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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:21:20 ; Search time 47.9168 Seconds
(without alignments)
2698.100 Million cell updates/sec

Title: US-09-303-232-6
Perfect score: 2640
Sequence: 1 MAPMLAALALLPVSQ.....LFTIATVALLSAPHIIVQ 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2640	100.0	501	Q9XZ14	Q9XZ14 heliothis v
2	2194	83.1	494	Q8T7S1	Q8T7S1 drosophila
3	2181	82.6	494	Q8T7S2	Q8T7S2 drosophila
4	2177	82.5	494	Q8T7S3	Q8T7S3 drosophila
5	2176.5	82.4	509	Q8T7S0	Q8T7S0 drosophila
6	2156.5	81.7	523	Q8T7R9	Q8T7R9 drosophila
7	1833	69.4	554	Q9VL79	Q9VL79 drosophila
8	1803.5	68.3	496	Q9XZ13	Q9XZ13 heliothis v
9	1800.5	68.2	807	Q8T7V5	Q8T7V5 drosophila
10	1786.5	67.7	545	Q9VW19	Q9VW19 drosophila
11	1705.5	64.6	525	Q81PE2	Q81PE2 drosophila
12	1258.5	47.7	502	Q9JHD6	Q9JHD6 mus musculus
13	1226.5	46.5	511	Q03481	Q03481 gallus gall
14	1145.5	43.4	480	Q81932	Q81932 caenorhabdi
15	1132	42.9	461	Q91197	Q91197 caenorhabdi
16	1124	42.6	273	Q9VJT9	Q9VJT9 drosophila

17	1085	41.1	554	5	062083	062083 caenorhabdi
18	1083.5	41.0	542	5	Q18556	Q18556 caenorhabdi
19	985	37.3	335	5	Q9NKD1	Q9NKD1 drosophila
20	982	37.2	537	5	Q8MUR0	Q8MUR0 apis mellif
21	978	37.0	515	5	Q46133	Q46133 locusta mig
22	973.5	36.9	537	5	Q9U941	Q9U941 myzus persi
23	970.5	36.8	499	11	Q8R4G9	Q8R4G9 mus musculu
24	970.5	36.8	504	11	Q8BV44	Q8BV44 mus musculu
25	966.5	36.6	499	11	Q8VHH6	Q8VHH6 mus musculu
26	964.5	36.5	567	5	Q9VC74	Q9VC74 drosophila
27	961	36.4	531	5	Q96632	Q96632 heliothis v
28	959.5	36.3	523	5	Q46128	Q46128 heliothis v
29	953.5	36.1	536	5	Q8T0Y9	Q8T0Y9 aplysia cal
30	951.5	36.0	552	5	Q91765	Q91765 myzus persi
31	951.5	36.0	568	5	Q9NFR5	Q9NFR5 drosophila
32	946.5	35.9	545	5	Q96631	Q96631 heliothis v
33	941	35.6	532	5	Q9U940	Q9U940 myzus persi
34	939.5	35.6	536	5	Q8T9S0	Q8T9S0 aplysia cal
35	939	35.6	533	5	Q8WRS1	Q8WRS1 chilo suppr
36	935	35.4	497	5	Q46135	Q46135 locusta mig
37	934	35.4	532	5	Q8MUB6	Q8MUB6 aphid gossy
38	932	35.3	494	11	Q8K0A7	Q8K0A7 mus musculu
39	930	35.2	595	5	P91764	P91764 myzus persi
40	926	35.1	494	11	Q9R0W9	Q9R0W9 mus musculu
41	920.5	34.9	496	6	Q8SPU6	Q8SPU6 bos taurus
42	920	34.8	517	5	Q96633	Q96633 heliothis v
43	918.5	34.8	512	11	Q91X60	Q91X60 mus musculu
44	917	34.7	452	13	Q918C7	Q918C7 gallus gall
45	916.5	34.7	495	11	Q8R493	Q8R493 mus musculu

ALIGNMENTS

RESULT 1

Q9XZ14	PRELIMINARY;	PRT;	501 AA.
ID	Q9XZ14;		
AC	Q9XZ14;		
DT	01-NOV-1999 (TREMBLrel. 12, Created)		
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	Putative nicotinic acetylcholine receptor alpha 7-2 subunit.		
OS	Heliothis virescens (Noctuid moth) (Owlet moth).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Lepidoptera; Glossata; Noctuoidea;		
OC	Noctuidae; Heliothinae; Heliothis.		
OX	NCBI_TaxID=7102;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Schulte T., Oellers N., Adamczewski M.;		
RT	"Putative alpha subunits of insect nicotinic acetylcholine receptors		
RT	more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than		
RT	to other insect nicotinic acetylcholine receptor alpha subunits.";		
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.		
CC	- - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).		
CC	- - SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.		
DR	EMBL; AF143847; AAD32698.1; -		
DR	InterPro: IPR006201; Neur_chan.		
DR	InterPro: IPR006202; Neur_chan_LBD.		
DR	InterPro: IPR006029; Neu_chan_memb.		
DR	Pfam; PF02931; Neur_chan_LBD; 1.		
DR	Pfam; PF02932; Neur_chan_memb; 1.		
DR	PRINTS; PR00252; NRIONCHANNEL.		
DR	TIGRFAMs; TIGR00860; LIC; 1.		
DR	PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.		
KW	Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;		
KW	transmembrane.		
SQ	SEQUENCE 501 AA; 56704 MW; 43CB0DC3960C78AB CRC64;		

Query Match 100.0%; Score 2640; DB 5; Length 501;
Best Local Similarity 100.0%; Pred. No. 5.1e-240; Indels 0; Gaps 0;
Matches 501; Conservative 0; Mismatches 0;

QY 1 MAPLAALALLALPVSEQGPHEKRLNALLANYNTLERPVANSEPLEVRFGLTQQOII 60
 DB 1 MAPLAALALLALPVSEQGPHEKRLNALLANYNTLERPVANSEPLEVRFGLTQQOII 60
 QY 61 DVDEKNOLLNTNLSLEWYNDYLNWDSYGGVKDLRTITPNKLRKPDVLMYNSADGGFD 120
 DB 61 DVDEKNOLLNTNLSLEWYNDYLNWDSYGGVKDLRTITPNKLRKPDVLMYNSADGGFD 120
 QY 121 GTYQTNVVRSGGSLVPPGIFKSTCKMDIAWFPDDQDCHDKMFKGWSWTYDGNQDLVLK 180
 DB 121 GTYQTNVVRSGGSLVPPGIFKSTCKMDIAWFPDDQDCHDKMFKGWSWTYDGNQDLVLK 180
 QY 181 DEAGDLSDFITNGEWYLGMPGKKNITTYACCPYVDVFTTMIIRRTLYYFFNLIVP 240
 DB 181 DEAGDLSDFITNGEWYLGMPGKKNITTYACCPYVDVFTTMIIRRTLYYFFNLIVP 240
 QY 241 CVLSSWALLGFTLPPDSGEKLTGVTLLSLTVFLNLVAETLPOVSDAIPPLGTYFNCI 300
 DB 241 CVLSSWALLGFTLPPDSGEKLTGVTLLSLTVFLNLVAETLPOVSDAIPPLGTYFNCI 300
 QY 301 MFVYASSVLTVVVLYNHHRTADITHMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMN 360
 DB 301 MFVYASSVLTVVVLYNHHRTADITHMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMN 360
 QY 361 TMRLELKERSSKSLANVLIDDDFRHGPPPPNSTASTGNLPGGCSIFRTDFRRSFVR 420
 DB 361 TMRLELKERSSKSLANVLIDDDFRHGPPPPNSTASTGNLPGGCSIFRTDFRRSFVR 420
 QY 421 PSTMEDVGGGSHHRELHLILRELOFTITARMKKADEAEELISDWKFAAMVVDRECLFVF 480
 DB 421 PSTMEDVGGGSHHRELHLILRELOFTITARMKKADEAEELISDWKFAAMVVDRECLFVF 480
 QY 481 TLFTIATVAVLLSAPHIIQV 501
 DB 481 TLFTIATVAVLLSAPHIIQV 501

RESULT 2

Q8T7S1 PRELIMINARY; PRT; 494 AA.
 AC Q8T7S1;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Nicotinic acetylcholine receptor Dalpha6 subunit variant type
 DE III.
 GN NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21969411; PubMed=11973307;
 RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
 RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
 RT Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
 RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
 RT Mediated A-to-I Pre-mRNA Editing.";
 RL Genetics 160:1519-1533(2002).
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC EMBL; AF321447; AAM13394.1;
 DR FlyBase; FBgn0032151; nACR-alpha-30D.
 DR InterPro; IPR006201; Neur_chan_memb.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR Pfam; PF02931; Neur_chan_LBD.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR TIGRfam; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;

KW Transmembrane.
 SQ SEQUENCE 494 AA; 56113 MW; 48327537229573FF CRC64;
 Query Match 83.1%; Score 2194; DB 5; Length 494;
 Best Local Similarity 82.6%; Pred. No. 5.7e-198;
 Matches 418; Conservative 31; Mismatches 37; Indels 20; Gaps 3;
 QY 2 APLAALAL-----LALLPVSEQGPHEKRLNALLANYNTLERPVANSEPLEVRFGLT 55
 DB 3 SPLASLSFLVLIIFLAIIKESCGPHEKRLNALLSTYNTLERPVANSEPLEVRFGLT 62
 QY 56 LQOIIDVDEKNOLLITNLSLEWYNDYLNWDSYGGVKDLRTITPNKLRKPDVLMYNSA 115
 DB 63 LQOIIDVDEKNOLLITNLSLEWYNDYLNWDSYGGVKDLRTITPNKLRKPDVLMYNSA 122
 QY 116 DEFGDTGYQTNVVRSGGSLVPPGIFKSTCKMDIAWFPDDQDCHDKMFKGWSWTYDGNQ 175
 DB 123 DEFGDTGYTNVVRSGGSLVPPGIFKSTCKMDITWFPDDQDCHDKMFKGWSWTYDGNQ 182
 QY 176 DLVLKDGAGDLSDFITNGEWYLGMPGKKNITTYACCPYVDVFTTMIIRRTLYYFF 235
 DB 183 DLVLNSDGDLSDFITNGEWYLLAMPKKNITTYACCPYVDITFIQIRRTLYYFF 242
 QY 236 NLIVPCVLISSMALLGFTLPPDSGEKLTGVTLLSLTVFLNLVAETLPOVSDAIPPLGT 295
 DB 243 NLIVPCVLISSMALLGFTLPPDSGEKLTGVTLLSLTVFLNLVAETLPOVSDAIPPLGT 302
 QY 296 YFCIMPMWASSVLTVVVLYNHHRTADITHMPQWIKSVFLQWLPWILRMSRPGKKITRK 355
 DB 303 YFCIMPMWASSVLTVVVLYNHHRTADITHMPQWIKSVFLQWLPWILRMSRPGKKITRK 362
 QY 356 TIMMNTMRLELKERSSKSLANVLIDDDFRHGPPPPNSTASTGNLPGGCSIFRTDFR 415
 DB 363 TILLSNRKLELKERSSKSLANVLIDDDFRH-----TISGSQTAIGSS----- 408
 QY 416 RSFVRPSTMEDVGGGSHHRELHLILRELOFTITARMKKADEAEELISDWKFAAMVVDRE 475
 DB 409 ASFGRPITVEHHTAICGNHKLHLILRELOFTITARMKKADEAEELISDWKFAAMVVDRE 468
 QY 476 CLFVFTLTITATVAVLLSAPHIIQV 501
 DB 469 CLIVFTLTITATVAVLLSAPHIIQV 494
 RESULT 3
 Q8T7S2 PRELIMINARY; PRT; 494 AA.
 AC Q8T7S2;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Nicotinic acetylcholine receptor Dalpha6 subunit variant type II.
 GN NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21969411; PubMed=11973307;
 RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
 RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
 RT Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
 RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
 RT Mediated A-to-I Pre-mRNA Editing.";
 RL Genetics 160:1519-1533(2002).
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC EMBL; AF321446; AAM13393.1;
 DR FlyBase; FBgn0032151; nACR-alpha-30D.
 DR InterPro; IPR006201; Neur_chan_memb; 1.
 DR InterPro; IPR006202; Neur_chan_LBD.

CC	-!	SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).	
CC	-!	SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.	
DR	EMBL:	AF321445; AAM13392.1;	
DR	FLYBase:	FBgn0032151; oACR-alpha-30D.	
DR	InterPro:	IPR006201; Neur_channel.	
DR	InterPro:	IPR006202; Neur_chan_LBD.	
DR	pfam:	PF02931; Neur_chan_LBD; 1.	
DR	pfam:	PF02932; Neur_chan_memb; 1.	
DR	TIGRFAMS:	TIGR00860; LIC; 1.	
DR	PROSITE:	PS00236; NEUROTR_ION_CHANNEL; 1.	
DR	Glycoprotein:	Ionic channel; Postsynaptic membrane; Receptor;	
KW	Transmembrane.		
SW	SEQUENCE	494 AA; 56095 MW; B46EBEDA63A92942 CRC64;	
Query Match			
Best Local Similarity 82.5%; Score 2177; DB 5; Length 494;			
Matches 414; Conservative 33; Mismatches 39; Indels 20; Gaps 3;			
QY	2	APMLAAL-----LALLPVSEQGPHEKRLNALLANYNTLPRPVANESEPLEVRFGLT	55
DB	3	SPLPASLSLEVLIIFLAIKESCGPHEKRLNLLSTYNTLPRPVANESEPLEVRFGLT	62
QY	56	LQIIDVDKQQLITNWLSEWYDYNLRWSEYGVGVDLRTITPNKWKPDVLYNSA	115
DB	63	LQIIDVDKQQLITNWLSEWYDYNLRWSEYGVGVDLRTITPNKWKPDVLYNSA	122
QY	116	DEGFDGTQTNVVRSGGSLYVPPGIFKSTCKMDIAWFPDQDCHDKMFGSWTYDGNOL	175
DB	123	DEGFDGTHNIVVYHGGSLYVPPGIFKSTCKMDITWFPDQDCHDKMFGSWTYDGNOL	182
QY	176	DLVLKDEAGDGLSDFITNGEWYLGMPGKKNITTYACCPPEYVDVTFITIRRTLYYFF	235
DB	183	DLVLNSEDGGLSDFITNGEWYLLAMPKKNITTYACCPPEYVDVTFITIRRTLYYFF	242
QY	236	NLIIVPCVLISMSALLGFTLPDPSGEKITLGVTILLSTVFLNLVAETLPQVSDAIPPLGT	295
DB	243	NLIIVPCVLISMSALLGFTLPDPSGEKITLGVTILLSTVFLNLVAETLPQVSDAIPPLGT	302
QY	296	YFNCIMFVASSVLTIVVVLNHYHRTADIHEMPQWIKSVFLQWLPWILMRSPGKKITRK	355
DB	303	YFNCIMFVASSVLTIVVVLNHYHRTADIHEMPQWIKSVFLQWLPWILMRSPGKKITRK	362
QY	356	TIMNTRMRELEKERSKSLANVLVDIDDDFRHGPPPNSTASTGNLPGCCSIFRTDFR	415
DB	363	TILLSNRKLEKERSKSLANVLVDIDDDFRH-----TISGQTAIGSS-----	408
QY	416	RSFVPSPTMEDVGGGLASHHRELHLILRELQFTIARMKKADEAEELISDKWFAAMVVDPR	475
DB	409	ASFGRPTTVEEHHTAIGCNHKDLHLILKELOFTIARMKKADEAEELISDKWFAAMVVDPR	468
QY	476	CLFVFTLTFTIATVALLSAPHIIQV 501	
DB	469	CLIVFTLTFTIATVLLSAPHIIQV 494	
RESULT 5			
Q8T7S0			
ID	Q8T7S0	PRELIMINARY; PRT: 509 AA.	
AC	Q8T7S0;		
DT	01-JUN-2002 (Tremblrel. 21, Created)		
DT	01-JUN-2002 (Tremblrel. 21, Last sequence update)		
DT	01-MAR-2003 (Tremblrel. 23, Last annotation update)		
DE	Nicotinic acetylcholine receptor Dalpha6 subunit variant type I.		
GN	NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephyrroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21969411; PubMed=11973307;		
RL	Genetics 160:1519-1533(2002).		

RT Mediated A-to-I Pre-mRNA Editing. *;
RL Genetics 160:1519-1533(2002).

DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DE 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 GN C4128 protein.
 OS NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
 GN Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang O., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadien E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleib J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Ananides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon K.Y., Beeson K.Y., Busan D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferrieria S., Frise E., Galie R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleib J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirkas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradscky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 RA

RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB003626; AAF52817.2;
 DR FlyBase; FBgn0032151; nacr-alpha-30D.
 DR InterPro; IPR006201; Neur_channel.
 DR InterPro; IPR006029; Neur_channel_memb.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 SQ SEQUENCE 554 AA; 63236 MW; D6C63EB7F5B32A35 CRC64;
 Query Match 69.4%; Score 1833; DB 5; Length 554;
 Best Local Similarity 65.0%; Pred. No. 7.4e-164;
 Matches 370; Conservative 36; Mismatches 67; Indels 96; Gaps 8;
 RA 4 MLCALALLALPVSQGPHEKRLNALLANYTLRPNVANESEPLEVREGLTQQIIDVD 63
 DB 11 LFLVLLFLAIIRKESQGPHEKRLNALLSTYTLRPNVANESEPLEVREGLTQQIIDVD 70
 QY 64 EKNQLITNWLSEWMDYNLRWNDSEYGVGKDLRITPNKLPDVLNYSNADGFDGTY 123
 DB 71 EKNQLITNWLSEWMDYNLRWNETEYGVGKDLRITPNKLPDVLNYSNADGFDGTY 130
 QY 124 QTNVVRSGGCLYPPGIFKSTCKMDIAWFFDOHCDMKFGSTWYDGNLDVLKDBA 183
 DB 131 FHNIVVKNHSGCLYPPGIFKSTCKIDITWFFDQHCMEKFGSTWYDGNLDVLNSED 190
 QY 184 GGLSDFTINGEWYLGIM-PGKNTITYACCP-----EPYVDVFTTMIIRR 229
 DB 191 GGLSDFTINGEWYLLGYHAGKEEDSLRLDPTTCRHYLYTNSPYI----- 239
 QY 230 TLYYFNLIIVPCVLSMALL-----GFTLPDPSGEKLT----- 263
 DB 240 ILFFQFCAMCANLIDGPTGLHIAAGFGRETDAGRNYTTIINSISKPCRRVHADNVGCCS 299
 QY 264 -----IG-----VTLLSLTVFLNLVAETLPQVSDAIP 292
 DB 300 SYRYTHITLKRYSLKYGPIGRTHYQCRARVITLLSLTVFLNLVAETLPQVSDAIP 359
 QY 293 LGTYFNCIMFVASSVLTVVVLYNHHRTADITHMPWIKSVFLOLWPLWRMRPGKKI 352
 DB 360 LGTYFNCIMFVASSVLTVVVLYNHHRTADITHMPWIKSVFLOLWPLWRMRPGKKI 419
 QY 353 TRKTTMTNRMRELKERSKSLANVLIDDDDFRHGPPPPNASTGNLPGGCSIFRT 412
 DB 420 TRKTTLLSNRMKELEKERSKSLANVLIDDDDFRH-----TISGQTAIGSS---- 468
 QY 413 DFRSRFVRPSTMEDVGGGLSGHRLHLRLILRELQITARMKKADEAEELISDWKFAAMV 472
 DB 469 ---ASFGRPPTVEEHHTATGCKNHLHLILKELQITARMKKADDEAEELISDWKFAAMV 525
 QY 473 DRECLFVETFTTIATVAVLLSAPHIIQ 501
 DB 526 DRECLIVFTFTTIATVAVLLSAPHIIQ 554
 RESULT 8
 Q9XZ13 PRELIMINARY; PRT: 496 AA.
 ID Q9XZ13
 AC Q9XZ13;

Qy	456	DEEAELISDWKFAAMVVDRLCFVFTLFTTIATVAVLLSAPHIIV	500
		: : : : :	
Db	762	DECNDIANDWKFAAMVVDRLCIIFTMFAILATIIVLLSAPHIIV	806

RESULT 10

Q9WV19 PRELIMINARY; PRT: 545 AA.

AC Q9WV19; 13, Created)

AD 01-MAY-2000 (TREMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE CG32538 protein.

DE NACR-ALPHA-18C OR CG8082 OR CG8109 OR CG32538.

GN Drosophila melanogaster (Fruit fly).

OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

ON NCBI_TaxID=7227;

OX [1]

RY SEQUENCE FROM N.A.

RP STRAIN=Berkeley;

RC MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Duhan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nuskens D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveril J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.;

RL Science 287:2185-2195(2000).

RL [2]

RY SEQUENCE FROM N.A.

RP Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,

RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nuncio J.,

RA

QY 467 FAAMVVDRCFLVFTFTTATVAVLLSAPHIIV 500
 ID. QBIPE2 PRELIMINARY; PRT; 525 AA.
 DB 507 FAAMVVDRLCLITFTTATVAVLLSAPHIIV 540

RESULT 11

QBIPE2
 AC QBIPE2;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE C04128-PC.
 GN NACRALPHA-30D.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Balow R.M., Basu A., Bayevdale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Hostin N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jallal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong E., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celnik S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Anantides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Dou L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferrier S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jallal M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochman S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Carlson J.W., Celnik S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003626; AAN10709.1;
 SQ SEQUENCE 525 AA; 60135 MW; CF95283C56EA90A9 CRC64;
 Query Match 64.6%; Score 1705.5; DB 5; Length 525;
 Best Local Similarity 63.2%; Pred. No. 7.3e-152;
 Matches 347; Conservative 43; Mismatches 84; Indels 75; Gaps 9;
 QY 2 APLAALAL-----LALLPVSEGGHEKRLNALLNANYNTLPRPVANSEPLEVRGLT 55
 DB 3 SPPLASUSLEVLILFLAIKESCGGHEKRLNALLNANYNTLPRPVANSEPLEVRGLT 62
 QY 56 LQIIDIYDEKNQLLITNWLSEWNYLWNSDSEYGVKDLRITPNKLRKPDVLMYNSA 115
 DB 63 LQIIDIYDEKNQLLITNWLSEWNYLWNSDSEYGVKDLRITPNKLRKPDVLMYNSA 122
 QY 116 DEFGDTYQTNVVRSGGCLYVPPGIFKSTCKMDIANFFDDOCHDKMGSTYDGNOL 175
 DB 123 DEFGDTGTHYTNVVRSGGCLYVPPGIFKSTCKMDIANFFDDOCHDKMGSTYDGNOL 182
 QY 176 DLVLKDGAGDLSDFITNGEWYLGIM-PGKNITITYACCP-----EPYVDVT 221
 DB 183 DLVLNSEDGGLSDFITNGEWYLLGYHAGKEEDSLRLPTICRYHLYTNSPYI--- 239
 QY 222 FTIMIRRTLYYFNLIVPCVLSSMALL-----GFTLPDPSGEKLTGV----- 266
 DB 240 -----ILFFQFNCAACANLIDGPTGLHIAAGFGRETDAGRNYTTIINSIKPCRVRH 291
 QY 267 -----TILLSLTVELNLVAETLPQVSDAIPLLGTYFNCIMFMAVSSVLTV 312
 DB 292 ADVGCCSSVRYTHITLKRYSKYGPIGRTIDHYQC-RAESTYFNCIMFMAVSSVLTV 350
 QY 313 VLVNHYHRTADIHEMPQWIKSVFLQWLPWILRMRSPGKKITRKTIMNTRMRELEKERS 372
 DB 351 VLVNHYHRTADIHEMPQWIKSVFLQWLPWILRMRSPGKKITRKTILLSNRKLEKERS 410
 QY 373 SKSLANVLDDIDDFRHGPPPPPNSTAGNLPGCCSIFRTDFRSFVRPSTMEDVGGGLG 432
 DB 411 SKSLANVLDDIDDFRH-----TISGSAITAGSS-----ASFGRPTTVEHHTAIG 456
 QY 433 SHHRELHLILRELOFITARMKKADEAEELISDNKFAAMVVDRCFLVFTTATVAVL 492
 DB 457 CNHKDLHLILKELOFITARMKKADEAEELIGDNKFAAMVVDRCFLVFTTATVAVL 516
 QY 493 LSAPHIIVQ 501
 DB 517 LSAPHIIVQ 525
 RESULT 12
 Q9JHD6


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Db 313 GLSVVTVLVQHHHDPOQAGKPRVWVRYLLNWCAMFLRMKKPGENI-----K 361
QY 365 EELK-----ERSSKLLANVLIDDDFRHGPPPNSTAGNL-----GPGCSIF 410
Db 362 PLCKSYKPHHSLKNTENVL-----FCHQPSNGNMYSYTHMPNCC--- 406
QY 411 RTDFRFRVSPSTMEDVGGGLG-----SHRELHL-----ILRELQFITAR 451
Db 407 -----PON-NDLGSKSGKITCPLSDNEHVKKALMDTIPVIVKILEEVQFIAMR 455
QY 452 MKKADAEALISDWKFAAMVVDRCLEVFILFIATVAVLLSAPHII 499
Db 456 FRKQDEGEICSEWKFAAAVIDRLCLVAFTLFAICTFTILMSAPNEI 503

RESULT 14
Q81932 PRELIMINARY; PRT; 480 AA.
AC Q81932;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Acetylcholine receptor protein 16, isoform b.
GN ACR-16.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Nelson J., Wohlmann P.;
RT "The sequence of C. elegans cosmid F25G6.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF022973; AAN84815.1;
KW Receptor.
SQ SEQUENCE 480 AA; 55274 MW; B5D6B707E50228A3 CRC64;

Query Match 43.4%; Score 1145.5; DB 5; Length 480;
Best Local Similarity 47.3%; Pred. No. 4.1e-99;
Matches 231; Conservative 71; Mismatches 135; Indels 51; Gaps 9;

QY 2 APLAALALLALLPVSGQGPHEKRLNALLANYNTLPRVANSEPLEVRFGLTLOQIID 61
Db 15 APTLGLS-----QERLYEDLMRNYNLERPVANHSEPVTVHLKVALQIID 61
QY 62 VDEKNQLITNWLSEWNDYNLWNSDEYGGVYKDLRITNKLWKPDPVLYMNSADEGFDG 121
Db 62 VDEKNQVYVYNAWLDTYNDNINLVMDKAEYGNITDVRFPAGKWKPDVLYNSYDTNFD 121
QY 122 TYQTNVVRGGSLYVPPGIFKSTCKMDIAWFPDQHDKMGFTWYDGNOLDLVLKD 181
Db 122 TYQTNMIVYTGVLVHWVPPGIFKSKICKIDIQWFPDQKCFKFGSWTYDGYKLD--LQP 179
QY 182 EAGG-DLSDFITNGEWGLHMPGKNTITYACCPYVDVFTIMIRRRRLTYFFNLIVP 240
Db 180 ATGFGDISVINGENALPLTTVERNEKFDCCPEPYDPVHFVLMRRRLTYGFLNIMP 239
QY 241 CVLISSMALGFTLPPDSGKELTGLVTILLSLVFLNLVAETLPQVSDAIPILGTYPNCI 300

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Db 240 CILTTMTLTGFTLPPDAGEKITLQITVLLSICFFLSIVSEMSPPTSEAVPLIGFTCC 299
QY 301 MFVASSVTVLVVLANVHRTADIHENPOWIKSVFLQWLFWILMRSPGKKITRKT--M 358
Db 300 MIVVTASTVFTVTVLNLHRTPTETHDGMPTNRLLLYWIPWILMRKRPGHNLTYASLPSL 359
QY 359 MNTRMRELELKERSSKSLLANVLIDDDFRHGPPPNSTASTGNLGPCCS 408
Db 360 FSTK-----PNRHSSELRINKNEHSLSRANSFADACRLNQYIMTQSVSNGLTSLG-S 412
QY 409 IFTDFRFRFVRSTMEDVGGGLGSHRE-----LHLILRELOFITARMKKADEEALIS 463
Db 413 I-----ESTMISSNGTTTDSVQQATLLILHLRIYHELKIVTKRMIEGDKREQACN 461
QY 464 DKWFAAMV 471
Db 462 NWKFAAMV 469

RESULT 15
P91197 PRELIMINARY; PRT; 461 AA.
AC P91197;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical 52.7 kDa protein.
GN D2092.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Gattung S., Maggi L.;
RT "The sequence of C. elegans cosmid D2092.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; U88167; AAB42223.1;
DR WormPep; D2092.3; CE09102.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_chan_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Hypothetical protein; Glycoprotein; Ionic channel;
KW Postsynaptic membrane; Transmembrane.
SQ SEQUENCE 461 AA; 52718 MW; 6182A7F827357B92 CRC64;

Query Match 42.9%; Score 1132; DB 5; Length 461;
Best Local Similarity 44.7%; Pred. No. 7.2e-98;
Matches 216; Conservative 86; Mismatches 127; Indels 54; Gaps 6;

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QY. 23 EKRLNALLANVTNLERPVANESSEPLEVRFGTLQOIIDVDEKNQLLITNIMLSLEWNDY 82
Db 26 ETKLFTDLLKGYNPLERPQVQSSQPLEVKIKFLQOILDVDEKNQIVSVNAWLSYTFD 85
QY 83 NLRWNDEYGGVKDLAI--TPNKLWKPDLVLMYNSADEGFGTYQTNTVVRSGSCLYVPP 140
Db 86 KIQWEPKYGIGQIDIRPGSSDHIWKPDVLLYNSAAEDFDSTKSNLLTYHTGTVVWIPP 145
QY 141 GIFKSTCKMDIAWFPDDQRCMDKFGSWYDGNQLDLVLKDEAGG----DLSDFITNGEW 196
Db 146 GVLKEVCQLDVTWFPDDQVCEMKFGSWFHGVAIDLQIDDDFTNGTQSMDLSTYLVNGEW 205
QY 197 YLIGMCKKNTITYACCPYVDVTFIMIRRTLYFFENLIVPCVLISSMALLGFTLPP 256
Db 206 QVISTNAKRVSYKCCPEPYTVNYLHIRRTLYGFNLITPSLLISMAILGFMFPP 265
QY 257 DSGEKLTLGVTILLSETVFLNLVAETLPOVSDAIPLLGTYENCIMFMVASSVVLTVVVLN 316
Db 266 DAGEKITLEVITLLAIVFLSMVSEWTPPTSEAVPLIGVFFSCCMLVVSASVVTIVVLN 325
QY 317 YHRTADIHEMPQWIKSVFLOLWPILRMSRPGKKITRKTIMNTRMRELELKERSSKSL 376
Db 326 LHFRSADSHENPLVRRVLEFLPWLLFMSRPGYKFKV-----PSN-----HAGYEAQIL 397
QY 377 LANVLDDDDFRHGPPPNSTASTGNLPGCCSIFRTDFRRSFVRPSTMEDVGGGLGSHHR 436
Db 364 -ANVIDSTDKMPKKPNPLD-----CNL-----PSN-----HAGYEAQIL 397
QY 437 ELHLILRELQFITARKKKADEAEELISDKFAAMVVDRECLFVFTLTITATVAVLLSAP 496
Db 398 LHSVTELRVVAVFYNKKEHDERIOTDRFAAMVVDRACLLLFTVIVISILAINMSAP 457
QY 497 HII 499
Db 458 HII 460
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Search completed: August 13, 2003, 15:29:11
Job time : 49.9168 secs

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50-105

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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:14:55 ; Search time 10.4907 Seconds
(without alignments)
2245.843 Million cell updates/sec

Title: US-09-303-232-6
Perfect score: 2640
Sequence: 1 MAPMLAALALLPVSQ.....LFTIATVALLSAPHIIVO 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1258.5	47.7	502	1	ACH7_HUMAN
2	1255.5	47.6	502	1	ACH7_MOUSE
3	1253	47.5	502	1	ACH7_CHICK
4	1246.5	47.2	502	1	ACH7_RAT
5	1240.5	47.0	499	1	ACH7_BOVIN
6	1237.5	46.9	498	1	ACH1_CAEEL
7	989.5	37.5	503	1	ACH3_HUMAN
8	977.5	37.0	499	1	ACH3_RAT
9	970.5	36.8	495	1	ACH3_BOVIN
10	964.5	36.5	567	1	ACH1_DROME
11	948.5	35.9	496	1	ACH3_CHICK
12	946.5	35.9	516	1	ACH1_MANSE
13	944	35.8	557	1	ACH1_SCHGR
14	943	35.7	576	1	ACH2_DROME
15	933	35.3	494	1	ACH6_HUMAN
16	924.5	35.0	528	1	ACH2_CHICK
17	922.5	34.9	529	1	ACH2_HUMAN
18	919.5	34.8	512	1	ACH3_CARAU
19	917	34.7	511	1	ACH2_RAT
20	915.5	34.7	494	1	ACH6_CHICK
21	914.5	34.6	493	1	ACH6_RAT
22	910.5	34.5	495	1	ACHP_RAT
23	908.5	34.4	519	1	ACH4_DROME
24	906	34.3	457	1	ACHA_BOVIN
25	900	34.1	521	1	ACH3_DROME
26	899.5	34.1	500	1	ACHN_RAT
27	897.5	34.0	627	1	ACH4_HUMAN
28	896	33.9	456	1	ACHA_CHICK
29	895	33.9	502	1	ACHN_HUMAN
30	891	33.8	622	1	ACH4_CHICK
31	890	33.7	457	1	ACHA_RAT
32	889	33.7	470	1	ACHP_CHICK
33	887	33.6	498	1	ACHP_HUMAN

34	886	33.6	457	1	ACHA_MOUSE
35	885.5	33.5	459	1	ACHN_CARAU
36	882.5	33.4	482	1	ACHA_HUMAN
37	881.5	33.4	461	1	ACHA_TORMA
38	881.5	33.4	630	1	ACH4_RAT
39	881	33.4	491	1	ACHN_CHICK
40	876.5	33.2	461	1	ACHA_TORCA
41	875.5	33.2	457	1	ACH2_XENLA
42	869.5	32.9	457	1	ACH1_XENLA
43	869	32.9	538	1	ACH8_CAEEL
44	863.5	32.7	456	1	ACHA_BRARE
45	858.5	32.5	466	1	ACHP_CARAU

ALIGNMENTS

RESULT 1
ACH7_HUMAN STANDARD; PRT; 502 AA.
ID ACH7_HUMAN Q15826; Q96RH2; Q99555; Q9BXH0;
AC P36544; Q15826; Q96RH2; Q99555; Q9BXH0;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
GN CHRNA7 OR NACHRA7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94195283; PubMed=8145738;
RA Peng X., Katz M., Gerzanich V., Anand R., Lindstrom J.;
RT "human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit
from the SH-SY5Y cell line and determination of pharmacological
properties of native receptors and functional alpha 7 homomers
expressed in Xenopus oocytes.";
RL Mol. Pharmacol. 45:546-554(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RA Logel J., Drebing C., Barnhart M., Antle C., Leonard S.;
RT Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97062879; PubMed=8906617;
RA Elliott K.J., Ellis S.B., Berckman K.J., Urrutia A.,
Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
2-beta 4 nicotinic acetylcholine receptor subunits and functional
expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
beta 4 subunits.";
RL J. Mol. Neurosci. 7:217-228(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97162233; PubMed=9009220;
RA Groot Kormelink P.J., Luyten W.H.M.L.;
RT "Cloning and sequence of full-length cDNAs encoding the human neuronal
nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and
expression of seven nAChR subunits in the human neuroblastoma cell
line SH-SY5Y and/or IMR-32.";
RL FEBS Lett. 400:309-314(1997).
RN [5]
RP REVISIONS.
RA Groot Kormelink P.J., Luyten W.H.M.L.;
RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Epidermal keratinocytes;
RA Arredondo J., Grando S.A.;
RT "Cloning cholinergic receptors in human keratinocytes.";

Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 [7]
 RN SEQUENCE OF 17-502 FROM N.A.
 RP TISSUE=Brain;
 RC Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M.T.,
 RA Lee J., Tian J., Giordano T.;
 RT "Cloning and sequence of the human $\alpha 7$ nicotinic acetylcholine
 receptor.";
 RL Drug Dev. Res. 30:252-256(1993).
 RN [8]
 RP SEQUENCE OF 24-502 FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=94245214; PubMed=818270;
 RA Chini B., Raimondi E., Elgoyhen A.B., Moralli D., Balzaretta M.,
 RA Heinemann S.F.;
 RT "Molecular cloning and chromosomal localization of the human $\alpha 7$ -
 nicotinic receptor subunit gene (CHRNA7).";
 RL Genomics 19:379-381(1994).
 RN [9]
 RP SEQUENCE OF 118-129 FROM N.A.
 RX MEDLINE=21818878; PubMed=11829490;
 RA Riley B., Williamson M., Collier D., Wilkie H., Makoff A.;
 RT "A 3-Mb map of a large segmental duplication overlapping the $\alpha 7$ -
 nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14.";
 RL Genomics 79:197-209(2002).
 RN [10]
 RP MASS SPECTROMETRY.
 RC TISSUE=Breast cancer;
 RX MEDLINE=21829512; PubMed=11840567;
 RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
 RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
 RA Zvelebil M.J.;
 RT "Cluster analysis of an extensive human breast cancer cell line
 protein expression map database.";
 RL Proteomics 2:212-223(2002).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
 CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
 CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- MASS SPECTROMETRY: MW=54157.68; METHOD=WALDI.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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 CC -----
 DR EMBL; X70297; CAA49778.1; -
 DR EMBL; U40583; AAA83561.1; -
 DR EMBL; U62436; AAB40114.1; -
 DR EMBL; Y08420; CAA69697.1; -
 DR EMBL; AF385585; AAK68111.1; -
 DR EMBL; L25827; -; NOT ANNOTATED_CDS.
 DR EMBL; Z23141; CAA80672.1; -
 DR EMBL; AF332758; AAK19515.1; -
 DR PIR; G02259; G02259.
 DR PIR; I37185; ACHUA7.
 DR Genew; HGNC:1960; CHRNA7.
 DR MIM; 118511; -
 DR GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. .; TAS.
 DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. .; TAS.
 DR GO; GO:0000187; P:activation of NMPK; TAS.
 DR GO; GO:0006832; P:small molecule transport; TAS.
 DR InterPro; IPR006029; Neur_chan_memb.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR InterPro; IPR006201; Neur_channel.

DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR PRINTS; PR0232; Neur_chan_memb; 1.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 22 BY SIMILARITY.
 FT CHAIN 23 502 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-7 CHAIN.
 FT DOMAIN 23 230 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 231 255 POTENTIAL.
 FT TRANSMEM 262 280 POTENTIAL.
 FT TRANSMEM 296 317 POTENTIAL.
 FT DOMAIN 318 469 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 470 490 POTENTIAL.
 FT DISULFID 150 164 BY SIMILARITY.
 FT DISULFID 212 213 ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 11 11 A -> G (IN REF. 1 AND 7).
 FT CONFLICT 58 58 S -> N (IN REF. 2 AND 6).
 FT CONFLICT 134 134 S -> P (IN REF. 2 AND 6).
 FT CONFLICT 364 364 C -> S (IN REF. 8).
 FT CONFLICT 375 375 A -> G (IN REF. 1).
 FT CONFLICT 409 413 RMACS -> AWPAP (IN REF. 8).
 SQ SEQUENCE 502 AA; 56449 MW; D94B3A482EAA0E42 CRC64;
 Query Match 47.7%; Score 1258.5; DB 1; Length 502;
 Best Local Similarity 48.68; Pred No. 1.4e-103;
 Matches 250; Conservative 75; Mismatches 138; Indels 51; Gaps 7;
 QY 8 LALLA-LLPVSEQGPHEKRLNALLNLYLERPVANSEPLEVRFGLTIQQIIDVDEN 66
 DB 10 LALAASLLHVSLOGEFQKLYKLVKNYPLERPVANDSQPLTVYFSLSLQIMDVDEKN 69
 QY 67 QLLITNWLSELDNLYNRNDSEYGGVKDLRTPNKWKPDVLYMNSADEGDTGTQTN 126
 DB 70 QVLTNTNWLQMSWTNHYLQNVSEYPGKTVRFPDGOIKWPKDILLYNSADERDATPHN 129
 QY 127 VVVRSGGCLYVPPGIFKSKMDIAWFPDDQHCMDKFGSWITVDGNQLDLVLKDEAGD 186
 DB 130 VLVNSSHCQYLPFGIFKSSCYIDVRWFPDVQHCCLKFGWSYGGWSLDLQGE---AD 186
 QY 187 LSDFITNGEYLIGMPGKNTITYACCPYVDVFTTMRRTLYFFNLIYVPCVLIS 246
 DB 187 ISGVIPNGEWDLVGIPGKRSERFYECKPEYVDVFTTMRRTLYYGLNLLIPCVLISA 246
 QY 247 MALLGFTLPDPSGEKLTGLVTILLSTVFLNVAETLPOVSDAIPLLGTYFNCIMFVAS 306
 DB 247 LALLVFLPADSGEKISLGITVLLSLTFVLLVAEIMPATSDSVPLIAQFASTMIIYGL 306
 QY 307 SVVTVVVLNTHHRTADIHEMPOWIKSVFLQWLFPWILMRSPRKKITRKTMMTRREL 366
 DB 307 SVVTVVIVLYHHDDPGGKMKPWTRVILLNWCANFLRMKRPGEKVPACQHKQRCSL 366
 QY 367 ELKERSKSLANVLDIDDDFRHGPPPNSTASTGNL-----GPGC 407
 DB 367 ASVEMSAVA-----PPP---ASGNLLYICFRGLDGVHCVPPTPDGSGVVC 407
 QY 408 SIFRTDFRSFVRPSTMEDV---GGGLSHHRLHLILRELQFITARKMKADEAEELSDW 465
 DB 408 G-----RMACSPTHDEHLHGQPGGPDPLAKILEEVRYIANRFRQCQSEAVCSEW 460
 QY 466 KFAAMVDRFCLFVFTLTFTTIATVAVLSAPHII 499
 DB 461 KFAACVVDRLCLMAFSVFTICTIGILMSAPNFV 494
 RESULT 2
 ACH7_MOUSE

10	LALAAALLHVSLOGEFORRLYKELVKNYNPLERPVANDSQPLTVYVFSLSLIQIMDVDEKN	69
67	QLLITNTIWSLEWNDYLRNWDSEYGGVKOLRITPNKLWKPDVLMYNSADEGFGCTGYQTN	126
70	QVLTTNIWLQMSWTDHYLQNMSEYPGVKVNFDPDQIWKPDILLYNSADERDATEFTN	129
127	VVVRSGGSLYVPPGIFKSKCKMDIAWFPDDQHCMDKFGSWTYDGNQLDLVLKDEAGD	186
130	VLVNASHCQYLPPIEFKSCYIDVRWFPDVOQCKLKFSGWSYGGWSLDLQMQE---	186
187	LSDFITNGEYWLIGMPCKKNTITVACCPYVVDVTFITIMIRRTLYYFENLIVPCVLIS	246
187	ISSYITNGEYWLIGMPCKKNTITVACCPYVVDVTFITIMIRRTLYYFENLIVPCVLIS	246
247	MALIGFLTPDPSGKGLTGVITLLSLVFLMLVAETLPQVSDAIPLLGTYFNCIMFVMS	306
247	LALLVFLPADSGEKISLIGITVLLSLVFLMLVAEIMPATSDSVPLIAQYFASFTMIIVGL	306
307	SVVLTVVVLVNYHRTADIHMPQWIKSVFLOMLPWILRMSRPGKKITRKTIMMNTMRRL	366
307	SVVTVTVLRYHHDPDGGKMPKTRITLLNWCAMFLRMKRPGEKVRPACQHKPRCSL	366
367	ELKERSS----KSLIANVLIDDDFR-----HGPPPNSTASTGNLPGCCSIFRTDFRRS	417
367	ASVELSAGAGPPTSGNGLLYI--GFRLEGMHCAPTDPSGVVVCGR--ACSPTHDEHLMH	422
418	FVRPSTMEDVGGGLGSHHRELHLTLRELQFTARMKKADEAEALISDMKFAAMVYDRFCL	477
423	GTHPSDGP-----DLAKILEEVRYTANFRCODESEVICSEWKFAACVYDRCL	472
478	FVFTLFTTIATVAVLLSAPHII 499	
473	MAFSVFTIICTIGILMSAPNEV 494	

RESULT 3

ACH7_CHICK

ID	ACH7_CHICK	STANDARD	PRT	502 AA.
AC	P22770;			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Neuronal acetylcholine receptor protein, alpha-7 chain precursor.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
ON	NCBI_TaxID=9031;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RC	MEDLINE=91097796; PubMed=1702646;			
RA	Couturier S., Bertrand D., Matter J.M., Hernandez M.C., Bertrand S.,			
RA	Miller N., Valera S., Barkas T., Ballivet M.;			
RT	"A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is			
RT	developmentally regulated and forms a homo-oligomeric channel blocked			
RT	by alpha-BTX.";			
RL	Neuron 5:847-856(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RC	MEDLINE=90315158; PubMed=2369519;			
RA	Schoeffer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.;			
RT	"Brain alpha-bungarotoxin binding protein cDNAs and mAbs reveal			
RT	subtypes of this branch of the ligand-gated ion channel gene			
RT	superfamily.";			
RL	Neuron 5:35-48(1990).			
RN	[3]			
RP	SEQUENCE OF 1-18 FROM N.A.			
RC	STRAIN=White leghorn; TISSUE=Erythrocyte;			
RC	MEDLINE=93049204; PubMed=1425587;			
RA	Matter-Sadzinski L., Hernandez M.C., Roztocil T., Ballivet M.,			
RA	Matter J.M.;			

RT "Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor.
 RT promoter develops during morphogenesis of the central nervous
 RT system.";
 RL EMBO J. 11:4529-4538(1992).
 RN [4]
 RP SEQUENCE OF 24-47.
 RC TISSUE=Brain;
 RX MEDLINE=85270494; PubMed=3860855;
 RA Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lal F.A.,
 RA Ray N., Raftery M.A.;
 RT "Brain and muscle nicotinic acetylcholine receptors are different but
 RT homologous proteins.";
 RT Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
 RL [5]
 RN MUTAGENESIS OF LEU-270.
 RP MUTAGENESIS OF LEU-270.
 RX MEDLINE=92049732; PubMed=1719423;
 RA Recah F., Bertrand D., Galzi J.-L., Devillers-Thierry A., Mulle C.,
 RA Hussy N., Bertrand S., Ballivet M., Changeux J.-P.;
 RT "Mutations in the channel domain alter desensitization of a neuronal
 RT nicotinic receptor.";
 RL Nature 353:846-849(1991).
 RN [6]
 RP MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC.
 RX MEDLINE=93024917; PubMed=1383829;
 RA Galzi J.-L., Devillers-Thierry A., Hussy N., Bertrand S.,
 RA Changeux J.-P., Bertrand D.;
 RT "Mutations in the channel domain of a neuronal nicotinic receptor
 RT convert ion selectivity from cationic to anionic.";
 RL Nature 359:500-505(1992).
 RN [7]
 RP FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -1- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
 CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DEVELOPMENTAL STAGE: ALPHA-7 TRANSCRIPTS TRANSIENTLY ACCUMULATE
 CC IN THE DEVELOPING OPTIC TECTUM BETWEEN E5 AND E16.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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DR EMBL; X52295; CAA36543.1; -;
 DR EMBL; X68246; CAA48317.1; -;
 DR EMBL; X68586; CAA48576.1; -;
 DR PIR; JN0113; JN0113.
 DR PDB; 1KC4; 17-APR-02.
 DR PDB; 1KL8; 17-APR-02.
 DR InterPro; IPR006029; Neu_channel_memb.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR InterPro; IPR006201; Neur_channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRfams; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 DR Posttranslational modification; Ionic channel; Signal;
 KW Transmembrane; Multigene family; 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 502 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-7 CHAIN.
 FT DOMAIN 24 230
 FT TRANSMEM 231 255
 FT TRANSMEM 262 280
 FT TRANSMEM 296 317
 FT DOMAIN 318 469 CYTOPLASMIC.

FT TRANSMEM 470 490
 FT DISULFID 150 164
 FT DISULFID 212 213
 FT
 FT CARBOHYD 46 46
 FT CARBOHYD 90 90
 FT CARBOHYD 133 133
 FT MUTAGEN 270 270
 FT
 FT CONFLICT 26 27
 FT SEQUENCE 502 AA; 56946 MW; 57325D4309AD2FD CRC64;
 SQ
 Query Match 47.5%; Score 1253; DB 1; Length 502;
 Best Local Similarity 48.8%; Pred. No. 4.2e-103;
 Matches 250; Conservative 81; Mismatches 145; Indels 36; Gaps. 8;
 QY 2 APLAALALLALLPVSEOGPEKRLNALLANTYNTLPRVANESEPLEVFLGLTLOQIID 61
 DB 5 ALMLWLLAAGLVRESLOGEFQRKLYKELLKNPLRPVANDSQPLTVYFTLSLQIMD 64
 QY 62 VDEKNQLLTITNWLSEWNDYLNLRWDSYGVKVDLRITPNKLMKPDVLMYNSADEGFDG 121
 DB 65 VDEKNQVLTITNWLQMYTQDHYLQWNVSEYGVKNVRFDPGLIWKPDILLYNSADERFA 124
 QY 122 TYOTNVVVRSGGSLYVPGIFKSTCKMDTAWFPDQHCMDKFGSWTYDGNQLDLVKD 181
 DB 125 TFEHTNVLNSSGHCOYLPFGIFKSSCYIDVRWFFDQKCNLKFSGSWTYGWSLDQMOE 184
 QY 182 EAGDGLSDFITNGEWYLGMPGKNTITYACCPPEYVDVFTIMIRRTLYFFENLVPC 241
 DB 185 ---ADISGYISNGEWDLVGIPGRATESFYECCKEYPDIITFTVMTTRRTLYYGLNLLIPC 241
 QY 242 VLISSMALLGFTLPPDSSGKLTGLVTILLSLTVFLNLVAETLPQVSDAIPLLGLTYFNCIM 301
 DB 242 VLISALALLVLLPADSGEKISLITVLLSILTVFLLVAEIMPATSDSVPLIAQYFASMT 301
 QY 302 FMYASSVVLTVVNLNHHRTADITHMPQWIKSVFLQWLPWLILMSRSGKKITKRTIMNT 361
 DB 302 IIVGLSVVTVIVLYVHHDPDGGKMPKWTIRILLNCWAFELRMKRPEDKVRPACQHKQ 361
 QY 362 RMRELEKERSKS---LLANVLIDIDDDFR---HGPPPNSTASTGNGLPGCSIFRT 412
 DB 362 RRCSSLSMEMNTVSGQCSNGNMLYI---GFGLDGVHCTPTDTSGVICGRM--TCS---- 413
 QY 413 DFRSRFVRPSTMEDVGGGLSGSH---RELHLILRELQITARKMKADEAEILISDKWF 467
 DB 414 -----PTEENL---LHSGHPSEGDPLAKILEEVRYIANFRDQDEEAICNWKF 462
 QY 468 AAMVVDRECLFVFTLETTIATVALLSAPHII 499
 DB 463 AASVVDRLCLMAFSVFTIICTIGILMSAPNFV 494

RESULT 4

ACH7_RAT
 ID ACH7_RAT STANDARD; PRT; 502 AA.
 AC Q05941;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
 GN CHRNA7 OR ACRN7.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93147931; PubMed=7678857;
 RA Sequela P., Wadiche J., Dineley-Miller K., Dani J.A., Patrick J.W.;
 RT "Molecular cloning, functional properties, and distribution of rat
 RT brain alpha 7: a nicotinic cation channel highly permeable to

[illegible]

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 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL: X93604; CAA63802.1; -
 DR InterPro: IPR006029; Neu_chan_memb.
 DR InterPro: IPR006202; Neur_chan_LBD.
 DR InterPro: IPR006201; Neur_chan.
 DR Pfam: PF02931; Neur_chan_LBD; 1.
 DR Pfam: PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 DR Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family; Alternativity; Splicing.
 FT SIGNAL 1 19
 FT CHAIN 20 499
 FT
 FT DOMAIN 20 227
 FT TRANSMEM 228 252
 FT TRANSMEM 259 277
 FT TRANSMEM 293 314
 FT DOMAIN 315 466
 FT TRANSMEM 467 487
 FT DISULFID 147 161
 FT DISULFID 209 210
 FT
 FT CARBOHYD 43 43
 FT CARBOHYD 87 87
 FT CARBOHYD 130 130
 FT VARSPLIC 262 290
 FT
 FT SEQUENCE 499 AA; 56002 MW; AEE5D0B382D042D5 CRC64;
 Query Match 47.0%; Score 1240.5; DB 1; Length 499;
 Best Local Similarity 49.4%; Pred. No. 5.3e-102;
 Matches 247; Conservative 78; Mismatches 152; Indels 23; Gaps 6;

QY 8 LALLA-LLPVSEQGPHEKRLNALLANNTLEPRVANESEPLEVRFGTLTQIIVDDEKN 66
 DB 7 LALAASLHLSVGEFORFKLYKLVKNYNLEPRVANDSLPLVYFSLSLQIIVDDEKN 66
 QY 67 QLLITNLTSLWNYDLNRNDSYGGVKDLRITPNKLWKPDLVLYNSADEGFGTGYQTN 126
 DB 67 QVLTNTNLTQWTDHYLQWNASSEYGVKTVRPDPDGOIKWPKDILLYNSADEREDATPHN 126
 QY 127 VVVRSGGSLVPPGIFKSTCKMDIAWPFDDQDCKMFGSWYDGNQLDLVLKDEAGD 186
 DB 127 VLVNSSGHCQYLPFGIFKSSYIDVRFPDFVQOQCKLFGSWSYGGWSLDLQWQE---AD 183
 QY 187 LSDFITNGEWLYGMPCKNTITVACCPVVDVFTIMIRRRRTLYFFNLIIVPCVLISS 246
 DB 184 ISGYPNGEMDLVGLGRSEKFEYCKEYPPDVTFTVSRRTLYGLNLLIPCVLISA 243
 QY 247 MALLGFTLPDPSGKELTGLVITLLSLAVFLNLVAETLPQVSDAIPILGTYFNCIMFVAS 306
 DB 244 LALLVFLLPADSGEKISGLITVLLSLVFMLLVAEIMPATSDSVPLIAQVFASTMIIVGL 303
 QY 307 SVVLTVVVLYNHHRTADIEHMPQIKSVFLQWLPHILRMSRPGKIKTKITMNTREL 366
 DB 304 SVVTVIVLVQHHHDPDGGKMPKTRVYLLNWCAMFLRMKRPDKYKRPACQHNRCSL 363
 QY 367 ELKERSV---KSLANVLDDDD--DFRHGPPPPNSTASTGNLPGGCSIFRTDFRRSFV 419
 DB 364 ASVMSAVAGPPATNGNLLYTGFLDTHMCAPTDPGCVVCGRV--ACSPHDEHLLHAG 421
 QY 420 RPSTMEDVGGGLGSHHRLHLILRELQFITARMKKADEAEELISDWKFAAMVDFCLFV 479
 DB 422 QPSEGD-----DLAKILEVRYIAHFRFCQDESEAVCSSEWKAACVVDRLCLMA 471

QY 480 FTLTIIATVAVLLSAPHII 499
 DB 472 FSVFTILCTIGILMSAPNFV 491
 RESULT 6
 ACHI_CAEEL STANDARD; PRT; 498 AA.
 ID AC48180;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acetylcholine receptor like protein, alpha-type chain precursor.
 GN F25G6.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=96196478; PubMed=8627624;
 RA Ballivet M., Alliod C., Bertrand S., Bertrand D.;
 RT "Nicotinic acetylcholine receptors in the nematode Caenorhabditis
 RT elegans".
 RL J. Mol. Biol. 258:261-269(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Nelson J., Wohldmann P.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: POSSIBLE ACETYLCHOLINE RECEPTOR.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL: X83887; CAA58764.1; -
 DR EMBL: AF022973; AAC25796.1; -
 DR PIR: S68588; S68588.
 DR HSP; P58154; 119B.
 DR WormPep; F25G6.3; CE09639.
 DR InterPro: IPR006029; Neu_chan_memb.
 DR InterPro: IPR006202; Neur_chan_LBD.
 DR InterPro: IPR006201; Neur_chan.
 DR Pfam: PF02931; Neur_chan_LBD; 1.
 DR Pfam: PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 DR Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
 KW Transmembrane; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 498
 FT
 FT DOMAIN 20 230
 FT TRANSMEM 231 252
 FT TRANSMEM 261 279
 FT TRANSMEM 295 314
 FT DOMAIN 315 472
 FT TRANSMEM 473 493
 FT DISULFID 147 161
 FT DISULFID 211 212
 FT
 FT CARBOHYD 43 43
 FT CARBOHYD 93 93
 FT
 FT ACETYLCHOLINE RECEPTOR LIKE PROTEIN,
 FT ALPHA-TYPE CHAIN.
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT POTENTIAL.
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT POTENTIAL.
 FT BY SIMILARITY.
 FT ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 498 AA; 57169 MW; E463ABB40AC9FA82 CRC64;

Query Match 46.9%; Score 1237.5; DB 1; Length 498;
 Best Local Similarity 47.5%; Pred. No. 9.7e-102;
 Matches 245; Conservative 80; Mismatches 140; Indels 51; Gaps 9;

QY 2 APMALALALLPVSQGPHEKRLNALLANYTLRPNVANESEPLEVRFGLTQQIID 61
 DB 15 APTAGSL-----QRRLYEDLMRYNNLRLRPNVANHSEPTVHLKVALQQIID 61

QY 62 VDEKNOLLITNLSLEWNYLNRWDSYGVKDLRITPNKLPKPDVLMYNSADEGPD 121
 DB 62 VDEKQVYVNAWLDYTWNDYVMDKAEIGNITDVRFPAGKWPDLVLYNSVDTFDS 121

QY 122 TYQTNVVRSGSCLYVPPGIFKSTCKMDIAFPDDQHCMDKFGSWTYDGNQLDLVLKD 181
 DB 122 TYQTNMIVYSTGLVHWVPPGIFKISCKIDIQWFFDEQKCFKFGSWTYDGVKLD--Lop 179

QY 182 EAGG-DLSDFINGEWLGMGPKKNTIYACCPYVDVTFIMIRRTLYFFNLIVP 240
 DB 180 ATGGFDISEYISNGEWALPLTTVERNEKPYDCPEYDPVDFHFLHMRRTLYGFNLMP 239

QY 241 CVLISSMALLGTLPPDSGEKLTGLVTILLSTVFLNLVAETLPQVSDAIPLLGYENCI 300
 DB 240 CILTLMLTLGTLPPDAGEKITLQITVLLSTICFLSVSEMSPTSEAVPLLGIFTC 299

QY 301 MFMVASSVLTVYVNLNHYHRTADIHEMPQWIKSVFLOLWPLWILMRSPGKTKITRKTII-M 358
 DB 300 MIWVTASTVTVVNLNHYRTETHDMGPWTRNLLLYWIPWILMRKPGHNLTYASLPSL 359

QY 359 MNTRELEKRSKSLANVLD-----IDDFRHGPPPPNPNSTAGNLGPGCS 408
 DB 360 FSTK-----PNRHSLSLRNKDNEHLSRANSEFADCRNLQYIMTQSVNSGLTSLG-S 412

QY 409 IFTDFRRSEVPSPMEDVGGGLSGSHRE-----LHLILRELQFTIARMKKADEAELIS 463
 DB 413 I-----PSTMISSNGTTTDSQQTLLILRIYHLEKIYTKRMIEGDKKEQACN 461

QY 464 DNKFAAMVDRCLFVFTLFTIARVALLSAPHII 499
 DB 462 NKKFAAMVDRCLVFTFIIVSTIGIFWSAPYLV 497

RESULT 7

ACH3_HUMAN
 ID ACH3_HUMAN STANDARD; PRT: 503 AA.
 AC P32297; Q15823; Q96RH3; Q99553; Q9BQ93;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
 GN CHRNA3 OR NACHRA3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90245296; PubMed=2336208;
 RA Fornasari D., Chini B., Taroni P., Clementi F.;
 RT "Molecular cloning of human neuronal nicotinic receptor alpha
 3-subunit";
 RL Neurosci. Lett. 111:351-356(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Thymus;
 RX MEDLINE=91114756; PubMed=1989896;
 RA Mihovilovic M., Roses A.D.;
 RT "Expression of mRNAs in human thymus coding for the alpha 3 subunit
 of a neuronal acetylcholine receptor";
 RL Exp. Neurol. 111:175-180(1991).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).

RX MEDLINE=97062879; PubMed=8906617;
 RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
 Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
 RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
 2-beta 4 nicotinic acetylcholine receptor subunits and functional
 expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
 beta 4 subunits";
 RL J. Mol. Neurosci. 7:217-228(1996).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=97162233; PubMed=9009220;
 RA Groot Kormelink P.J., Luyten W.H.M.L.;
 RT "Cloning and sequence of full-length cDNAs encoding the human neuronal
 nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and
 expression of seven nAChR subunits in the human neuroblastoma cell
 line SH-SY5Y and/or IMR-32";
 RL FEBS Lett. 400:309-314(1997).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=99118870; PubMed=9921897;
 RA Rempel N., Heyers S., Engels H., Slegers E., Steinlein O.K.;
 RT "The structures of the human neuronal nicotinic acetylcholine receptor
 beta2- and alpha3-subunit genes (CHRNA2 and CHRNA3)";
 RL Hum. Genet. 103:645-653(1998).
 RN [6]
 RP SEQUENCE FROM N.A. AND VARIANT LEU-21. INS.
 RX MEDLINE=21342809; PubMed=11450844;
 RA Lev-Lehman E., Bercovich D., Xu W., Stockton D.W., Beaudet A.L.;
 RT "Characterization of the human beta4 nAChR gene and polymorphisms in
 CHRNA3 and CHRNA4";
 RL J. Hum. Genet. 46:362-366(2001).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP SEQUENCE OF 30-503 FROM N.A.
 RC TISSUE=Brain;
 RA Anand R., Lindstrom J.;
 RL Submitted (JUN-1990) to the EMBL/GenBank/DBJ databases..
 RN [9]
 RP SEQUENCE OF 6-493 FROM N.A.
 RC TISSUE=Epidermal keratinocytes;
 RA Arredondo J., Grando S.A.;
 RT "Cloning cholinergic receptors in human keratinocytes";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 MEMBRANE.
 CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE
 OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

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CC CC -!- ALTERNATIVE PRODUCTS:
CC CC Event=Alternative splicing; Named isoforms=2;
CC CC Name=1;
CC CC Name=2;
CC CC IsoId=P32297-1; Sequence=Displayed;
CC CC IsoId=P32297-2; Sequence=VSP_000073;
CC CC Note=No experimental confirmation available;
CC CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC CC -----
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CC CC -----
CC CC EMBL; M86383; AAC84176.1; -
CC CC EMBL; M37981; AAA59942.1; -
CC CC EMBL; U62432; AAB40110.1; -
CC CC EMBL; Y08418; CAA69695.1; -
CC CC EMBL; AJ007783; CAA07682.1; -
CC CC EMBL; AJ007784; CAA07682.1; JOINED.
CC CC EMBL; AJ007785; CAA07682.1; JOINED.
CC CC EMBL; AJ007786; CAA07682.1; JOINED.
CC CC EMBL; AJ007787; CAA07682.1; JOINED.
CC CC EMBL; BC001642; AAH01642.1; -
CC CC EMBL; BC002996; AAH02996.1; -
CC CC EMBL; BC000513; AAH00513.1; -
CC CC EMBL; AF385584; AAK68110.1; -
CC CC EMBL; X53559; CAA37625.1; -
CC CC PIR; A37040; A37040.
CC CC PIR; A53956; A53956.
CC CC Genew; HGNC:1957; CHRNA3.
CC CC MIM; 118503; -
CC CC GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. ; TAS.
CC CC GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. ; TAS.
CC CC GO; GO:0005215; F:transporter activity; TAS.
CC CC GO; GO:0007165; P:signal transduction; TAS.
CC CC GO; GO:0006832; P:small molecule transport; TAS.
CC CC InterPro; IPR006029; Neu_channel_memb.
CC CC InterPro; IPR006202; Neu_channel_LBD.
CC CC InterPro; IPR006201; Neu_channel.
CC CC Pfam; PF02931; Neur_chan_LBD; 1.
CC CC Pfam; PF02932; Neur_chan_memb; 1.
CC CC PRINTS; PR00252; NRIONCHANNEL.
CC CC TIGRFAMs; TIGR00860; LIC; 1.
CC CC PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
CC CC Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
CC CC Transmembrane; Multigene family; Alternative splicing; Polymorphism.
CC CC SIGNAL 1 29
CC CC CHAIN 30 503
CC CC DOMAIN 30 238
CC CC TRANSMEM 239 263
CC CC TRANSMEM 271 289
CC CC TRANSMEM 305 326
CC CC DOMAIN 327 475
CC CC TRANSMEM 476 495
CC CC DISULFID 157 171
CC CC DISULFID 221 222
CC CC CARBOHYD 53
CC CC CARBOHYD 170 170
CC CC VARSPPLIC 1 5
CC CC VARIANT 21 21
CC CC CONFLICT 5
CC CC CONFLICT 11 14
CC CC CONFLICT 100 100
CC CC CONFLICT 132 133
CC CC CONFLICT 235 235

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FT CONFLICT 430 430 L -> V (IN REF. 1).
SQ SEQUENCE 503 AA; 57309 MW; 8A9EBC5D71AEC7D6 CRC64;

Query Match 37.5%; Score 989.5; DB 1; Length 503;
Best Local Similarity 38.5%; Pred. No. 9.2e-80;
Matches 200; Conservative 92; Mismatches 166; Indels 61; Gaps 5;

QY 1 MAPMLAALALLPVSQEPHEKRLNALLNANTLERPVANSEPLEYRFGTLTLOQII 60
Db 11 LSPRLLLLSLLPVARASEAEHRLFERLFEDYNEIIRPVANVSDPVIHFVMSQLV 70
QY 61 DVEDEKQOLLITNLSLEWYNDYLNWNSYGVGKDLRITPNKLWKPDVLMWYNSADSGFD 120
Db 71 KYDEVNQIMETNWLKQIWDYDKWNPDSYGAEFMRVPAQIKWDPDIIVLYNNVAGDFQ 130
QY 121 GTYQTNVVRSGGSCLYVPGIFKSTCKMDIANFPDDQHCMDKFKGWTYDGNOLDVLK 180
Db 131 VDDTKTALLKYGTGTWIPPAIFKSSCKIDVTFFDYQNTMKFGWSYDKAKIDLVL 190
QY 181 DEAGGDLSDFITNGEYWLIGMPGKKNITTYACPEYVDVTFITMIRRTLYYFFNLIVP 240
Db 191 G-SSMNLKDYWESGEWAILKAPGYKHDIKYNCCCEIYDPDITYSLYIRRLPLFTINLIIP 249
QY 241 CVLISSMALIGFTLPDPSGEKLTGLVTLISLWFLNLVAETLPQVSDAIPLLGYFNCI 300
Db 250 CLLISFLTVLVFYLPSDCGKVKLCISVLSLVFLVLTITETIPSTSLVPLIGEYLLFT 309
QY 301 MFMVASSVLTVVVLYNHYHRTADITHMPQWIKSVFLOLWILRMSRPGKKITRKTIMN 360
Db 310 MIFVTLISIVITVFLNVHYRTPTHTNPSVNVKTVFLNLLPRVMPMTRP----- 357
QY 361 TRMRELEKERSKSLIANVLDIDDDFRHGGPPPNSTASTGNL-----GPGCS----- 408
Db 358 -----TSNEGNAQKPRPLYGAELSNLCNCFSAESKCGKGYPC 395
QY 409 -----IFRTDFRSFVRPSTMEDVGG--GLGSHHRELHLTLRELOFTARMKK 454
Db 396 QDGMGCGYCHRRRIKISFNLSANLRSSESVDVLSLSLSLSPEIKAEIQSVKYIAENKA 455
QY 455 ADEEAELISDMKFAAMVVDRCFLVFVTLFTIIATVAVLL 493
Db 456 QNEAKEIQDDWKVYAMVIDRFLWVFTLVCLIGTAGLFL 494

RESULT 8
ACH3_RAT
ID ACH3_RAT STANDARD; PRT; 499 AA.
AC P04757;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
GN CHRNA3 OR ACRA3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86118671; PubMed=3753746;
RA Boulter J., Evans K., Goldman D.J., Martin G., Treco D.,
RA Heinemann S.F.,
RA Patrick J.;
RA "Isolation of a cDNA clone coding for a possible neural nicotinic
RT acetylcholine receptor alpha-subunit.";
RL Nature 319:368-374(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041184; PubMed=2444984;
RA Boulter J., Connolly J.G., Deneris E.S., Goldman D.J., Heinemann S.F.,
RA Patrick J.;
RT "Functional expression of two neuronal nicotinic acetylcholine
RT receptors from cDNA clones identifies a gene family.";

```


Proc. Natl. Acad. Sci. U.S.A. 84:7763-7767(1987).
 [3]
 SEQUENCE OF 1-21 FROM N.A.
 TISSUE=Liver;
 RX MEDLINE=94193711; PubMed=8144606;
 RA Yang X., McDonough J., Fyodorov D., Morris M., Wang F.,
 RA Deneris E.S.;
 RT "Characterization of an acetylcholine receptor alpha 3 gene promoter
 and its activation by the POU domain factor SCIP/Tst-1.";
 RL J. Biol. Chem. 269:10252-10264(1994).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES
 CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-3 SUBUNIT CAN BE
 CC COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC
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 CC
 CC EMBL: X03440; CAA27170.1; -
 CC EMBL: L31621; AAA1673.1; -
 CC EMBL: U04961; AAA18001.1; -
 CC InterPro: IPR006029; Neu_chan_memb.
 CC InterPro: IPR006202; Neur_chan_LBD.
 CC InterPro: IPR006201; Neur_channel.
 CC Pfam: PF02931; Neur_chan_LBD; 1.
 CC Pfam: PF02932; Neur_chan_memb; 1.
 CC PRINTS: PR00252; NRIONCHANNEL.
 CC TIGRFAMs: TIGR00860; LIC; 1.
 CC PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.
 CC Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 499 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-3 CHAIN.
 FT DOMAIN 26 234 EXTRACELLULAR.
 FT TRANSMEM 235 259
 FT TRANSMEM 267 285
 FT TRANSMEM 301 322
 FT DOMAIN 323 471 CYTOPLASMIC.
 FT TRANSMEM 472 491
 FT DISULFID 153 167
 FT DISULFID 217 218
 FT CARBOHYD 49 49
 FT CARBOHYD 166 166
 FT CARBOHYD 499 AA; 56997 MW; D66C49LE832B9C34 CRC64;
 Query Match 37.0%; Score 977.5; DB 1; Length 499;
 Best Local Similarity 40.2%; Pred. No. le-78;
 Matches 201; Conservative 95; Mismatches 177; Indels 27; Gaps 8;
 QY 3 PMAALALALLPVSEQGPHEKRLNALLANTLERPVANSEPLEVRFGTLTLOQITDV 62
 Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
 QY 63 DEKNOLLITNWLSEWYDNLRWNSDEYGGVKDLRITPNKLWKPDLVLYNSADSGFDGT 122
 Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
 QY 69 DEVNQIMETNLKQIWDNDYKLUKWRPSYQGGVEFMVRVPAEKTWKPDIVLYNNADGDFQVD 128
 Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
 QY 123 YOTNVVVRSGGSLVPPGPIKSTCKMDIATWPPDDQHCDFGWSWTYDGNOLDVLVKDE 182
 Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
 Db 129 DKTALLKYGTGVTWIPPAIFKSSCKIDVTYFPDYQNTMTKFGWSYDKAKIDLVLIG- 187

QY 183 AGDLSDFITNGEYWLIGMPGKNTITYACCEPPYVDVTFITMIRRTLYFFNLIVPCV 242
 Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
 Db 188 SSMNLKDYWESGEWALIKAPGYKHEIKYNCCEIYQDITYSLYIRLFLFYINLIIPCL 247
 QY 243 LISSMALLGFTLPPGSGEKLTLGVTTLLSLTVFLNLVAETLPOVSDAIPLLGTYFNCMF 302
 Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
 Db 248 LISFTLVLYFIPSCGGEKVTLCISVLLSLTVFLVITETIPSTSLVPLIGEYLLFTWI 307
 QY 303 MYASSVVLTVVVLNVHRTADIHMPQWIKSVFLQWLPWILRMSRP--GKTKRKT-IMM 359
 Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
 Db 308 FVTLSTIVITFVLNVHYRTPPTHTWTVKAVFLNLLPRVMEVTRPTSGEGDTPKTRTEY 367
 QY 360 NTRMRELEKERS-SKSLLANVLDDDDFRHGGPPPNSTASTGNLPGGCSIFR---TDPR 415
 Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
 Db 368 GAELSLLNCFSRADSKSC-----KEGYPCQDGTGCGY-----CHHRRVKISNFS 410
 QY 416 RSFVRPSTMEDVGG--GLGSHHREHLHLILRELQFITARMKKADEEAELISDNKFAAMVVD 473
 Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
 Db 411 ANLTRSSSESNAVLSLSALSPEIKAEIQSVKYAENKMAQNVAKIEQDDMKVYAVVID 470
 QY 474 RECLFVFTLTITATVAVILL 493
 Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
 Db 471 RIFLWVFIIVLCIGTAGLFL 490
 RESULT 9
 ACH3_BOVIN STANDARD; PRT; 495 AA.
 ID ACH3_BOVIN
 AC Q07263;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update).
 DE Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
 GN CHRNA3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92319195; PubMed=1620271;
 RA Criado M., Alamo L., Navarro A.;
 RT "Primary structure of an agonist binding subunit of the nicotinic
 RT acetylcholine receptor from bovine adrenal chromaffin cells.";
 RL Neurochem. Res. 17:281-287(1992).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
 CC TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X57032; CAA40348.1; -
 DR PIR: S60589; S60589.
 DR InterPro: IPR006029; Neu_chan_memb.
 DR InterPro: IPR006202; Neur_chan_LBD.
 DR InterPro: IPR006201; Neur_channel.
 DR Pfam: PF02931; Neur_chan_LBD; 1.
 DR Pfam: PF02932; Neur_chan_memb; 1.
 DR PRINTS: PR00252; NRIONCHANNEL.
 DR TIGRFAMs: TIGR00860; LIC; 1.
 DR PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.

KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 FW Transmembrane; Multigene family.
 FT STGNAL 1 21 POTENTIAL.
 FT CHAIN 22 495 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-3 CHAIN.
 FT DOMAIN 22 230 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 231 255 POTENTIAL.
 FT TRANSMEM 263 281 POTENTIAL.
 FT TRANSMEM 296 318 POTENTIAL.
 FT DOMAIN 319 467 CYTOPLASMIC (BY SIMILARITY).
 FT TRANSMEM 468 487 POTENTIAL.
 FT DISULFID 149 163 BY SIMILARITY.
 FT DISULFID 213 214 ASSOCIATED WITH RECEPTOR ACTIVATION
 (BY SIMILARITY).
 FT CARBOHYD 45 45 N-LINKED (GLNAC. . .) (POTENTIAL).
 FT CARBOHYD 162 162 N-LINKED (GLNAC. . .) (POTENTIAL).
 SQ SEQUENCE 495 AA; 56914 MW; 322825629821EA07 CRC64;
 Query Match 36.8%; Score 970.5; DB 1; Length 495;
 Best Local Similarity 39.8%; Pred. No. 4.3e-78;
 Matches 198; Conservative 93; Mismatches 181; Indels 25; Gaps 7;
 QY 5 LAALALLLPVSEQGPHEKRLNALLANTLERPVANSEPLEVRFGTLTQIIVDVE 64
 DB 7 LRRLLLLLLPVASTDAERHLERLFEDYNEIRPVANVSDPVIIQFVMSQLVKVDE 66
 QY 65 KNOLLITNLSLEWYNDYINLRWNSDEYGGVKDLRITPNKLWKPDLVMSADSGFGDTYQ 124
 DB 67 VNOIMETNLKQIWNQYKLNWPSDYDGAERFVPAEKIWKPDIVLYNNAVGDFQVDDK 126
 QY 125 TNVVRSGGCLYVPGIFKSTCKMDIAWPFDDOCHDMKFGSWYDGNOLDLVLKDEAG 184
 DB 127 TKALLKYTGVTWTPPAIFKSSKIDVTYFPDYQNTKMFQGSWSDYKAKIDLVLIG-SS 185
 QY 185 GDLSDFTINGEWLIGMPGKNITTYACCPPEPVVDVTFTIMIRRTLYFFNLIVPCVLI 244
 DB 186 MNLKDYWESGEWAIKAPGVKHKDKYCNCEIYDITYSLYIRRLFYINLIPLCLI 245
 QY 245 SSMAILGFTLPDSGEKLTGVTLLSLTVFLNLVAETLPQVSDAIPLLCTYNCIMFW 304
 DB 246 SFTLVFLYLPSCGGERVTCISVLLSLTVFLVITETIPSTSLVPLIGEYLLTFMFV 305
 QY 305 ASSVVLTVVNLVHRTADITHMPWIKSVFLQWLPILWLRMSRPGK---KITRKTIMMNT 361
 DB 306 TLSIVITVFLNVHRTPTTHTPAWVKTIIFLNLPRVMTWRPASNEGTFQRPFYSA 365
 QY 362 RMRELELKRSSKSLANVLIDDDFRHGGPPPNSTASTGNLPGCSIFR---TDFRRSF 418
 DB 366 ELSNLNCFRLESKVC-----KEGYP-----CODGLCG-YCHHRRAKISNFSANL 409
 QY 419 VRPSTMEDVGG--GLGSHHRELHLILRELOFITARMKKADEEAEELISDWKFAAMVDVDFC 476
 DB 410 TRSSSSSEDAVLSLSALSPEIKAIQSVKYIAENMKQAQNEAKEIQDDWKYVAMVIDRIF 469
 QY 477 LFVETLTITATVALL 493
 DB 470 LWVFILCYILGTAGLFL 486
 RESULT 10
 ACHI_DROME
 ID ACHI_DROME STANDARD; PRT; 567 AA.
 AC P09478; Q9VC74;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Acetylcholine receptor protein, alpha-like chain 1 precursor.
 GN NACK-ALPHA-96AA OR ACRB OR ALS OR ACR96AA OR G5610.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;

RN SEQUENCE FROM N.A.
 RC STRAIN=Oregon-R;
 RX MEDLINE=88283626; PubMed=2840281;
 RA Bossy B., Ballivet M., Spierer P.;
 RT "Conservation of neural nicotinic acetylcholine receptors from
 RL Drosophila to vertebrate central nervous systems.";
 RMBO J. 7:611-618(1988).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballaw R.M., Basu A., Bayendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei X., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 [3]
 RN REVISIONS.
 RP STRAIN=Berkley;
 RC MEDLINE=22426069; PubMed=12537572;
 RX Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: CNS IN EMBRYOS.
 CC -!- DEVELOPMENTAL STAGE: LATE EMBRYONIC, LATE PUPAL AND SECOND INSTAR
 CC LARVAE STAGES.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

DR Pfam: PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 22
 FT CHAIN 23 496 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT DOMAIN 23 231 ALPHA-3 CHAIN.
 FT TRANSMEM 232 256 EXTRACELLULAR.
 FT TRANSMEM 264 282
 FT TRANSMEM 298 319
 FT DOMAIN 320 468 CYTOPLASMIC.
 FT TRANSMEM 469 488
 FT DISULFID 150 164
 FT DISULFID 214 215
 FT CARBOHYD 46
 FT CARBOHYD 163
 FT CARBOHYD 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 496 AA; 57027 MW; FD25BC02A9B601FF CRC64;
 Query Match 35.9%; Score 948.5; DB 1; Length 496;
 Best Local Similarity 37.7%; Pred. No. 3.8e-76;
 Matches 195; Conservative 89; Mismatches 168; Indels 65; Gaps 6;
 QY 7 ALALLALPVSEQ-----PREKRLNALLANYNTLERPVANSEPLEVRFGTLQOIIDV 62
 DB 6 ALLTAAVCILFQCGGSEPEHRLYAALFKYNOQVVRPVKNASDPVILQEVSMQVKV 65
 QY 63 DEKNQLITNIWLSLEWYNDYLNLRNDESEYGVKDLRITPNKLNKPDVLYMNSADEGFGDT 122
 DB 66 DEVNQIMETNLKHLWYNDYKLRNPDVYGGAFIRVPSQIWKPDVLYNNAVGDFQVD 125
 QY 123 YQTNVYVRSGSLYVPPGIFKSTCKMDIAWFDDQHCMDKFGSWTYDGNQLDLVLKDE 182
 DB 126 DKTKALKYTGDTWTPPALFKSKCKIDVYFFDYQNCMTKFGSWYDKAKIDLVLIGS 195
 QY 183 AGGDLSDFITNGEYLYGMGPKKNTITYACCPYVDVTFIMIRRTLYFFNLIYPCV 242
 DB 186 T-MNLKDYWESEGAIIKAPGYKHDIKNCCEEYTDITYSLVIRLPLFTYINMIIPCL 244
 QY 243 LISSMALLGTLPPDSEKLTGLVTILLSTVLNVAETLPQVSDAIPLLGYFNCIMF 302
 DB 245 LISFLTVLYLPSCDGEKVTLCISVLLSTVLLVITETIPSTSLVPLIGETLFTMI 304
 QY 303 MVASSVLTVVVLYNHYHRTADIHEMPOWIKSVFLQWLPWILRMSRPGKTKITRMNTR 362
 DB 305 FVLSIVITVFLVNLVHYRTKTHMPVWVTFIENLLPRIMETRP----- 350
 QY 363 MRELEKERSKSLANVLDDDFRHGPPPPNSTASTGNLG----- 404
 DB 351 -----TSDEENQKPKPFTSEFSLNCFNSSEIKCKKDGFCVQD 390
 QY 405 PGCSIFR-----TDFRSFVRSTMEDVGG--GLGSHHRELHLILRELQFIARKKAD 456
 DB 391 MACSCCOYQRMKTSDFSGNITRSSSESVDPLSFVSLSPEMRDAIESVYIAENMKQN 450
 QY 457 EEAEELISDMKFAAMVDFRCFLVFTFTIATVAVLL 493
 DB 451 EAKEIQDDWKYVAMVIDRIELWFLVILCILGTAGLFL 487

RESULT 12.

ACH1_MANSE

ID ACH1_MANSE

AC P91766;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Acetylcholine receptor protein, alpha-like chain precursor (MARAL).

GN ACRA1.

OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
 OC Sphingidae; Sphinginae; Manduca.
 OX NCBI_TaxID=7130;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98424077; PubMed=9753155;
 RA Eastham H.M., Lind R.J., Eastlake J.L., Clarke B.S., Towner P.,
 RA Reynolds S.E., Wolstenholme A.J., Wonnacott S.;
 RT "Characterization of a nicotinic acetylcholine receptor from the
 RT Insect Manduca sexta";
 RL Eur. J. Neurosci. 10:879-889(1998).
 CC -I- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE (BY SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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 CC -----
 CC EMBL; Y09795; CAA70928.1;
 DR InterPro: IPR006029; Neur_chan_memb.
 DR InterPro: IPR006202; Neur_chan_LBD.
 DR InterPro: IPR006201; Neur_channel.
 DR Pfam: PF02931; Neur_chan_LBD; 1.
 DR Pfam: PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 DR Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 21
 FT CHAIN 22 516 POTENTIAL.
 FT FT ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-
 FT FT LIKE CHAIN.
 FT FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 22 243
 FT TRANSMEM 244 264 POTENTIAL.
 FT TRANSMEM 274 294 POTENTIAL.
 FT TRANSMEM 306 326 POTENTIAL.
 FT DOMAIN 327 465 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 466 486 POTENTIAL.
 FT DISULFID 149 163 BY SIMILARITY.
 FT DISULFID 222 223 ASSOCIATED WITH RECEPTOR ACTIVATION
 FT FT (BY SIMILARITY).
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 516 AA; 58720 MW; E7A71E8C45D13BD2 CRC64;
 Query Match 35.9%; Score 946.5; DB 1; Length 516;
 Best Local Similarity 39.7%; Pred. No. 6.1e-76;
 Matches 195; Conservative 84; Mismatches 171; Indels 41; Gaps 6;
 QY 21 PHEKRLNALLANYNTLERPVANSEPLEVRFGTLQOIIDVDEKNQLITNIWLSLEWN 80
 DB 23 PDAKRLYDLDLSNKNLVRPVLNVSADLTAVRIKLKLSQLDVNLKQIMTNTLWVEQSWY 82
 QY 81 DYNLNRNDSYGGVKDLRITPNKLNKPDVLYMNSADEGFGDTYQTNVYVRSGSLYVPP 140
 DB 83 DYKLSWEPREYGVGVEMLHVPDHIWRPDIVLYNNAAGNFVETLKATKATNYTGVVERPP 142
 QY 141 GIEKSTCKMDIAWFPDDQHCMDKFGSWTYDGNQLDLVLKDEAGG-----DLSDFIT 192
 DB 143 AIYKSCSEIDVEYFFPDQHCVMKFGSWTYDGNQLDLVLKDEAGG-----DLSDFIT 202
 QY 193 NGEWYLGMPGKKNITITYACCPYVDVTFIMIRRTLYFFNLIYPCVLISSMALLGF 252

Db 203 SVWDILEVPAVRNEKPYCCDPYLDITENITMRRKTLFTYVNLIIIPCMGISFLVLVF 262

Qy 253 TLPPDSGEKLTGVTILLSTVFLNLVAETLPQVSDAIPLLGYFNCIMPMWASSVVLTV 312

Db 263 YLPSDGEKVSLSILLSTVFLNLVAETLPQVSDAIPLLGYFNCIMPMWASSVVLTV 322

Qy 313 VVLYNHYRTADIHEMPOWIKSVFLQWLPWILMSRPGCKI---TRKTMNTMTRMRELELK 369

Db 323 VVLYNHYRTADIHEMPOWIKSVFLQWLPWILMSRPGCKI---TRKTMNTMTRMRELELK 382

Qy 370 ERSGKSLANVLDDDDFRHGRPPNPSTASTGNLGP--GCSIFRTDFRRSFVRPSTMEDV 427

Db 383 DESPGV-----PAPRPPPCAPPLAPCAACA-----PAPAL 416

Qy 428 GGGIGSHR--ELHLRLRELQFTIARMKKADEAEILSDMKFAAMVVDRCLEVFIFTI 485

Db 417 CDALRRWHRCPELHKAIDGINIADOTRKEESTRVKEDWKYVAVMLDRPFLFIETLAVV 476

Qy 486 IATVAVLLSAP 496

Db 477 VGSAGIILQAP 487

RESULT 13

ACH1_SCHGR STANDARD; PRT; 557 AA.

AC P23414;

DT 01-NOV-1991 (Rel. 20, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Acetylcholine receptor protein, alpha-L1 chain precursor.

OS Schistocerca gregaria (Desert locust).

OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

OC Neoptera; Orthoptera; Orthoptera; Caelifera; Acridomorpha;

OC Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.

OX NCBI_TaxID=7010;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91092263; PubMed=1702381;

RA Marshall J., Buckingham S.D., Shingai R., Lunt G.G., Goosey M.W.,

RA Darlison M.G., Sattelle D.B., Barnard E.A.;

RT "Sequence and functional expression of a single alpha subunit of an

RT insect nicotinic acetylcholine receptor."

RL EMBL J. 9:4391-4398(1990).

CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN

CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND

CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA

CC MEMBRANE.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

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CC -----

DR EMBL: X55439; CAA35081.1; -

DR PIR: S12359; S12359.

DR InterPro: IPR006029; Neu_chan_memb.

DR InterPro: IPR006029; Neu_chan_LBD.

DR InterPro: IPR006201; Neu_chan.

DR Pfam: PF02931; Neu_chan_LBD; 1

DR Pfam: PF02932; Neu_chan_memb; 1

DR PRINTS: PR00252; NRIONCHANNEL.

DR TIGRFS: TIGR00860; LIC; 1.

DR PROSITE: PS00236; NEUROTR ION CHANNEL; 1.

KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;

KW Transmembrane; Multigene family.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 557 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-L1

FT DOMAIN 24 244

FT TRANSMEM 245 266

FT TRANSMEM 274 294

FT TRANSMEM 308 329

FT TRANSMEM 330 500

FT TRANSMEM 501 523

FT DISULFID 151 165

FT DISULFID 224 225

FT CARBOHYD 47 47

FT CARBOHYD 235 235

FT DOMAIN 382 400

FT DOMAIN 406 422

SQ SEQUENCE 557 AA; 63026 MW; 168389C887DFE3E CRC64;

Query Match 35.8%; Score 944; DB 1; Length 557;

Best Local Similarity 36.9%; Pred. No. 1.1e-75;

Matches 201; Conservative 96; Mismatches 181; Indels 66; Gaps 7;

Qy 1 MAPMLAALALLLPVSEQGPEKRLNALLANYTLERPVANESEPLEVRFGLTLQQII 60

Db 5 LPFMLLLLLLLLHPAAANPDARLYDOLLSNYNRLRPVSNNDTVLVKGRLSLQI 64

Qy 61 DVDEKNOLLITNLSLEWYNDYLNWNSYGGVKDLRITPNKLPDVLNYSADSGFD 120

Db 65 DLNLKQILTTNVWLEHEMODHFRWDPAEYGGVTELYPSEHILWLPDIYLYNAGEYV 124

Qy 121 GTYTNNVRSYGSLYVPGIPIKSTCKMDIANFPDDQHCMDKFGSWTDGQDLV-- 178

Db 125 VTTMTKAVLHHTGKVVTTPPAIFKSCIEDVRYFPDQOTCFMKFGSWTDGQDLKHI 184

Qy 179 -----LKDEAGGDLSDFITNGEWYLGMPKKNITTYACCPPEYVDVTFIMIRRTLY 232

Db 185 NQYDDNKVKVGDIDREYYPVEMDILGVPAERHEKYYPCAEYPDIFENILRRKTLF 244

Qy 233 YFENLIVPCVLISSMALLGTLPPDGEKLTGVTILLSTVFLNLVAETLPQVSDAIP 292

Db 245 YTVNLIVPCVGISYLVFLPADSGEKIALCISILLSTQTFMFLISEIPSTSLAPL 304

Qy 293 LGYFNCIMPMWASSVVLTVVLYNHYRTADIHEMPOWIKSVFLQWLPWILMSRPGCK-- 350

Db 305 LGKYLFTVVLGVSIVITIMLVNHYRKPSTHMAPWVRKVFIRRLKLLMLMRVPEQL 364

Qy 351 -KITRKTIMMTRMRELEKERSKSLA--NYLIDIDDDFRH----- 389

Db 365 ADLASKRLRLHAKNSLSAAAAAASAAASPSDLSRHHHLHQHQLHLHLQ 424

Qy 390 GPPPPNST-ASTGNLPGGCSIFRTDFRRSFVRPSTMEDVGGGLGS----- 433

Db 425 RGGCGNLHSATNRFSGSAGF-----GGLPSVVGDLGSLSDVATRK 466

Qy 434 -HREHLILRELQFTIARMKKADEAEILSDMKFAAMVVDRCLEVFETLTIIATVAVL 492

Db 467 KYFELEKAIHNVLFIONHMQRDEDAEDQDMGFMVAVMLDRFLFIETIASIVGTAIL 526

Qy 493 LSAP 496

Db 527 CEAP 530

RESULT 14

ACH2_DROME

ID ACH2_DROME STANDARD; PRT; 576 AA.

AC P17644; Q9VC73;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Acetylcholine receptor protein, alpha-like chain 2 precursor.

GN Drosophila melanogaster (fruit fly).

OS Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

QY	234	FENLIVPCVLISSMALLGFTTPPSGGKLTGLGVITLLSVFLNLVAETLPQVSDAIPLL	293
Db	265	TYNLIPCGISYLSVLYLPADSGEKIALCISILLSTQMFLLIIEIIPSTSLAPLL	324
QY	294	GYFNCIMFVASSVVLTVVLYNHYHRTADTHEMPOWIKSVFQLQWLPWILMRSPCKKIT	353
Db	325	GXYLLFTMLLVGLSVVITIIINHYKPSHKMRPWIRFFIIRLPLKLLMRVP----	379
QY	354	RKTIMMTRMRELEKRSKSLIANVLIDIDDDFRHGPPPPNS--TASTGNLGP--GCS-IF	410
Db	380	-KDLLDLAANKINYGLAFSKTEGQALMDQMNSGSSPDSLRRMQGRVAGAGCGNGMH	438
QY	411	RTDFRFSVRSTMEDVGGGLGS-----HHREHLILRE	444
Db	439	VTTATNRF--SGLVGALGGSLTSGYNGLPVSLVSGLDLSDLSVDAARKKYKPFPELEKAIHN	496
QY	445	LQFITARMKKADAEALISDMKFAAMVYVDRFLCVFTLFTIATVAVLLSAPHI	498
Db	497	VNFIOHHMQRQDEFNAEDQMGFVAMVMDRLFLWLFMIASLVGTGVTILGEAPSL	550
		[1]	
RESULT 15			
ACH6 HUMAN			
ID	ACH6_HUMAN	STANDARD:	PRT: 494 AA.
AC	Q15825;		
DC	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	Neuronal acetylcholine receptor protein, alpha-6 chain precursor.		
GN	CHRNA6.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NCBI_Taxid	9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-Substantia nigra;		
RC	MEDLINE-97062879; PubMed-8906617;		
RA	Ellrott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,		
RA	Chavez-Noriega L.E., Johnson E.C., Velliccebi G., Harpold M.M.;		
RT	"Comparative structure of human neuronal alpha 2-alpha 7 and beta		
RT	2-beta 4 nicotinic acetylcholine receptor subunits and functional		
RT	expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and		
RT	beta 4 subunits.";		
RL	J. Mol. Neurosci. 7:217-228(1996).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Groot Kormelink P.J.;		
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	Ebihara M., Ohba H., Yoshikawa T.;		
RT	"Alu and other elements in the promoter of human nAChR A6 gene		
RT	(CHNRA6) direct transcriptional repression.";		
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-Skin;		
RC	MEDLINE-22388257; PubMed-12477932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		

```
Db 94 KLRDPMYDGIETLRVPADKIWRPDIVLYNNVGDQVEGKTKALKYNGMITWTPPAI 153
Qy 143 FKSTCKMDIAWFPDQHQCDKMGSWTYDGNQDLVLKDEAGG--DLSDFITNGEWYLI 200
Db 154 FKSSCPMDITFFPDHQNCSLKFGSWTYDKAEIDLLI---IGSKVDMNDFWENSEWEI 210
Qy 201 MPQKKNITTYACCPPEPVVOTFTIMIRRTLYYFFNLIVPCVLISSMALLGFTLPDPS 260
Db 211 ASGYKHDIKYNCCIEIYTDITYSFYIRRLPMFYTNLIIPCLFTSFTLVLYVLPDCE 270
Qy 261 KLTGLVTLLSLVFLNVAETLPQVSDAIPLLGTYFNCIMFMVASSVLTVVVLYNHH 320
Db 271 KVTLCISVLLSVFLVLTITETIPSTSLVPLVGEYLLFTMIEFTLSIVVTVFLNIH 330
Qy 321 TADIHEMPOWIKSVFLQWLPWILRMSRPGKKITRKTTIMMNTMRLELEKERSKSLIAN 380
Db 331 TPPTHMPRWKVTVFLKLLPQVLLMRWPLDK-TRGT---GSDAVPRCLARRPAKGLAS 385
Qy 381 LDIDDDFRHGPP-----PPNSTASTGNLPGGCSIFRTDFRRSFVRPS--TWEDVG 428
Db 386 -----HGEPRHLKECFCHKSNELA-----TSKRRLSHQPLQWVVEN-- 422
Qy 429 GGLGSHHRELHLILRELQFITARMKKADEAEELISDMKFAAMVVDRECLFVFTLT 488
Db 423 ---SEHSPEVEDVINSVOFAENKMSHNETKEVEDDMKYVAMVVDVFLWVFIIVCV 479
Qy 489 VAVLL 493
Db 480 AGLFL 484
```

Search completed: August 13, 2003, 15:26:13
Job time : 12.4907 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:21:45 ; Search time 18.7131 Seconds
(without alignments)
2574.698 Million cell updates/sec

Title: US-09-303-232-6
Perfect score: 2640
Sequence: 1 MAPMLALALLLPVSEQ.....LFTTIATVAVLLSAPHIVQ 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1260	47.7	502	1 ACHUA7	nicotinic acetylch
2	1255.5	47.6	502	2 A57175	nicotinic acetylch
3	1253	47.5	502	2 JN0113	nicotinic acetylch
4	1252.5	47.4	502	2 G02259	alpha 7 neuronal n
5	1246.5	47.2	502	2 T01378	nicotinic receptor
6	1237.5	46.9	498	2 S68588	nicotinic acetylch
7	1226.5	46.5	511	2 JH0173	alpha-bungarotoxin
8	1132	42.9	461	2 T25671	hypothetical prote
9	1083.5	41.0	542	2 T19862	hypothetical prote
10	1081	40.9	560	2 T19622	hypothetical prote
11	989	37.5	503	2 A53956	nicotinic acetylch
12	982.5	37.2	502	2 A37040	nicotinic acetylch
13	970.5	36.8	495	2 S60589	acetylcholine rece
14	970.5	36.8	499	2 A24572	nicotinic acetylch
15	964.5	36.5	567	1 ACPFA1	nicotinic acetylch
16	944	35.8	557	2 S12359	nicotinic acetylch
17	943	35.7	576	1 ACPFA2	nicotinic acetylch
18	929.5	35.2	494	2 T09289	nicotinic acetylch
19	924.5	35.0	528	1 ACPH2N	nicotinic acetylch
20	919.5	34.8	512	2 A37014	nicotinic acetylch
21	919	34.8	511	2 A40110	nicotinic acetylch
22	910	34.5	500	2 S12899	nicotinic acetylch
23	909.5	34.5	495	2 B35721	nicotinic acetylch
24	906.5	34.3	517	2 A30992	probable nicotinic
25	906	34.3	457	1 ACBOA1	nicotinic acetylch
26	905	34.3	457	1 ACHUA1	nicotinic acetylch
27	901	34.1	521	1 ACPFNN	nicotinic acetylch
28	900	34.1	503	2 JH0174	nicotinic acetylch
29	897.5	34.0	627	2 JC4021	nicotinic acetylch

30	896	33.9	456	1 ACHHAN	nicotinic acetylch
31	895	33.9	502	2 S10505	nicotinic acetylch
32	891	33.8	622	1 ACH4N	nicotinic acetylch
33	890	33.7	457	2 S13872	nicotinic acetylch
34	890	33.7	470	2 A39218	nicotinic acetylch
35	888	33.6	625	2 A26456	nicotinic acetylch
36	887	33.6	498	2 G02421	nicotinic acetylch
37	885.5	33.5	459	2 S14703	nicotinic acetylch
38	885	33.5	457	2 A24383	nicotinic acetylch
39	883.5	33.5	445	2 I49458	acetylcholine rece
40	881	33.4	491	1 ACPHNN	nicotinic acetylch
41	879.5	33.3	461	2 I50548	acetylcholine rece
42	876.5	33.2	461	1 ACRYAL	nicotinic acetylch
43	875.5	33.2	457	2 A28529	nicotinic acetylch
44	869.5	32.9	457	2 S08162	nicotinic acetylch
45	862	32.7	559	2 E89134	protein F25G6.4 [1

ALIGNMENTS

RESULT 1

ACHUA7

nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human
N:Alternate names: cholinergic nicotinate receptor alpha-7 chain
C:Species: Homo sapiens (man)
C>Date: 12-Aug-1996 #sequence_revision 31-Jan-1997 #text_change 22-Jun-1999
C:Accession: I37185; A54194; S60309
R:Peng, X.; Katz, M.; Gerzanich, V.; Anand, R.; Lindstrom, J.
Mol. Pharmacol. 45, 546-554, 1994
A:Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from th
omers expressed in Xenopus oocytes.
A:Reference number: I37185; MUID:94195283; PMID:8145738
A:Accession: I37185

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-502 <PEN>

A:Cross-references: EMBL:X70297; NID:9496606; PION:CAA49778.1; PID:9496607

A:Experimental source: brain neuroblastoma cell line SHSY-5Y

R:Chini, B.; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzaretti, M.; Heinemann, S.

Genomics 19, 379-381, 1994

A:Title: Molecular cloning and chromosomal localization of the human alpha-7-nicotini

A:Reference number: A54194; MUID:94245214; PMID:8188270

A:Accession: A54194

A:Molecule type: mRNA

A:Residues: 24-363, 'S', 365-374, 'A', 376-408, 'AWPAP', 414-502 <CHI>

A:Cross-references: GB:223141; NID:9457736; PIDN:CAA80672.1; PID:9457737

A:Experimental source: retina

C:Comment: this acetylcholine receptor is blocked by alpha-bungarotoxin and is locali

C:Genetics:

A:Gene: GDB:CHRNA7

A:Cross-references: GDB:138751; OMIM:118511

A:Map position: 15q14-15q14

A>Note: defects in this gene have been associated with mental retardation and schizop

C:Superfamily: acetylcholine receptor

C:Keywords: brain; glycoprotein; heteropentamer; ion channel; neurotransmitter recept

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pr

F:262-280/Domain: transmembrane #status predicted <TR1>

F:296-317/Domain: transmembrane #status predicted <TR2>

F:470-488/Domain: transmembrane #status predicted <TR3>

F:46-90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:150-164/Disulfide bonds: #status predicted

F:365,413/Binding site: phosphate (Ser) (covalent) #status predicted

F:415/Binding site: phosphate (Thr) (covalent) #status predicted

F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 47.7%; Score 1260; DB 1; Length 502;

Best Local Similarity 48.5%; Pred. No. 2 6e-99;

Matches 247; Conservative 75; Mismatches 137; Indels 50; Gaps 6;

Qy 12 ALLPVSSQGPHEKRLNALLANTYLERPVANSEPLEVRFGTLQOIIDVDEKKNOLLIT 71
 Db 15 SLLHVSLLQSGFQKLYKELVGNKYNPLRPVANDSQPLTVYFSLSLQIMDVDEKKNOLLIT 74
 Qy 72 NIWLSLEWYNDYNLRWNSDSEYGVKDLRITPNKLNKPDVLMYNSADEGFGDTYQTNVVR 131
 Db 75 NIWLSWMTDHYLQWNVSEYGVKDLRITPNKLNKPDVLMYNSADEGFGDTYQTNVVR 134
 Qy 132 GGSCLYVPPGIFKSTCKMDIAWPFDDQCHDMKFGSWTYDGNOLDLVKDEAGGDLSDFI 191
 Db 135 SGHCQYLPPIKSSCYIDVRWPFDDQCHDMKFGSWTYDGNOLDLVKDEAGGDLSDFI 191
 Qy 192 TNGEWYLLGMPGKNTITYACCPPEYVDVTFITIMRRRTLYFFNLIYPCVLISSMALLG 251
 Db 192 PNGEDLVGIPGRSERFEYCKEPEYVDVTFITIMRRRTLYFFNLIYPCVLISSMALLG 251
 Qy 252 FTLPDPSGEKLTGLVITLLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFYASSVLT 311
 Db 252 FLTPDPSGEKLTGLVITLLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFYASSVLT 311
 Qy 312 VVVLNYHRTADITHMPQWIKSVFLQWLPWILRMSRPGKKTIRKTIIMNTRMRELELKER 371
 Db 312 VIVLYHHDPDGGKMPKWTIRILLNWCANFLMRKPGEDKVRPACQHKQRCSLASVEM 371
 Qy 372 SSKSLIANVLIDDDFRHGGPPPNSTASTGNL-----GPGCSIFRT 412
 Db 372 SAV-----GPPP-----ASGNLLYIGRGLDGVHCVPDTPDSGVVCG---- 408
 Qy 413 DFRSFVYRSTMEDV---GGGLGSHHRELHLILRELOFITARMKKADEAEELISDWKFAAM 470
 Db 409 ---RMACSPHDEHLLGGPPEGDPDLAKILEEVRYIANFRQDESEAVCSSEWKAAC 465
 Qy 471 VDRFCLFVFTLTITATVALLSAPHII 499
 Db 466 VDRCLCLMAFSVFTICTIGILMSAPNFV 494

RESULT 2
 A57175
 nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Aug-1999
 C:Accession: A57175
 R:Orr-Urtreger, A.; Seldin, M.F.; Baldini, A.; Beaudet, A.L.
 Genomics 26, 399-402, 1995
 A:Title: Cloning and mapping of the mouse alpha7-neuronal nicotinic acetylcholine receptor
 A:Reference number: A57175; MUID:95324936; PMID:7601470
 A:Accession: A57175
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-502 <ORR>
 A:Cross-references: GB:L37663; NID:g790853; PIDN:AAC42053.1; PID:g790854
 C:Superfamily: acetylcholine receptor
 C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein;
 F:1-23/Domain: signal sequence #status predicted <Sig>
 F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain; neuronal #status predi
 F:21-254/Domain: transmembrane #status predicted <TR1>
 F:262-280/Domain: transmembrane #status predicted <TR2>
 F:296-317/Domain: transmembrane #status predicted <TR3>
 F:470-488/Domain: transmembrane #status predicted <TR4>
 F:46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:365,413,427/Binding site: phosphate (Ser) (covalent) #status predicted
 F:415/Binding site: phosphate (Thr) (covalent) #status predicted
 F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 47.68; Score 1255.5; DB 2; Length 502;
 Best Local Similarity 49.68; Pred. No. 6.3e-99;
 Matches 249; Conservative 78; Mismatches 148; Indels 27; Gaps 7;

Qy 8 LALLPVSEQGPHEKRLNALLANTYLERPVANSEPLEVRFGTLQOIIDVDEKKN 66
 Db 10 LALAAALLVSLQGEFORRKYKELVGNKYNPLRPVANDSQPLTVYFSLSLQIMDVDEKKN 69

Qy 67 QLLITNIWLSLEWYNDYNLRWNSDSEYGVKDLRITPNKLNKPDVLMYNSADEGFGDTYQTN 126
 Db 70 QVLTITNIWLSWMTDHYLQWNVSEYGVKDLRITPNKLNKPDVLMYNSADEGFGDTYQTN 129
 Qy 127 VVVRSGSCLYVPPGIFKSTCKMDIAWPFDDQCHDMKFGSWTYDGNOLDLVKDEAGG 186
 Db 130 VLVNASHGHCQYLPPIKSSCYIDVRWPFDDQCHDMKFGSWTYDGNOLDLVKDEAGG 186
 Qy 187 LSDFITNGEWYLLGMPGKNTITYACCPPEYVDVTFITIMRRRTLYFFNLIYPCVLISS 246
 Db 187 ISSYIPNGEWDLMGIPGKNEKEFEYCKEPEYVDVTFITIMRRRTLYFFNLIYPCVLISA 246
 Qy 247 MALLGFTLPDPSGEKLTGLVITLLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFYAS 306
 Db 247 LALLVLLPADSGEKISLIGITVLLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFYAS 306
 Qy 307 SVVLTVVVLNYHRTADITHMPQWIKSVFLQWLPWILRMSRPGKKTIRKTIIMNTRMREL 366
 Db 307 SVVVTIVLVRYHHDPDGGKMPKWTIRILLNWCANFLMRKPGEDKVRPACQHKPRCSL 366
 Qy 367 ELKERSS---KSLIANVLIDDDFR-----HGPPPNSTASTGNLPGCSIFRTDFRRS 417
 Db 367 ASVELSAGAGPPTSGNLLYI---GFRGLEGMHCAPTDSGVVCGRL--ACSPTHDEHLMH 422
 Qy 418 FVPRSTMEDVGGGLGSHHRELHLILRELOFITARMKKADEAEELISDWKFAAMVDRFCL 477
 Db 423 GTHPSGDP-----DLAKILEEVRYIANFRQDESEVICSSEWKAACVDRCL 472
 Qy 478 FVFTLTITATVALLSAPHII 499
 Db 473 MAFSVFTICTIGILMSAPNFV 494

RESULT 3
 JN0113
 nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken
 N:Alternate names: alpha-bungarotoxin-binding protein alpha chain
 C:Species: Gallus gallus (chicken)
 C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1999
 C:Accession: JN0113; JH0172; S28018; B25738; S26566
 R:Couturier, S.; Bertrand, D.; Matter, J.M.; Hernandez, M.C.; Bertrand, S.; Millar, N.
 Neuron 5, 847-856, 1990
 A:Title: A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is development
 A:Reference number: JN0113; MUID:91097796; PMID:1702646
 A:Accession: JN0113
 A:Molecule type: DNA
 A:Residues: 1-502 <COU>
 A:Cross-references: GB:X68586; NID:g287756; PIDN:CAA48576.1; PID:g287757
 A:Experimental source: white leghorn; brain
 R:Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
 Neuron 5, 35-48, 1990
 A:Title: Brain alpha-bungarotoxin binding protein cDNAs and MABs reveal subtypes of t
 A:Reference number: JH0172; MUID:90315158; PMID:2369519
 A:Accession: JH0172
 A:Molecule type: mRNA
 A:Residues: 1-502 <SCH>
 A:Cross-references: EMBL:X52295; NID:g63077; PIDN:CAA36543.1; PID:g63078
 A:Experimental source: brain
 R:Matter-Sadzinski, L.; Hernandez, M.C.; Rostocil, T.; Ballivet, M.; Matter, J.M.
 EMBO J. 11, 4529-4538, 1992
 A:Title: Neuronal specificity of the alpha7 nicotinic acetylcholine receptor promoter
 A:Reference number: S28018; MUID:93049204; PMID:1425587
 A:Accession: S28018
 A:Molecule type: DNA
 A:Residues: 1-18 <MAS>
 A:Cross-references: EMBL:X68246; GB:S49751; NID:g65319; PIDN:CAA48317.1; PID:g65320
 A:Experimental source: white leghorn; erythrocyte
 R:Conti-Tronconi, B.M.; Dunn, S.M.J.; Barnard, E.A.; Dolly, J.O.; Lai, F.A.; Ray, N.;
 Proc. Natl. Acad. Sci. U.S.A. 82, 5208-5212, 1985
 A:Title: Brain and muscle nicotinic acetylcholine receptors are different but homolog
 A:Reference number: A94055; MUID:85270494; PMID:3860855
 A:Accession: B25738
 A:Molecule type: protein

A:Residues: 24-25, 'ET', 28-41, 'X', 43-45, 'X', 47 <CON>
 C:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localized
 C:Genetics:
 A:Introns: 19/1; 65/3; 80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3
 C:Superfamily: acetylcholine receptor
 C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein;
 F:1-23/Domain: signal sequence status predicted <SIG>
 F:24-302/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predicted
 F:231-254/Domain: transmembrane #status predicted <TR1>
 F:262-280/Domain: transmembrane #status predicted <TR2>
 F:296-317/Domain: transmembrane #status predicted <TR3>
 F:470-488/Domain: transmembrane #status predicted <TR4>
 F:46,90,133/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:365,367,413,427,465/Binding site: phosphate (Ser) (covalent) #status predicted
 F:415/Binding site: phosphate (Thr) (covalent) #status predicted
 F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 47.5%; Score 1253; DB 2; Length 502;
 Best Local Similarity 48.8%; Pred. No. 1e-98;
 Matches 250; Conservative 81; Mismatches 145; Indels 36; Gaps 8;

QY 2 APMALALLALLPVSEQPEHEKRLNALLNANYTLERPVANSEPLEVRFGTLTQOIID 61
 DB 5 ALMLWLLAAGLVRESLQGEFQKLYKELKNYPLERPVANDSPLTYFTLSLQIMD 64
 QY 62 VDEKNOLLITNIWLSLEWNDYLNLRWNSYGGVKDLRITPNKLPKDVLMYNSADEGFDG 121
 DB 65 VDEKNQVLTNIWLOWMTDHYLQWNVSEYPGVKVRFDPGLIWKPDILLYNSADERFPA 124
 QY 122 TYQTNVVRSGLYVPPGIFKSTCKMDIAWFPDDQDCHDKMFGSWTYDGNLDLVLKD 181
 DB 125 TPTNTNVLNSSGHCQLPPLGIFKSCYIDVRWFPDQVCKNLKFGSWTYGGWSLDLQMOE 184
 QY 182 EAGGDLSDITNGEWYLGMPGKNTITYACCPYVDVTFTIMRRRTLYFFENLIVPC 241
 DB 185 ---ADISGYISNGEWDLVGIPKRSERFYECCKEPYDITFTVTRRRRTLYGLNLLIPC 241
 QY 242 VLISSMALGFTLPDPSGKELGLVITLLSVFLNVAETLPQVSDAIPLLGLTYFNCIM 301
 DB 242 VLISALALLVFLPADSGEKISLIGITVLLSVFLLVAEIMPATSDSVPLIAQYFASTM 301
 QY 302 FMVASSVLTVVVLYNHHRTADIHMPQWIKSVFLOWLPWILRMSRPGKIKTRKTMNT 361
 DB 302 IIVGLSVVTVIVLQYHHHDPDGGKMPKWTTRVILLNWCAMFLRMKPGEDKVRPACQHKQ 361
 QY 362 RMRELKERSKS-----LLANVLIDDDFR-----HGPPPNSTASTNLGPGCSIFRT 412
 DB 362 RCCLSSMEMNTVSGOCSNGNMLYI--GFRGLDGVHCTPTTDSGVICGM--TCS---- 413
 QY 413 DFRSRFVRPTMEDVGGGLGSHH-----RELHLILRELQFITARMKKADEEAELISDKWF 467
 DB 414 -----PTEENL---LHSGHPSEGDPLAKILEEVRYIANRFRQDEEAICNEWK 462
 QY 468 AAMVDRFCLFVFTFTIATVAVLLSAPHII 499
 DB 463 AASVDRCLCMAFSVFTIICITIGILMSAPNFV 494

RESULT 4
 G02259
 alpha 7 neuronal nicotinic acetylcholine receptor - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
 C:Accession: G02259
 R:Leonard, S.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: H00936
 A:Accession: G02259
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-502 <LEO>
 A:Cross-references: EMBL:U40583; NID:g1125076; PIDN:AAA83561.1; PID:g1125077
 C:Superfamily: acetylcholine receptor

Query Match 47.4%; Score 1252.5; DB 2; Length 502;
 Best Local Similarity 48.4%; Pred. No. 1.1e-98;
 Matches 249; Conservative 74; Mismatches 140; Indels 51; Gaps 7;

QY 8 LALLA-LLPVSSQGPHEKRLNALLNANYTLERPVANSEPLEVRFGTLTQOIIDVDEKN 66
 DB 10 LALAAALLHVSLQGEFQKLYKELKNYPLERPVANDSPLTYFTLSLQIMDVK 69
 QY 67 QLLITNIWLSLEWNDYLNLRWNSYGGVKDLRITPNKLPKDVLMYNSADEGFDGYQT 126
 DB 70 QVLTNTNWLQWMTDHYLQWNVSEYPGVKVRFDPGQIWKPDILLYNSADERDATFTN 129
 QY 127 VVRSGLYVPPGIFKSTCKMDIAWFPDDQDCHDKMFGSWTYDGNLDLVLKDEAGD 186
 DB 130 VLVNPSGHCQLPPLGIFKSCYIDVRWFPDQVCKNLKFGSWYGGWSLDLQMOE--AD 186
 QY 187 LSDFTNGEWYLGMPGKNTITYACCPYVDVTFTIMRRRTLYFFENLIVPCVLIS 246
 DB 187 ISGYIPNGEWDLVGIPKRSERFYECCKEPYDITFTVTRRRRTLYGLNLLIPC 246
 QY 247 MALLGFTLPDPSGKELGLVITLLSVFLNVAETLPQVSDAIPLLGLTYFNCIMFVAS 306
 DB 247 LALLVFLPADSGEKISLIGITVLLSVFLLVAEIMPATSDSVPLIAQYFASTMI 306
 QY 307 SVVLTVVVLYNHHRTADIHMPQWIKSVFLOWLPWILRMSRPGKIKTRKTMNTRMREL 366
 DB 307 SVVTVTVIVLQYHHHDPDGGKMPKWTTRVILLNWCAMFLRMKPGEDKVRPACQHK 366
 QY 367 ELKERSKSLANVLIDDDFRHGPPPNSTASTGNL-----GPGC 407
 DB 367 ASVMSAVA-----PPP-----ASGNLLYIGFRGLDGVHCTPTTDSGVVVC 407
 QY 408 SIFRTDFRSFVRPTMEDV--GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW 465
 DB 408 G-----RMACSPHDEHLLHGQPGEPDOLAKILEEVRYIANRFRQDESEAVCSEW 460
 QY 466 KFAAMVDRFCLFVFTFTIATVAVLLSAPHII 499
 DB 461 KFAACVDRCLCMAFSVFTIICITIGILMSAPNFV 494

RESULT 5
 T01378
 nicotinic receptor alpha 7 chain - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
 C:Accession: T01378
 R:Seguela, P.; Wadiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W.
 J. Neurosci. 13, 596-604, 1993
 A:Title: Molecular cloning, functional properties, and distribution of rat brain alpha
 A:Reference number: Z14310; MUID:93147931; PMID:7678857
 A:Accession: T01378
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-502 <SEG>
 A:Cross-references: EMBL:S53987; NID:g264770; PIDN:AAAB25224.2; PID:g5705903
 A:Experimental source: brain
 C:Superfamily: acetylcholine receptor

Query Match 47.2%; Score 1246.5; DB 2; Length 502;
 Best Local Similarity 49.4%; Pred. No. 3.7e-98;
 Matches 248; Conservative 78; Mismatches 149; Indels 27; Gaps 7;

QY 8 LAL-LLLPVSSQGPHEKRLNALLNANYTLERPVANSEPLEVRFGTLTQOIIDVDEKN 66
 DB 10 LALAAALLHVSLQGEFQKLYKELKNYPLERPVANDSPLTYFTLSLQIMDVK 69
 QY 67 QLLITNIWLSLEWNDYLNLRWNSYGGVKDLRITPNKLPKDVLMYNSADEGFDGYQT 126
 DB 70 QVLTNTNWLQWMTDHYLQWNVSEYPGVKVRFDPGQIWKPDILLYNSADERDATFTN 129
 QY 127 VVRSGLYVPPGIFKSTCKMDIAWFPDDQDCHDKMFGSWTYDGNLDLVLKDEAGD 186

Db 130 VLVNASGCOYLPPGIFKSSCYIDVRWFFPDVQCKLKFSGWSYGGWSLDQHOE---AD 186
Qy 187 LSFDFITNGEWYLGMPGKKNITACCPPEYVDVTFITIMRRRTLYFFNLVPCVLISS 246
Db 187 ISSVIPNGEWDLMGIPKRNKEFYECCKEYPPDVTVTVTMRRTLYGLNLLIPCVLISA 246
Qy 247 MALLGFTLPDPGSEKLTGLVTILLSTVFNVAETLPQVSDAIPLLGTFFNCFMFWAS 306
Db 247 LALLVFLPADSGEKISIGITVLLSTVFNVAETLPQVSDAIPLLGTFFNCFMFWAS 306
Qy 307 SVLTVVVLVNYHRTADIEHMPQWIKSVFQWLPWILRMSRPGKKTIRKTIIMNTRMREL 366
Db 307 SVVTVVILVYHHDDPGGKMPKWTIRILLNWCANFLMRKPGEDKVRPAQCKHPRCSL 366
Qy 367 ELKERS--KSLANVLDDDFR-----HGPPPPNSTASTGNLPGGCSIFRTDFRRS 417
Db 367 ASVELSAGAGPPTSGNLLYI--GFRGLEGMHCAPTDSGVVCGRL--ACSPHDEHLMH 422
Qy 418 FVRPSTMEDVGGGLSGSHHRELHLILRELQFIATMKKADEAEELISDKWFAAMVVDRCFL 477
Db 423 GAHPSDGP-----DLAKILEVRVIANRRCODESEVICSEWKFACVVDPLCL 472
Qy 478 FVFTLTIIATVALLSAPHII 499
Db 473 MAFSVFTIICITIGILSAPNFV 494

RESULT 6
S68588
nicotinic acetylcholine receptor alpha-1 chain precursor (clone Ce21) - Caenorhabditis e
C:Species: Caenorhabditis elegans
C:Date: 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 20-Aug-1999
C:Accession: S68588; S57496
R:Ballivet, M.; Alliod, C.; Bertrand, S.; Bertrand, D.
J. Mol. Biol. 258, 261-269, 1996
A:Title: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans.
A:Reference number: S68587; MUID:96196478; PMID:8627624
A:Accession: S68588
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-498 <BAL>
A:Cross-references: EMBL:X83887; NID:g872087; PIDN:CAA58764.1; PID:g872088
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-498/Product: nicotinic acetylcholine receptor alpha-1 chain #status predicted <MAT>

Query Match 46.9%; Score 1237.5; DB 2; Length 498;
Best Local Similarity 47.5%; Pred. No. 2.1e-97;
Matches 245; Conservative 80; Mismatches 140; Indels 51; Gaps 9;
Qy 2 APLAALLALLPVSQGPHEKRLNALLANYNTLERPVANESLEPVRFLTQLOIID 61
Db 15 APTGLS-----QERLYEDLMRYNLERPVANHSEPTVHLKVALQLOIID 61
Qy 62 VDERKQLITNWLSEWNYNLRWNSDEYGGVKDLRITPNKLNKPKDVLNYSADGFDG 121
Db 62 VDERKQVYVNAWLDYTNWNLVMDKAEYGNITDVRFPAGKINPKDVLNYSVDTFNDS 121
Qy 122 TYQTNVVRSGCLYVPPGIFKSTCKMDIAWFFPDQCHDMKFGSWTYDGNOLDVLKD 181
Db 122 TYQTNMIVYGLVHHVWPPGIFKSTCKMDIAWFFPDQCHDMKFGSWTYDGYKLD--LQP 179
Qy 182 EAGG-DLSDFITNGEWYLGMPGKKNITACCPPEYVDVTFITIMRRRTLYFFNLVPC 240
Db 180 ATGDFDISEYLSNGEAWPLTTVERNEKFYCCPEYPDVHFVHLHMRRTLYYGNLIMP 239
Qy 241 CVLISSMALLGFTLPDPGSEKLTGLVTILLSTVFNVAETLPQVSDAIPLLGTFFNCF 300
Db 240 CILTTLMTLGLFTLPDAGEKITLQITVLLSCFFLSIVSEMSPTSEAVPLLGIFFTCC 299
Qy 301 MFWASSVVLVNYHRTADIEHMPQWIKSVFQWLPWILRMSRPGKKTIRKTI--M 358

Db 300 MIVVSTASTVTVVNLNHYETPTHDMGPWTRNLLLYWIPILMRKPGHNLIVASPLS 359
Qy 359 MNTRMRELELKERSKSLANVLID-----IDDFRHGPPPPNSTASTGNLPGCCS 408
Db 360 FSTK-----PNHSESLIRNIKDNEHLSRANSFADACRLNQYITQTSVSNGLTSLG-S 412
Qy 409 IFRDTRRSFVRSTMEDVGGGLSGHRE-----LHLILRELQFIATMKKADEAEELIS 463
Db 413 I-----PSTMISSNGTTDVSQATLILHRIYHELKIVTARMIEGDEKQEOACN 461
Qy 464 DKWFAAMVDRFCFLFVFTLETTIATVALLSAPHII 499
Db 462 NWKFAAMVDRCLYVETIIVSTIGIFWSAPLV 497

RESULT 7
JH0173
alpha-bungarotoxin-binding protein alpha-2 chain precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Aug-1999
C:Accession: JH0173
R:Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
Neuron 5, 35-48, 1990
A:Title: Brain alpha-bungarotoxin binding protein cDNAs and Mabs reveal subtypes of t
A:Reference number: JH0172; MUID:90315158; PMID:2369519
A:Accession: JH0173
A:Molecule type: mRNA
A:Residues: 1-511 <SCH>
A:Cross-references: GB:X52296; NID:g63081; PIDN:CAA36544.1; PID:g63082
A:Experimental source: brain
A:Note: this sequence is similar to acetylcholine receptor alpha chains
C:Comment: Alpha-bungarotoxin binding proteins are localized to extrasynaptic pseudod
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-510/Product: alpha-bungarotoxin binding protein alpha-2 chain #status predicted
F:239-262/Domain: transmembrane #status predicted <TM1>
F:270-288/Domain: transmembrane #status predicted <TM2>
F:304-323/Domain: transmembrane #status predicted <TM3>
F:479-496/Domain: transmembrane #status predicted <TM4>
F:54/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 46.5%; Score 1226.5; DB 2; Length 511;
Best Local Similarity 46.6%; Pred. No. 1.9e-96;
Matches 246; Conservative 75; Mismatches 134; Indels 73; Gaps 9;
Qy 5 LAALLALLPVSQGPHEKRLNALLANYNTLERPVANESLEPVRFLTQLOIIDVDE 64
Db 16 LWASLFLSFFKVSQGESORRLYRDLNRYNLERPVNDSQPIVVELQLSLQIIDVDE 75
Qy 65 KQOLLITNWLSEWNYNLRWNSDEYGGVKDLRITPNKLNKPKDVLNYSADGFDGTYQ 124
Db 76 KQVLLITNAWLMQVWDYLSWQYEPYQVGNLRFPDQIIVPDPILLYNSADERDATFH 135
Qy 125 TNVVRSGCLYVPPGIFKSTCKMDIAWFFPDQCHDMKFGSWTYDGNOLDVLKDEAG 184
Db 136 TNVLRVYSGSQYIPPGILKSTCIDVWFFPDQCHDMKFGSWTHSGWLDLQMLE--- 192
Qy 185 GDLSDFITNGEWYLGMPGKKNITACCPPEYVDVTFITIMRRRTLYFFNLVPCVLI 244
Db 193 ADISNYISNGEAWLVGPGKRNELYECCKEYPDVTVITMRRTLYYGLNLLIPCVLI 252
Qy 245 SSMAALLGFTLPDPGSEKLTGLVTILLSTVFNVAETLPQVSDAIPLLGTFFNCFMFW 304
Db 253 SGLALLVFLPADSGEKISIGITVLLSTVFNVAETLPQVSDAIPLLGTFFNCFMFW 312
Qy 305 ASSVVLTVVLYNYHRTADIEHMPQWIKSVFQWLPWILRMSRPGKKTIRKTIIMNTRM 364
Db 313 GLSVVTVVLVQLQFHDPQAGKMPRWVRIILNWCANFLMRKPGEDKVRPAQCKHPRCS 361
Qy 365 ELELK-----ERSKSLANVLDDDFRHHGPPPPNSTASTGNL-----GPGCSIF 410

Db 362 PLCKSYKPKHPSLKNTEENVL-----PGHQPSNGNMIIYHTMENPCC--- 406
Qy 411 RTDFRRSVRPSTMEDVGGGLG-----SHRELHL-----ILRELQFTAR 451
Db 407 -----PQN-NDLGSGSGKTCPLSDNEHVKQKALMDTIPVIVKILEEVOFTAMR 455
Qy 452 MKKADAEALISDWKFAAMVVDVRFCLFVFTLTITATVAVLLSAPHII 499
Db 456 FRKODEGEEICSEKFAAAVIDRLCLVAFTLFAICTTILMSAPNFI 503

RESULT 8
T25671
hypothetical protein D2092.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T25671
R:Gattung, S.; Maggi, L.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid D2092.
A:Reference number: Z20067
A:Accession: T25671
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-461 <GAT>
A:Cross-references: EMBL:U88167; PIDN:AAB42223.1; GSPDB:GN00019; CESP:D2092.3
A:Experimental source: strain Bristol N2; clone D2092
C:Genetics:
A:Gene: CESP:D2092.3
A:Map position: 1
A:Introns: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2
C:Superfamily: acetylcholine receptor

Query Match 42.9%; Score 1132; DB 2; Length 461;
Best Local Similarity 44.7%; Pred. No. 1.9e-88;
Matches 216; Conservative 86; Mismatches 127; Indels 54; Gaps 6;

Qy 23 EKRLNALLANYTLERPVANSEPLEVRFGTLQIIDIYDEKNQLITNINWLSLEWNDY 82
Db 26 ETKLFTDLKGYNPLRPVQNSQPLEVKIKLFLQQLIDVDEKNQIVSNWNLSTWFDH 85
Qy 83 NLRWNSDSEGVKDLRI--TPNKLWKPDLVLYNSADEGDTGTQTNVVRSGGSLVYPP 140
Db 86 KLQWEPKYGIGDIIRFPSSDHIWKRPDVLNLYNSAAEDFSTFKSNLLTYHTGTVMWIP 145
Qy 141 GIFKSTKMDIANFPDDQDCMKFGSWTYDGNQLDLVLDKDEAG--DLSDFITNGEW 196
Db 146 GVLKVCOLDVTFEPDDQVCMKFGSWTFHGAIDLQIDDDTNGTQSMDLSTLYLVNGEW 205
Qy 197 YLIGMPGKNTITYACCPYVDVTFIMIRRTLYFFNLIVPCVLISSMALLGFTLPP 256
Db 206 QVISTNAKRVSYKCCPEPYPTVNYLHRRRTLYYGENLIIPSLISLMAILGFMFPP 265
Qy 257 DSGEKLTLGVTILLTLVNLVAETLPQVSDAIPLLGTYFCINMFVASSVLTVVVNL 316
Db 266 DAGEKITVETILLAILVFFLSVMSEMTPTSEAVPLIGVFSCCMLWSASVFTVWLN 325
Qy 317 YHRTADIHEMPQWIKSVFLQWLPILRMSRPGCKITRKTIMNTRMRELELERSKSL 376
Db 326 LHFRSADSHENMPLVRVLLLEFLPWLFLMSRPGYKVK----- 363
Qy 377 LANVLIDDDFRIGPPPPNSTASTGNLPGCSTIFRTDFRSFVRPSTMEDVGGGLSHHR 436
Db 364 -ANVIDSTDKMPKPKNPLD-----CNL-----PSN-----HAGYEAQIL 397
Qy 437 ELHLILRELOFTIARMKKADEAEALISDWKFAAMVVDVRFCLFVFTLTITATVAVLLSAP 496
Db 398 LLHSVHTELRVVAFYVFNKEEDHRIQTDRFAAMVVDVRFCLFVFTLTITATVAVLLSAP 457
Qy 497 HII 499
Db 458 HII 460

RESULT 9

T19862
hypothetical protein C40C9.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T19862
R:Hembry, C.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19188
A:Accession: T19862
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-542 <WIL>
A:Cross-references: EMBL:Z70266; PIDN:CAA94206.1; GSPDB:GN00028; CESP:C40C9.2
A:Experimental source: clone C40C9
C:Genetics:
A:Gene: CESP:C40C9.2
A:Map position: X
A:Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1;
C:Superfamily: acetylcholine receptor

Query Match 41.0%; Score 1083.5; DB 2; Length 542;
Best Local Similarity 42.8%; Pred. No. 3.2e-84;
Matches 232; Conservative 86; Mismatches 152; Indels 75; Gaps 13;

Qy 10 LLALLPVSEGGPHEKRLNALLANYTLERPVANSEPLEVRFGTLQIIDIYDEKNQLL 69
Db 17 LFHLLTEVHSADEYRLADLRHNYDPYERPVANASEPLVSVKVIYQQLIDVDEKNQVI 76
Qy 70 ITNINWLSLEWNDYLNWNSDSEGVKDLRI--TPNKLWKPDLVLYNSADEGDTGTQTNV 127
Db 77 TLVAMIEYQWTDYKWKDPSEYGGIKDIRIPGNANAIWKRPDVLNLYNSADENFSTVPVY 136
Qy 128 VYRSGGSLVYPPGIFKSTCKMDIANFPDDQDCMKFGSWTYDGNQLDLVLDKDEAGDL 187
Db 137 VSYTGDVLQVPPGILKLSCKIDITYFPDDQDCMKFGSWTYDGNQLDLVLDKDEAGDL 196
Qy 188 SD-----FITNGEWLIGMPGKNTITYACCPYVDVTFIMIRRTLYFFNLIVP 240
Db 197 SDGIDVQYVQNGENLLAVPARHETNIFD--EQYPSLFFYLLIQRRTLYGLNLIIP 254
Qy 241 CVLISSMALLGFTLPPDSGEKTLGVTILLTLVNLVAETLPQVSDAIPLL-----G 294
Db 255 SFLISLMTVLGFTLPPDAGEKITLITILLSVCFLSWADMTPTSEAVPLIGLIIFSG 314
Qy 295 TYFNCTMFWVASSVLTVVVNLVYHRTADIHEMPQWIKSVFLQWLPILRMSRPGCKITR 354
Db 315 AFFSCMLVSVASVFTVVLVNLHNRKPETHMSPELRELLLIWLPWLLLMRRPG----- 369
Qy 355 KTMNTRMRELELERSKSLIANVLIDDDFRHGGPPPPNSTASTGNLGP--GCSIFRT 412
Db 370 KITFNCTHLKAEKAEKAKGSIKNGV-----GPKRP-----TDSVHPSGLSLMKN 416
Qy 413 -----DFRRSF-----VRPSTM-----ED-VGGGGLSHHREL 438
Db 417 IKLGRQOTIDFEYEFHVNHLMPVAPSEMTPRVTYSKYMAESYVEDVVTMLNKMQA 476
Qy 439 HLILRELOFTIARMKKADEAE--LISDWKFAAMVVDVRFCLFVFTLTITATVAVLLS 494
Db 477 CLEKNISSOTARMKKMEEDERDEQAANDWKFAMVVDVRFCLFVFTLTITATVAVLLS 536
Qy 495 APHII 499
Db 537 SPHLI 541

RESULT 10
T19622
hypothetical protein C31H5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T19622

R:Kershaw, J.
Submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19622
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-560 <WIL>
A:Cross-references: EMBL:Z93778; PIDN:CA07843.1; GSPDB:GN00019; CESP:C31H5.3
A:Experimental source: clone C31H5
C:Genetics:
A:Gene: CESP:C31H5.3
A:Map position: 1
A:Introns: 24/1; 70/3; 139/2; 270/1; 336/3; 372/2; 456/3
C:Superfamily: acetylcholine receptor

Query Match 40.9%; Score 1081; DB 2; Length 560;
Best Local Similarity 39.4%; Pred. No. 5.5e-84;
Matches 218; Conservative 88; Mismatches 155; Indels 92; Gaps 8;
Qy 20 GPHEKRLNALLANYNTPRVANESEPLEVRFGTLTQQIIDVDEKQKLLITNIWLSLEW 79
Db 28 GDHRRLYAKLAENYKLRPVNESEAVVLLGMDYQQILDIDKQHMNSNVWLRMSW 87
Qy 80 NDYNLRNDSYGVKDLRITPNKLPDVLNYSADGFGDYQTNVVRSGSCLYVP 139
Db 88 TDHLYTWDPSFEGNIKEVRLPINNIWKPDLVLLNSVDQDFSTWPNVAVLYTGNVTWIP 147
Qy 140 PGIFKSTCKMDIAWFPDDQCHDMKFGSYDGNQDLVLKDEAGGDLSDFITNGEWYLI 199
Db 148 PAIRSSCAIDIAFPDQCHDMKFGSYDGFDTLI---NTTISPAIKPNEGWEELL 204
Qy 200 GMPGKKNITTYACPEYVDVTFITRRLTYFFNLIYVPCVLISSMALLGFTLPDPSG 259
Db 205 GLTSQRSIFFECCPEYVDVTFVTSIRRLTYGFFNLLPCMLISSALLSFTLPADCG 264
Qy 260 EKLTLGVTILLSTVFLNVAETLPQVSDAIPLLGTGFNCIMEWASSVVLTVVVLNYYH 319
Db 265 EKLMLGVTIFMSLCVFMIMAEAMPQSDALPLIQIIFSCIMFQVGSVATVIALNFHH 324
Qy 320 RTADIHE-MPQWIKSVFLOLWPLILMRSP-----GKTRITKTIIMNTRMR 364
Db 325 RSPQYKPMKFKLTLLGLWPLTLLGMERPDVLESHVGAHSDNKKQKQVILIEVERH 384
Qy 365 ELEKERSKSLANVLIDID-----DDFRHGGPPPNSTAST--GNLPGCCSIFRDFR 415
Db 385 ILTRPNNGHSAVDKAYHLDLSTGNPHSDAKKSPSPKRTSASIMGTG----- 433
Qy 416 RSFVRPSTMEDVGGGLGS----- 433
Db 434 ----LPTT--QMNGALDSSINKYCTKVTTRPLENGSATINHKSSPQINPINNNIYKCAN 487
Qy 434 -----HREHLHLILRELQFITARMKADAEALISDWKFAAMVVDRCFLVFTFTIIA 487
Db 488 NQKTFQEDRHFHLLNELRVISARVKEAMHALQADMEASRVVDRCFLAFSAFLMC 547
Qy 488 TVAVLLSAPHIIV 500
Db 548 TAIISNAPHLFV 560

RESULT 11
A53956
nicotinic acetylcholine receptor alpha-3 chain precursor, neuronal - human
C:Species: Homo sapiens (man)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 20-Aug-1999
R:Mihoilovic, M.; Roses, A. D.
C:Accession: A53956; S21338
A:Title: Expression of mRNAs in human thymus coding for the alpha3 subunit of a neuronal
A:Reference number: A53956; MUID:91114756; PMID:1989896
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-503 <MIH>
A:Cross-references: GB:M37981; NID:g189252; PIDN:AAAS9942.1; PID:g189253
R:Anand, R.; Lindstrom, J.
Submitted to the EMBL Data Library, June 1990
A:Description: Nucleotide sequence of the mature human nicotinic acetylcholine receptor
A:Reference number: S21338
A:Accession: S21338
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 30-503 <ANA>
A:Cross-references: EMBL:X53559; NID:g34985; PIDN:CAA37625.1; PID:g34986
C:Genetics:
A:Gene: GDB:CHRNA3
A:Cross-references: GDB:125219; OMIM:118503
A:Map position: 15q24-15q24
C:Superfamily: acetylcholine receptor
C:Keywords: neurotransmitter receptor

Query Match 37.5%; Score 989; DB 2; Length 503;
Best Local Similarity 38.9%; Pred. No. 3.3e-76;
Matches 202; Conservative 91; Mismatches 164; Indels 62; Gaps 6;
Qy 1 MAPLAALALLALLPVSEQGPHEKRLNALLANYNTPRVANESEPLEVRFGTLTQQII 60
Db 12 VAPRL-LLLLLLLPVARASEAEHRLFERLFEDYNEIIRPVANVSDPVIIHFEVMSQLV 70
Qy 61 DVDEKQKLLITNIWLSLEWYDNLNNDSEYGVKDLRITPNKLPDVLNYSADGFGD 120
Db 71 KVDEVNQIMETNLWLKQIWNNDYKLNKPNPSDYGAEFRVPAQKIKWPKDVLVNNVAGDF 130
Qy 121 GTQTNVVRSGSCLYVPVPGIFKSTCKMDIAWFPDDQCHDMKFGSYDGNQDLVLK 180
Db 131 VDDTKALLKYTGVTWIPPAIFKSSCKIDVTFYFDYQNTMKFGSMDKAKIDLVI 190
Qy 181 DEAGGDLSDITNGEWYLIQMGPKKNTIYACPEYVDVTFITRRLTYFFNLIYV 240
Db 191 G-SSMNLKDYSEGEWALIKAPGYKHDIKYNCEEIYDITYSLYIRRLPLFYTNLIIP 249
Qy 241 CVLISSMALLGFTLPDPSGKLTGVTILLSTVFLNVAETLPQVSDAIPLLGTYNFI 300
Db 250 CLTISFTLVFVLPDSCGEKVTLCISVLLSLTVFLVITETIPSTSLVPLIGEYLLFT 309
Qy 301 MEVASSVVLTVVVLNYYHRTADITHMPQWIKSVFLOLWPLILMRSPGKKITRKTIMN 360
Db 310 MIFVTLISIVTVFVLNYYHRTPTTHMPWSVKTVFVLNLLPRVMTPTP----- 357
Qy 361 TRMRELKERSKSLANVLIDIDDDFRHGGPPPNSTASTGNL-----GPGCS----- 408
Db 358 -----TSNEGNAQKPRPLYGAELSNLNCFSRAESKGCCKEGYPC 395
Qy 409 -----TFRTDFRSFVRPSTMEDVGG--GLGSHHRELHLILRELQFITARMKK 454
Db 396 QDQCMGCGYCHRRRIKISFNLSANLRSSESSESDAVLSLSALSPEIKAEIQSVKYIAENKA 455
Qy 455 ADEAEALISDWKFAAMVVDRCFLVFTFTIIATVAVLL 493
Db 456 QNEAKEIQDDWKVYAMVIDRIFLWVFTLVLCILGTAGLFL 494

RESULT 12
A37040
nicotinic acetylcholine receptor alpha-3 chain precursor, neuronal (version 2) - huma
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C:Accession: A37040; S24595
R:Fornasari, D.; Chini, B.; Tarroni, P.; Clementi, F.
Neurosci. Lett. 111, 351-356, 1990
A:Title: Molecular cloning of human neuronal nicotinic receptor alpha-3-subunit.
A:Reference number: A37040; MUID:90245296; PMID:2336208
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-502 <FOR>
A:Cross-references: EMBL:X52239; NID:g177897; PIDN:AAC84176.1; PID:g177898

C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-502/Product: nicotinic acetylcholine receptor alpha-3 chain #status predicted <MAT>

Query Match 37.2%; Score 982.5; DB 2; Length 502;
Best Local Similarity 38.9%; Pred. No. 1.2e-75;
Matches 199; Conservative 89; Mismatches 163; Indels 61; Gaps 5;

QY 8 LALLALLPVSEQEPHEKRLNALLANTLERPVANESPEVRFGLTLQOIIDVDEKQ 67
DB LLLLSLLPVARASEAERLFEFLFEDYNEIRPVANVSDVVIHFVSSQLVYKVDVQ 76
QY 68 LLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 127
DB IMETNLWLKQIWNKYKLNWPSDYGAEFRVPAEKIWPDIIVLYNNVAGDFQVDDK 136
QY 128 VVRSGSCLYVPPGIFKSTCKMDIANFPDQDCHMKFGSWTYDGNQLDLVLKDEAGD 187
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 195
QY 137 LLKTYGEVTPWIPPAIFKSSCKIDVTYFPDYQNTKMGFSWYDKAKIDLVLIG-SSMNL 247
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 255
QY 188 SDFITNGEWYLGMPGKKNITTYACCPPEPVVDVTFITMIRRRRLTYFFNLIIVPCVLIS 307
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 315
QY 248 ALLGFTLPDPSGKGLTGVTLLSLVFLNVAETLPQVSDAETPLGLTYFNCIMFVASS 367
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 376
QY 256 TVLVFVLPSCDGEKVTLCISVLLSLVFLVITETIPSTSLVIPLIGEYLLFTMIEV 401
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 408
QY 308 VLTITVVLVNYHHHTADIHEMPQIKSVFLOLWLPWILRMSRPGKTIKTRIMNTRMLE 461
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 468
QY 316 IVITVFLVNYHTPTTHTMPVAVKTIIFLLPLRVPMFTMRP----- 502
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 509
QY 368 LKERSKSLLANVLIDDDFRHGPPPPNSTASTGNL-----GPGCS----- 558
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 565
QY 409 -----TSNEGNAQKPRLYCAELSNLNCPSRAESKCKEYPCQDGMCGY 605
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 612
QY 402 CHRRIKISFNFSANLRSSESVDVAVLSALSPEIKAEIOQVYIAENMKRAQNEAKEI 660
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 667
QY 462 ISDMKFAAMVDFRCLFVETLFIATVAVLL 493
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 499
QY 462 QDDWKYVAMVIDRFLWVETLFCILGTAGLFL 493
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 500

RESULT 13
S60589
acetylcholine receptor alpha chain precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
C;Accession: S60589
R;Criado, M.; Alamo, L.; Navarro, A.
Neurochem. Res. 17, 281-287, 1992
A;Title: Primary structure of an agonist binding subunit of the nicotinic acetylcholine
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-495/Product: acetylcholine receptor alpha chain #status predicted <MAT>

Query Match 36.8%; Score 970.5; DB 2; Length 495;
Best Local Similarity 39.8%; Pred. No. 1.2e-74;
Matches 198; Conservative 93; Mismatches 181; Indels 25; Gaps 7;

QY 5 LAALLALLPVSEQEPHEKRLNALLANTLERPVANESPEVRFGLTLQOIIDVDE 64
DB LRLRLRLRLVASTDAEHRFLERFLFEDYNEIRPVANVSDVVIHFVSSQLVYKVD 66

QY 65 KNOLLITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQ 124
DB VQOIMETNLWLKQIWNKYKLNWPSDYGAEFRVPAEKIWPDIIVLYNNVAGDFQVDDK 126
QY 125 TNVVRSGSCLYVPPGIFKSTCKMDIANFPDQDCHMKFGSWTYDGNQLDLVLKDEAG 184
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 185
QY 185 GDLSDFITNGEWYLGMPGKKNITTYACCPPEPVVDVTFITMIRRRRLTYFFNLIIVPCVLI 244
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 245
QY 245 SSMALLGFTLPDPSGKGLTGVTLLSLVFLNVAETLPQVSDAETPLGLTYFNCIMFV 304
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 305
QY 305 ASSVLTIVVVLVNYHHHTADIHEMPQIKSVFLOLWLPWILRMSRPGK---KITRKTMMNT 361
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 365
QY 306 TLSIVITVFLVNYHTPTTHTMPVAVKTIIFLLPLRVPMFTMRPAGNEGTQRPFPYSA 418
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 419
QY 362 RMRELKERSKSLLANVLIDDDFRHGPPPPNSTASTGNLPGCSIFR---TDFRRSF 409
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 418
QY 419 VRPSTMEDVGG--GLGSHHRELHLILRELOQITARMKKADEAEELISDMKFAAMVDRFC 476
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 477
QY 410 TRSSSESVDVAVLSALSPEIKAEIOQVYIAENMKRAQNEAKEIQQDMKYVAMVIDRIF 469
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 470
QY 477 LPVFTLFTIATVAVLL 493
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 493

RESULT 14
A24572
nicotinic acetylcholine receptor alpha-3 chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 08-Nov-1996
C;Accession: A24572
R;Boulter, J.; Evans, K.; Goldman, D.; Martin, G.; Treco, D.; Heinemann, S.; Patrick, Nature 319, 368-374, 1986
A;Title: Isolation of a cDNA clone coding for a possible neural nicotinic acetylcholine
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-499/Product: nicotinic acetylcholine receptor alpha chain #status predicted <MAT>

Query Match 36.8%; Score 970.5; DB 2; Length 499;
Best Local Similarity 39.8%; Pred. No. 1.2e-74;
Matches 199; Conservative 91; Mismatches 180; Indels 33; Gaps 7;

QY 3 PMLAALLALLPVSEQEPHEKRLNALLANTLERPVANESPEVRFGLTLQOIIDV 62
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 68
QY 63 DEKNOLLITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 122
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 128
QY 123 YQTNVVRSGSCLYVPPGIFKSTCKMDIANFPDQDCHMKFGSWTYDGNQLDLVLKDE 182
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 187
QY 129 DKTALLKYTGEVTPWIPPAIFKSSCKIDVTYFPDYQNTKMGFSWYDKAKIDLVLIG- 187
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 188
QY 183 AGGDSDFITNGEWYLGMPGKKNITTYACCPPEPVVDVTFITMIRRRRLTYFFNLIIVPCV 242
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 247
QY 188 SSMNLKDYWESEWAIKAPGYKHEIKYNCCEIYQDIYSLYIRPLFLFYINLIIPCL 247
DB LLLTITNLSLEWNYNLRWNSDYGGVGLRITPNKLPKPDVLMYNSADEGFGDTYQTN 243
QY 243 LISSMALLGFTLPDPSGKGLTGVTLLSLVFLNVAETLPQVSDAETPLGLTYFNCIMF 302

Db 248 LISFLVLYPSDCGKVTLCISVLLSTVFLVITETISTSLVILPGLLEYLFTMI 307
QY 303 MVASSVLTAVVLYNYHRTADITHMPQWIKSVFLOLWILRMSRP--GKTIKTKT-IMM 359
Db 308 FVTLISVITVFLVNYHRTPTTHMTWKAFLNLLPRVMTPTSGEGDTPKTRTEV 367
QY 360 NTRMRELEKERSKSLANVLDDDDFRHGPP-----PNSTASTGNLGPCCSIFRT 412
Db 368 GAELSNNLNCFSRCRLQKQGLR-----PLPRWDLMLPHRRYKISN-----408
QY 413 DFRSFVRSTMEDVGG--GLGSHRHRLHLILRELOFITARMKKADEAEELISDWKFAAM 470
Db 409 -FSANTRSSSSSVANVLSLSALSPETKEATIOSVYIAENMKAAQNAKEIQDDWKYVAM 467
QY 471 VDRFCLFVFTFTIATVAVLL 493
Db 468 VIDRIFLWVILCVILGTAGLFL 490

RESULT 15
ACFPAL
nicotinic acetylcholine receptor alpha-1 chain precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jun-2002
C:Accession: S00381; A38801
R:Bossy, B.; Ballivet, M.; Spierer, P.
EMBO J. 7, 611-618, 1988
A:Title: Conservation of neural nicotinic acetylcholine receptors from Drosophila to vertebrates
A:Reference number: S00381; MUID:88283626; PMID:2840281
A:Accession: S00381
A:Molecule type: DNA
A:Residues: 1-567 <BOS>
A:Cross-references: GB:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576
A:Accession: A38801
A:Molecule type: mRNA
A:Residues: 1-567 <BO2>
A:Cross-references: EMBL:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576
A:Note: 538-Tyr was also found
C:Genetics:
A:Gene: FlyBase:nACR-alpha-96Aa
A:Cross-references: FlyBase:FBgn0000036
A:Map position: 3R 96A
A:Introns: 64/3; 79/3; 116/2; 176/3; 330/2; 401/1; 499/3
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-567/Product: nicotinic acetylcholine receptor alpha-like chain #status predicted <M>
F:22-240/Domain: extracellular #status predicted <EXT>
F:240-264/Domain: transmembrane #status predicted <TM1>
F:272-290/Domain: transmembrane #status predicted <TM2>
F:306-325/Domain: transmembrane #status predicted <TM3>
F:326-513/Domain: intracellular #status predicted <INT>
F:514-532/Domain: transmembrane #status predicted <TM4>
F:45-233/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:149-163,222-223/Disulfide bonds: #status predicted

Query Match 36.5%; Score 964.5; DB 1; Length 567;
Best Local Similarity 36.5%; Pred. No. 4.8e-74;
Matches 198; Conservative 95; Mismatches 158; Indels 91; Gaps 9;

QY 21. PHEKRLNALLANTLERPVANSEPLEVRFGLTLOQIIDVDEKNOLLITNIWLSLEWN 80
Db 23. PDARKLYDDLSNLRNLRPVGNNSDRLTVMKGLRSLQIDVNLKNQIMTNNVWVEQWN 82
QY 81. DYNLRWNDSEYGGKDLRITPNKLVKPDVLMYNSADEGFDGCTYQTNVVRSGGSLYVPP 140
Db 83. DYKLNWPDYGGVDTLHVPSHHTWHPDVLVNNADNGYEVTIMTKALHHHTGKVVWKP 142
QY 141. GIFKSTCKMDIAWPFDDQHCMDKFGSWTYDGNOLDL-VLKD-----EAGGDLSEFIT 192
Db 143. AIYKSFCEIDVEYFPDEQTCFMKFGSWTYDGYWVDLRHLKQTADSDNIEVGIDLDQYI 202

QY 193 NGEWYLIGMPGKKNTITYACCPPEYVDVTFITMIRRTLYFFNLIVPCVLISSMALLGF 252
Db 203 SVENDIMRVPANRNEKFYSCCEPYLDIVFNLTLRKTLFTVNLIIPCVGISFLSVLF 262
QY 253 TLPPDSGEKLTGLVITLLSLTVFLNVAETLPQVSDAIPLLGYFNCIMFMASSVVLTV 312
Db 263 YLPSSDSGEKISLCISILLSTVFFLLAEIIPPTSLSVPLLGKYLFTMMLVLSVVVTI 322
QY 313 VVLNYHRTADITHMPQWIKSVFLOLWILRMSRPKKITRKTIMMNTMRLELKERS 372
Db 323 AVLNVNFRSPVTHRMAPVWORFIQILPKLLCIERPKKE-----EPEEQ 367
QY 373 SKSLLANVL-----DID-----DDFRHG-----pppp 394
Db 368 PPEVLTDVYHLPPDVVKFVNYDSKRGDYGIPALPASHREFDLAAAGGISAHCFAPPLP 427
QY 395 NS-----TASTGNLGPCC-----SIFRTDFRRSFVRPSTMEDVGGGLSHHR 436
Db 428 SSLPLPGADDDLFSPSGLNGDISPGCCPAAAAAADLSPTFEKP-----YAR 475
QY 437 ELHLILRELOFITARMKKKADEAEELISDWKFAAMVVDRECLFVFTLTITATVAVLLSAP 496
Db 476 EMEKTTIEGSRFIAQHVKNKDKFESVEDMKYVAMVLDRMFLWIFATACVVGTALIILOAP 535
QY 497 HI 498
Db 536 SL 537

Search completed: August 13, 2003, 15:30:22
Job time : 19.7131 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:14:30 ; Search time 43.9474 Seconds
(without alignments)
1809.483 Million cell updates/sec

Title: US-09-303-232-6

Perfect score: 2640

Sequence: 1 MAPMLAALALLPVSQGG.....LFTIIATVALLSAPHIIIV 501

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description
1	2640	100.0	501	21	AA50816	H. virescens acetylcholine receptor protein from clone Hva7-2.
2	1803.5	68.3	496	21	AA50815	H. virescens acetylcholine receptor protein from clone Hva7-2.
3	1609	60.9	770	21	AA50814	D. melanogaster acetylcholine receptor protein from clone Hva7-2.
4	1570.5	59.5	498	22	ABB60432	Drosophila melanogaster acetylcholine receptor protein from clone Hva7-2.
5	1283	48.6	311	22	ABB63683	Drosophila melanogaster acetylcholine receptor protein from clone Hva7-2.
6	1258.5	47.7	502	15	AAW44153	Human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
7	1258.5	47.7	502	18	AAW09025	Human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
8	1258.5	47.7	502	21	AAW24088	Human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
9	1258.5	47.7	502	21	AAW24089	Nicotinic acetylcholine receptor protein from clone Hva7-2.

10	1258.5	47.7	502	22	AAW50012	Wild-type human alpha 2 subunit of neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
11	1258.5	47.7	502	23	ABB82435	Human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
12	1258.5	47.7	502	23	ABG70492	Human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
13	1254.5	47.5	502	19	AAW69216	V274T variant human neuronal alpha-bun mutant human alpha
14	1253	47.5	502	18	AAW12368	Neuronal alpha-bun mutant human alpha
15	1252.5	47.4	502	22	AAW50015	Neuronal alpha-bun mutant human alpha
16	1248.5	47.3	502	22	AAW50016	Neuronal alpha-bun mutant human alpha
17	1242.5	47.1	502	22	AAW50017	Neuronal alpha-bun mutant human alpha
18	1226.5	46.5	511	18	AAW12369	Neuronal alpha-bun mutant human alpha
19	1080	40.9	554	22	AAE12824	Caenorhabditis elegans neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
20	1080	40.9	554	24	AAW96318	Caenorhabditis elegans neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
21	989.5	37.5	504	18	AAW09022	Human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
22	962.5	36.5	470	22	AAW50014	Human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
23	946.5	35.9	504	23	ABB82431	Human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
24	946.5	35.9	504	23	ABG70488	Human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
25	943	35.7	576	22	ABB61954	Drosophila melanogaster acetylcholine receptor protein from clone Hva7-2.
26	942	35.7	448	22	AAW50018	Human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
27	940.5	35.6	504	15	AAW44156	Human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
28	933	35.3	494	18	AAW09018	Human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
29	933	35.3	494	23	ABB82434	Human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
30	933	35.3	494	23	ABG70491	Human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
31	933	35.3	580	22	ABB62727	Drosophila melanogaster acetylcholine receptor protein from clone Hva7-2.
32	922.5	34.9	529	15	AAW44155	Human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
33	922.5	34.9	529	16	AAW73966	Human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
34	922.5	34.9	529	18	AAW09021	Human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
35	922.5	34.9	529	23	ABB82430	Human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
36	922.5	34.9	529	23	ABG31800	Human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
37	922.5	34.9	529	23	ABG61850	Prostate cancer-associated human neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
38	922	34.9	479	22	AAE12823	Caenorhabditis elegans neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
39	922	34.9	479	24	ABP96317	Caenorhabditis elegans neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
40	918.5	34.8	631	23	AAO17243	Modified acetylcholine receptor protein from clone Hva7-2.
41	915	34.7	622	23	AAO17245	Modified acetylcholine receptor protein from clone Hva7-2.
42	915	34.7	622	23	ABB08885	Modified hen ACR s neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
43	910.5	34.5	495	11	AAW07143	Neuronal nicotinic acetylcholine receptor protein from clone Hva7-2.
44	908.5	34.4	519	22	ABB62694	Drosophila melanogaster acetylcholine receptor protein from clone Hva7-2.
45	906	34.3	552	22	ABB61667	Drosophila melanogaster acetylcholine receptor protein from clone Hva7-2.

ALIGNMENTS

RESULT 1
AA50816
ID AA50816 standard; Protein; 501 AA.

XX
AC
AA50816;

XX
DT 17-FEB-2000 (first entry)

XX
DE H. virescens acetylcholine receptor protein from clone Hva7-2.

XX
DE Acetylcholine receptor; nicotinic; insect; insecticide; screening;
KW neurotransmission; plant protection agent; conductance; AChR.

XX
OS Heliothis virescens.

XX
PN DE19819829-AL.

XX
PD 11-NOV-1999.

XX
PF 04-MAY-1998; 98DE-1019829.

XX
PR 04-MAY-1998; 98DE-1019829.

XX
PA (FARB) BAYER AG.

XX
PI Adamczewski M, Oellers N, Schulte T;

XX
DR WPI; 2000-014207/02.

XX
DR N-PSDB; AAZ24477.

XX
PT New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides

XX Example 1a; Page 22-23; 26pp; German.
 XX This invention describes a novel nucleic acid (NA) encoding a nicotinic
 CC acetyl-choline receptor (I) from insects which can be used as an
 CC insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
 CC (also vectors containing it, its regulatory regions, and antibodies
 CC directed against (I)-encoded proteins) are used to screen for: (a) plant
 CC protection agents that alter conductance of AChR, potentially useful as
 CC insecticides; or (b) genes which encode polypeptides that are involved in
 CC formation of functionally related AChR in insects. (I) are also used to
 CC isolate and characterize the specified regulatory regions and for
 CC recombinant production of (II). This sequence represents an
 CC acetyl-choline receptor isolated from *Heliothus virescens*.
 XX SQ Sequence 501 AA;

Query Match 100.0%; Score 2640; DB 21; Length 501;
 Best Local Similarity 100.0%; Pred. No. 5.9e-270;
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MAPMLAALALLPVSEGGPHERKLLNALLANTLERPVANSEPLEVRFGLTLOQII 60
 Db 1 MAPMLAALALLPVSEGGPHERKLLNALLANTLERPVANSEPLEVRFGLTLOQII 60
 Oy 61 DVDEKNOLLITNIWLSLEWNDYINLRWNSDYGGVKDLRITPNKLNKPDVLMYNSADEGFD 120
 Db 61 DVDEKNOLLITNIWLSLEWNDYINLRWNSDYGGVKDLRITPNKLNKPDVLMYNSADEGFD 120
 Oy 121 GYTQTNVVRSGGSLVPPGIFKSTCKMDIAWPPFDDQHCMDKFGSWTYDGNLDLVK 180
 Db 121 GYTQTNVVRSGGSLVPPGIFKSTCKMDIAWPPFDDQHCMDKFGSWTYDGNLDLVK 180
 Oy 181 DEAGDLSDFITNGEWYLGMPGKNTITYACCPYVDVFTTIRRTLYFFNLIVP 240
 Db 181 DEAGDLSDFITNGEWYLGMPGKNTITYACCPYVDVFTTIRRTLYFFNLIVP 240
 Oy 241 CVLISSMALLGFTLPDPSGKLTGLVITLLSLVFLNVAETLPQVSDAIPLLGYFNCI 300
 Db 241 CVLISSMALLGFTLPDPSGKLTGLVITLLSLVFLNVAETLPQVSDAIPLLGYFNCI 300
 Oy 301 MFVASSVVLTVVVLNYHHRHADTHEMPQWIKSVFLOLWPLWLRMSRPGKTKITRMN 360
 Db 301 MFVASSVVLTVVVLNYHHRHADTHEMPQWIKSVFLOLWPLWLRMSRPGKTKITRMN 360
 Oy 361 TRMRELEKERSKSLANVLIDDDFRHGPPPPNSTASTGNLPGGCSIFRTDFRSEVR 420
 Db 361 TRMRELEKERSKSLANVLIDDDFRHGPPPPNSTASTGNLPGGCSIFRTDFRSEVR 420
 Oy 421 PSTMEDVGGGLGSHHRELHLILRELQFITARMKKADEAEELISDWKFAAMVVDRECLFV 480
 Db 421 PSTMEDVGGGLGSHHRELHLILRELQFITARMKKADEAEELISDWKFAAMVVDRECLFV 480
 Oy 481 TLFITIAVALLSAPHIIVQ 501
 Db 481 TLFITIAVALLSAPHIIVQ 501

RESULT 2
 ID AAY50815 standard; Protein; 496 AA.
 XX AC AAY50815;
 XX DT 17-FEB-2000 (first entry)
 XX DE H. *virescens* acetyl-choline receptor protein from clone Hva7-1.
 XX KW Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
 XX KW neurotransmission; plant protection agent; conductance; AChR.
 XX OS *Heliothus virescens*.
 XX

PN DEL9819829-AL.
 XX 11-NOV-1999.
 XX 04-MAY-1998; 98DE-1019829.
 XX 04-MAY-1998; 98DE-1019829.
 XX (FARB) BAYER AG.
 XX Adamczewski M, Oellers N, Schulte T;
 XX WPI; 2000-014207/02.
 XX N-PSDB; AAZ24476.
 XX New nucleic acid encoding a nicotinic acetylcholine receptor from
 XX insects, used to identify potential insecticides
 XX Example 1a; Page 17-19; 26pp; German.
 XX This invention describes a novel nucleic acid (NA) encoding a nicotinic
 CC acetyl-choline receptor (I) from insects which can be used as an
 CC insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
 CC (also vectors containing it, its regulatory regions, and antibodies
 CC directed against (I)-encoded proteins) are used to screen for: (a) plant
 CC protection agents that alter conductance of AChR, potentially useful as
 CC insecticides; or (b) genes which encode polypeptides that are involved in
 CC formation of functionally related AChR in insects. (I) are also used to
 CC isolate and characterize the specified regulatory regions and for
 CC recombinant production of (II). This sequence represents an
 CC acetyl-choline receptor isolated from *Heliothus virescens*.
 XX SQ Sequence 496 AA;

Query Match 68.3%; Score 1803.5; DB 21; Length 496;
 Best Local Similarity 68.7%; Pred. No. 1.9e-181;
 Matches 347; Conservative 53; Mismatches 78; Indels 27; Gaps 7;
 Oy 2 APMIAALALLPVSEGGPHERKLLNALLANTLERPVANSEPLEVRFGLTLOQII 60
 Db 12 APAGLLLLCLLWPRGARGCYHEKRLHLLHDHYNLVRPVPVNESDPLQLSGLTLMQII 71
 Oy 61 DVDEKNOLLITNIWLSLEWNDYINLRWNSDYGGVKDLRITPNKLNKPDVLMYNSADEGFD 120
 Db 72 DVDEKNOLLITNIWLSLEWNDYINLRWNSDYGGVKDLRITPNKLNKPDVLMYNSADEGFD 131
 Oy 121 GYTQTNVVRSGGSLVPPGIFKSTCKMDIAWPPFDDQHCMDKFGSWTYDGNLDLVK 180
 Db 132 STYPTNVVRNGSLVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGLDLQLQ 191
 Oy 181 DEAGDLSDFITNGEWYLGMPGKNTITYACCPYVDVFTTIRRTLYFFNLIVP 240
 Db 192 DEGGDISSEFTNGEWELIGVPGGRNEIYNCCPEYIDITFAVIRKTKLYFFNLIVP 251
 Oy 241 CVLISSMALLGFTLPDPSGKLTGLVITLLSLVFLNVAETLPQVSDAIPLLGYFNCI 300
 Db 252 CVLISSMALLGFTLPDPSGKLTGLVITLLSLVFLNVAETLPQVSDAIPLLGYFNCI 311
 Oy 301 MFVASSVVLTVVVLNYHHRHADTHEMPQWIKSVFLOLWPLWLRMSRPGKTKITRMN 360
 Db 312 MFVASSVVLTVVVLNYHHRHADTHEMPQWIKSVFLOLWPLWLRMSRPGKTKITRMN 370
 Oy 361 TRMRELEKERSKSLANVLIDDDFRHGPPPPNSTASTGNLPGGCSIFRTDFRSEVR 420
 Db 371 PPPDLELRERSKSLANVLIDDDFRH-----PQAQO-----PQCCRY---YRGG--- 414
 Oy 421 PSTMEDVGGGLGSH-----HRELHLILRELQFITARMKKADEAEELISDWKFAAMVVDRE 475
 Db 415 -----EENGAGLAHSCFGVDYELSLILKEIRVITQDMRKDDDEDADISDWKFAAMVVDRL 470
 Oy 476 CLFVFTLTITIAVALLSAPHIIV 500
 Db 471 CLIFTTITIAVALLSAPHIIV 495

RESULT 3
 ID AAY50814
 XX AAY50814 standard; Protein; 770 AA.
 AC AAY50814;
 XX
 DT 17-FEB-2000 (first entry)
 DE D. melanogaster acetyl-choline receptor protein from clone Da7.
 DE Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
 KW neurotransmission; plant protection agent; conductance; AChR.
 KW
 XX Drosophila melanogaster.
 XX DE19819829-A1.
 PN
 XX
 PD 11-NOV-1999.
 XX
 XX 04-MAY-1998; 98DE-1019829.
 PF
 XX 04-MAY-1998; 98DE-1019829.
 PR
 XX (FARB) BAYER AG.
 PA
 XX Adamczewski M, Oellers N, Schulte T;
 PI WPI; 2000-014207/02.
 XX N-PSDB; AAZ24475.
 DR
 XX New nucleic acid encoding a nicotinic acetylcholine receptor from
 PT insects, used to identify potential insecticides
 PT
 XX Example 1a; Page 12-14; 26pp; German.
 PS
 XX This invention describes a novel nucleic acid (NA) encoding a nicotinic
 CC acetyl-choline receptor (I) from insects which can be used as an
 CC insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
 CC (also vectors containing it, its regulatory regions, and antibodies
 CC directed against (I)-encoded proteins) are used to screen for: (a) plant
 CC protection agents that alter conductance of AChR, potentially useful as
 CC insecticides, or (b) genes which encode polypeptides that are involved in
 CC formation of functionally related AChR in insects. (I) are also used to
 CC isolate and characterize the specified regulatory regions and for
 CC recombinant production of (II). This sequence represents an
 CC acetyl-choline receptor isolated from *Drosophila melanogaster*.
 XX
 XX Sequence 770 AA;
 Query Match 60.9%; Score 1609; DB 21; Length 770;
 Best Local Similarity 60.8%; Pred. No. 1.4e-160;
 Matches 319; Conservative 57; Mismatches 65; Indels 84; Gaps 10;
 QY 10 LIALPVSQ----GPKRLLNALLANTLERPVANSEPLEVRFGTLQOIIDVDEK 65
 DB 295 LLIYLNLSAKVCLAGYHEKRLLHLLDPYNTLERPVNLSDELQLSFGLTLQIIDVDEK 354
 QY 66 NOLLITNIWLSLEWNDYLNLRWNSDSEYGVKDLRITPNKLRKPDVLMYNSADEGFGDTYQT 125
 DB 355 NOLLVTNWKLEWNDNLRWNTSDYGVKDLRIPPHRIKPDVLMYNSADEGFGDTYQT 414
 QY 126 NVVRSGLXVPVPGIFKSTCKMDIAWFPDDQHCMDKFGSWTYDGNOLDVLVDEAGG 185
 DB 415 NVVVRNNGSCLVYPVPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGFOLDLQDEYGG 474
 QY 186 DLSDFITNGEWLYLIGMPGKKNITTYACCPPEYVDVTFITIMIRRTLYFFNFNLIIVPCVLIS 245
 DB 475 DISSVYLVNGEWELLVPGKRNIYYNCCPEPIDITFAIIIRRTLYFFNFNLIIVPCVLIA 534
 QY 246 SMALLGFTLPPDSGEKLTGLVITLISLVFLNVAETLPQVSDAIPLIGTYNCFMFWA 305
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 535 SMALLGFTLPPDSGEKLSGLGVTLLISLVFLNVAETMPATSDAVPL----- 581
 QY 306 SSVLTVVVLNYHRTADIHEMPQWIKSVFLOLWPLMRSPGKKITRK---TIMMNT 362
 DB 582 -----WIRIVFLCWLPLMRSPGRLILEFTTFCSDTS 617
 QY 363 -----MRELEKERSKSLANVLIDDDFRHG--PPPNSTASTGMLGPCSIFRFD 413
 DB 618 SERKHQILSDVELKERSKSLANVLIDDDFRHRCRPMTPG-----GTLPHNPAFYRTV 672
 QY 414 FRRSVRPSTMEDVG--GGLGS-----HUR-----ELHLILRELOFTARMKKA 455
 DB 673 YGQG-----DDGSIGDIGSTRMPDAVTHCTCKSTSEYELGLILKEIRFTDQLRKD 724
 QY 456 DEAEALISDWKFAAMVVDRCFLVFETLTITATVAVLLSAPHIIV 500
 DB 725 DECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIV 769
 RESULT 4
 ID ABB60432
 XX ABB60432 standard; Protein; 498 AA.
 AC ABB60432;
 XX
 DT 26-MAR-2002 (first entry)
 DE Drosophila melanogaster polypeptide SEQ ID NO 8088.
 DE Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 KW
 XX Drosophila melanogaster.
 OS WO200171042-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 23-MAR-2001; 2001WO-US09231.
 PF
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 XX N-PSDB; ABL04535.
 DR
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from *Drosophila* and for elucidating cell signalling and cell-cell
 PT interactions
 PT
 XX Disclosure; SEQ ID NO 8088; 21pp + Sequence Listing; English.
 PS
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins.
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 498 AA;
 Query Match 59.5%; Score 1570.5; DB 22; Length 498;
 Best Local Similarity 61.1%; Pred. No. 8.6e-157;
 Matches 319; Conservative 44; Mismatches 84; Indels 75; Gaps 9;
 SQ

[illegible]

RESULT 5
ABB63683

ABB63683
ID ABB63683 standard; Protein; 311 AA.

AC ABB63683;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEO ID NO 17841.

XX Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
KW
KW

XX OS *Drosophila melanogaster*.

XX PN : WO200171042-A2

XX
PD
27-SEP-2001

23-MAR-2001: 2001WO-US09231.

XX
PR 23-MAR-2000. 2000US-191637D

PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.

PA (PEKE) PE CORP NY.

XX
PI
venter JC, Adams M, Li PWD, Myers EW:

XX
DR WPI: 2001-656860/75.

DR N-PSDB; ABL07786

PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from *Drosophila* and for elucidating cell signalling and cell-cell
PT interactions -

XX
TJ

PS Disclosure; SEQ ID NO 17841; 21pp + Sequence Listing; English.
XX
CC
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SO Sequence 311 AA;

RESULT 6

AAW44 153
ID AAW44153 standard: Protein: 502 AA:

XX AAW44153:

14-MAY-1998 (first entry)

XX
DE Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.

Human: neuronal nicotinic acetylcholine receptor: alpha-7 subunit: XX KW

KW Human; neuronal nicotinic acetylcholine
KW brain tissue: screening; NACHR; antibody.

XX
OS
Hom sapiens.

XX	Key	Location/Qualifiers
FH		

FT	key	Peptide	1..23
FT			

FT /label= signal

229..256
FT Domain

```
FT /label= TMD1
FM /set= 04000000
```

```
FT      /note= "transm  
FE      250  294  
FE      260  294
```

```

FT      Domain
      262...284
      , /label = TMD2
FT

```

```

EI /label= IMDZ
EI /note= "transm

```

FT	Domain	290..317	/HCC-CRASH
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FT /label= TMD3

FT /note= "transm

Misc-difference 343

```
FT /note= "encode
FE 152 187
FE domain
```

```

F1 Domain
462...48/
/label = TMD4

```

```
FT
/label= TMD4
/note= "transm
```

FT Domain 318..461
 FT /label= cytoplasmic_loop
 XX WO9420617-A2.
 XX 15-SEP-1994.
 XX 08-MAR-1994; 94WO-US02447.
 XX 08-MAR-1993; 93US-0028031.
 XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
 XX (SIBI-) SIBIA NEUROSCIENCES INC.
 XX Elliott KJ, Ellis SB, Harpold MM;
 XX WPI; 1994-303024/37.
 XX N-PSDB; AAV12197.
 XX Human neuronal nicotinic acetylcholine receptor subunits and DNA -
 PT also transformed cells useful for screening cpds. which modulate
 PT activity of the receptor
 XX
 XX Claim 7; Page 80-81; 99pp; English.
 XX
 CC The present sequence represents a human neuronal nicotinic acetylcholine
 CC receptor (NACHR) subunit. The cells expressing the alpha and/or beta
 CC NACHR subunits may be used in a method of screening compounds to
 CC identify any which modulate the activity of human neuronal NACHR.
 CC Subunit specific antibodies may be used to monitor the distribution
 CC and expression density of various subunits in normal vs diseased brain
 CC tissues. Testing of single receptor subunits or specific receptor
 CC subunit combinations with a variety of potential agonists or antagonists
 CC provides information with respect to the function and activity of the
 CC individual subunits and should lead to the identification and design of
 CC compounds that are capable of very specific interaction with one or
 CC more receptor subtypes. The resulting drugs should exhibit fewer
 CC unwanted side effects than drugs identified e.g. screening with cells
 CC that express a variety of subtypes.
 XX
 SQ Sequence 502 AA;
 Query Match 47.7%; Score 1258.5; DB 15; Length 502;
 Best Local Similarity 48.6%; Pred. No. 9e-124;
 Matches 250; Conservative 75; Mismatches 138; Indels 51; Gaps 7;
 QY 8 LALLA-LLPVSEOGPEKRLNALLANYNTERPVANSEPLEVRGLTLOQIIDVDENK 66
 DB 10 LALAASLLHVSLOGEFQRLKYLKLVNYPNPLRPVANDSQPLTVYFSLQLQIMDVDEKN 69
 QY 67 QLLITNIWLSLEWNDYNLRWNSDEYGGVKDLRTTPNKLWKPVDVLYMNSADEGFDGTYQTN 126
 DB 70 QVLTNTIWLQMSWTDHYLQWNSYEPGVKTVPDPGQIWKPDILLYNSADERDAFFHTN 129
 QY 127 VVVRSGGSLYVPPGIFKSTCKMDIAWFFPDQHCMDKFGSWTYDGNQLDLVLKDBAGD 186
 DB 130 VLNVSSGHCOYLPPLGIFKSCYIDVWFFDVQHCKLFGSGWSGLDLQMQE---AD 186
 QY 187 LSDFITNGEWLYIGMPGKNTITYACCPPEYVDVTFITMIRRTLYFFNLIIVPCVLISS 246
 DB 187 ISGYIPNGEWDLVIGFPGKSERIECKEPEYDPDVTFTVTRRTLYGNGLLIPCVLIISA 246
 QY 247 MALLGTLTPDPSGEKITLGVTLLSVTLFNLVAETLPQVSDAIPLLGTGYFNCIMPMVAS 306
 DB 247 LALLVLLPADSGEKISLGTIVLLSVTFMLLVAEIMPATSDSVPLIAQYFASTMIIVGL 306
 QY 307 SVVLTVVVLYNHRHTADIEMQWIKSVFLQWLPWLIRMSRPGKKITRKTIMMNTMRREL 366
 DB 307 SVVTVIVLYQHHHPDGGKMPKRWTRVILLNCAWFLMKRPGEDKVRPACQHKQRCSL 366
 QY 367 ELKRSKSLIANVLDDDFRHGPPPNSTASTGNL-----GPGC 407
 DB 367 ASVEMSAV-----PPP---ASNGNLLYIGRGLDGVHCVTPDPGSGVVC 407

QY 408 SIFRTDFRRSFVRPSTMEDV--GGGLGSHRELHLILRELQFTTARMKADEAEELISDW 465
 DB 408 G-----RMACSPTHDEHLLHGGOPGPDPLAKILEEVRYIANFRQDESEAVCSEW 460
 QY 466 KFAAMVVDRCFLVFTLTIIATVAVLLSAPHII 499
 DB 461 KFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494

RESULT 7
 AAW09025
 ID AAW09025 standard; Protein; 502 AA.
 XX AAW09025;
 DT 09-APR-1997 (first entry)
 XX
 DE Neuronal nicotinic acetylcholine receptor alpha-7 subunit.
 DE
 XX Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
 KW Ligand-gated receptor.
 XX
 OS Homo sapiens.
 XX
 PN WO9641876-A1.
 XX
 PD 27-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US09775.
 XX
 PR 07-JUN-1995; 95US-0484722.
 XX
 PA (SIBI-) SIBIA NEUROSCIENCES INC.
 XX
 PI Elliott KJ, Harpold MM;
 XX
 DR WPI; 1997-065463/06.
 DR N-PSDB; AAT48239.
 XX
 PT Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
 PT used in screening to determine the effect of drugs on the receptor
 PS
 PS Disclosure; Page 73-74; 108pp; English.
 CC
 CC The alpha-7 subunit (AAW09025) of the human neuronal nicotinic
 CC acetylcholine receptor (nAChR) can be expressed in transfected
 CC host cells carrying alpha-7 subunit DNA (see also AAT48239). Host
 CC cells, esp. mammalian cells or amphibian oocytes, expressing the
 CC recombinant alpha-7 subunit, opt. in combination with other
 CC recombinant alpha and/or beta subunits (see also AAW09018-24,
 CC AAW09026-27), can be used to examine the function of human AChR and
 CC to identify cpds. that modulate its activity.
 XX
 SQ Sequence 502 AA;
 Query Match 47.7%; Score 1258.5; DB 18; Length 502;
 Best Local Similarity 48.6%; Pred. No. 9e-124;
 Matches 250; Conservative 75; Mismatches 138; Indels 51; Gaps 7;
 QY 8 LALLA-LLPVSEOGPEKRLNALLANYNTERPVANSEPLEVRGLTLOQIIDVDENK 66
 DB 10 LALAASLLHVSLOGEFQRLKYLKLVNYPNPLRPVANDSQPLTVYFSLQLQIMDVDEKN 69
 QY 67 QLLITNIWLSLEWNDYNLRWNSDEYGGVKDLRTTPNKLWKPVDVLYMNSADEGFDGTYQTN 126
 DB 70 QVLTNTIWLQMSWTDHYLQWNSYEPGVKTVPDPGQIWKPDILLYNSADERDAFFHTN 129
 QY 127 VVVRSGGSLYVPPGIFKSTCKMDIAWFFPDQHCMDKFGSWTYDGNQLDLVLKDBAGD 186
 DB 130 VLNVSSGHCOYLPPLGIFKSCYIDVWFFDVQHCKLFGSGWSGLDLQMQE---AD 186
 QY 187 LSDFITNGEWLYIGMPGKNTITYACCPPEYVDVTFITMIRRTLYFFNLIIVPCVLISS 246

Db 187 ISGYPNGEWDLVGIPIKRSERFECCKEYPPDVTFTVWRRRTLYGLNLLIPCVLISA 246
 Qy 247 MALLGFTLPPDSGEKLTGLVTLISLTVFLNLVAETLPQVSDAIPGLGTYFNCIMFVMS 306
 Db 247 LALLVFLPADSGEKISLGITVLLSLTVFLNLVAEIMPATSDSVPLIAQYFASTMIIVGL 306
 Qy 307 SVVLTVVVLYNHHRTADIHEMPQWIKSVFLOLWLPWILMRSPGKKITRKTMMTRREL 366
 Db 307 SVVTVTVLQYHHHDPDGKMPKWTIRVILLNWCWFLMRKRPGEKVRPACQHKQRCSL 366
 Qy 367 ELKERSKSLLANVLDIDDDFRHGPPPNSTASTGNI-----GPGC 407
 Db 367 ASVEMSAVA-----PPP-----ASGNLLYIGFRCGLDVHCVPTDPSGVC 407
 Qy 408 SIERTDFRRSVRFPSTMEDV--GGGLGSHHREHLHLIRELQFITARMKKADEAEELISDW 465
 Db 408 G-----RMACSPTHDEHLHGQPPGDPDLAKILEEVRYIANFRCDSEAVCSW 460
 Qy 466 KFAAMVVDRLCLFVFTFTTIATVAVLLSAPHII 499
 Db 461 KFAACVVDRLCLMAFSVFTIITIGILMSAPNFV 494

RESULT 8

AAB24088

ID AAB24088 standard; Protein; 502 AA.

XX

AC AAB24088;

XX

DT 29-JAN-2001 (first entry)

XX

DE Human PRO2145 protein sequence SEQ ID NO:77.

XX

KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
 KW proliferation; tumorigenesis; identification; cancer; cytostatic;
 KW neutropic; neuroprotective; antiinflammatory; immunosuppressive;
 KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
 KW neuronal disorder; glioma disorder; astrocytic disorder; angiogenic;
 KW hypothalamic disorder; glandular disorder; macrophagal disorder;
 KW epithelial disorder; stromal disorder; blastocoele disorder;
 KW inflammatory disorder; immunologic disorder.

XX Homo sapiens.

OS

XX

PN WO200053755-A2.

XX

PD 14-SEP-2000.

XX

PF 06-JAN-2000; 2000WO-US00376.

XX

PR 08-MAR-1999; 99WO-US05028.

XX

PR 02-JUN-1999; 99WO-US12252.

XX

PR 23-JUN-1999; 99US-0141037.

XX

PR 07-JUL-1999; 99US-0143048.

XX

PR 26-JUL-1999; 99US-0145698.

XX

PR 30-NOV-1999; 99WO-US28313.

XX

PR 20-DEC-1999; 99WO-US30911.

XX

PR 05-JAN-2000; 2000WO-US00219.

XX

PA (GETH) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;

XX

PI Watanabe CK, Wood WI;

XX

DR WPI; 2000-572270/53.

XX

DR N-PSDB; AAC58395.

XX

PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
 treatment, diagnosis and prevention of cancer -
 XX
 PS Claim 61; Fig 58; 286pp; English.
 XX

CC The present invention describes an isolated antibody that binds to
 one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO355,
 PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
 PRO1025, PRO1030, PRO1097, PRO1107, PRO1153, PRO1182, PRO1184,
 PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,
 PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
 growth. The PRO polypeptides and nucleotides are useful in the
 treatment, diagnosis and prevention of cancer. The antibodies and other
 anti-tumour compounds may be used to treat various conditions, including
 those characterised by overexpression and/or activation of the amplified
 PRO genes. Exemplary conditions or disorders to be treated with such
 antibodies and other compounds include benign or malignant tumours
 (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
 colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic
 carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
 leukaemias and lymphoid malignancies, other disorders such as neuronal,
 glioma, astrocytic, hypothalamic and other glandular, macrophagal,
 epithelial, stromal and blastocoele disorders, and inflammatory,
 angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
 primers and hybridisation probes used in the isolation of the human PRO
 sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
 PRO polynucleotide and protein sequences given in the exemplification of
 the present invention.

XX Sequence 502 AA;

Query Match 47.7%; Score 1258.5; DB 21; Length 502;

Best Local Similarity 48.6%; Pred. No. 9e-124;

Matches 250; Conservative 75; Mismatches 138; Indels 51; Gaps 7;

Qy 8 LALLA-LLPVSEOGPEKRLNLLNANYTLERPVANESPELEVRFGTLTQIIVDDEKN 66
 Db 10 LALAASLLHVSLOGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDVDEKN 69
 Qy 67 QLITNITWLSLEWYDYNLRWNSDYGVGKDLRITPNKLRKPDVLYMNASDEGFDGTQTN 126
 Db 70 QVLTNITWLSQWTDHVLQWNVSEYPCVKTVPDGIWKPDILLYNSADERFATHTN 129
 Qy 127 VVVRSGSCLYVPPGIFKSTCKMDIAWFPDDOHCMDKMGFSWYDGNLDLVLKDEAGD 186
 Db 130 VLVNSSGHCOYLPPIGIFKSSCYIDVRWFPDQVHCKLFGSWSYGVSLDQMOE---AD 186
 Qy 187 LSDFITNGEWYLGMPGKKNITVYACCPYVDVDTFTIMIRRTLYYFFNLVPCVLIS 246
 Db 187 ISGYIPNGEWDLVGIPIKRSERFECCKEYPPDVTFTVWRRRTLYGLNLLIPCVLISA 246
 Qy 247 MALLGFTLPPDSGEKLTGLVTLISLTVFLNLVAETLPQVSDAIPGLGTYFNCIMFVMS 306
 Db 247 LALLVFLPADSGEKISLGITVLLSLTVFLNLVAEIMPATSDSVPLIAQYFASTMIIVGL 306
 Qy 307 SVVLTVVVLYNHHRTADIHEMPQWIKSVFLOLWLPWILMRSPGKKITRKTMMTRREL 366
 Db 307 SVVTVTVLQYHHHDPDGKMPKWTIRVILLNWCWFLMRKRPGEKVRPACQHKQRCSL 366
 Qy 367 ELKERSKSLLANVLDIDDDFRHGPPPNSTASTGNI-----GPGC 407
 Db 367 ASVEMSAVA-----PPP-----ASGNLLYIGFRCGLDVHCVPTDPSGVC 407
 Qy 408 SIERTDFRRSVRFPSTMEDV--GGGLGSHHREHLHLIRELQFITARMKKADEAEELISDW 465
 Db 408 G-----RMACSPTHDEHLHGQPPGDPDLAKILEEVRYIANFRCDSEAVCSW 460
 Qy 466 KFAAMVVDRLCLFVFTFTTIATVAVLLSAPHII 499
 Db 461 KFAACVVDRLCLMAFSVFTIITIGILMSAPNFV 494

RESULT 9

AAB82690

ID AAB82690 standard; Protein; 502 AA.

XX

AC AAB82690;

XX

DT XX 15-OCT-2001 (first entry)

DE XX Nicotinic acetylcholine receptor alpha7.

KW XX Nicotinic acetylcholine receptor; nAChR; human;

KW XX acetylcholine binding protein; AChBP; mollusc;

KW XX ligand-binding protein; ligand-gated ion channel; crystal;

KW XX drug design; protein co-ordinate data; schizophrenia;

KW XX Alzheimer's disease; nicotine addiction; Tourette's syndrome;

KW XX therapy; neurotropic; neuroprotective.

OS XX Homo sapiens.

XX XX

XX XX

FT XX Key Location/Qualifiers

FT XX Region 108..115

FT XX /note= "conserved ligand-binding region, residues

FT XX Trp108 and Tyr115 are essential"

FT XX Region 171..173

FT XX /note= "conserved ligand-binding region, residues

FT XX Trp171 and Tyr173 are essential"

FT XX Region 210..217

FT XX /note= "conserved ligand-binding region, residues

FT XX Tyr210, Cys212, Cys213 and Tyr217 are

FT XX essential"

XX XX WO200158951-A2.

XX XX

XX XX 16-AUG-2001.

XX XX

XX XX 09-FEB-2001; 2001WO-EP01457.

XX XX

XX XX 10-FEB-2000; 2000EP-0200443.

XX XX 31-OCT-2000; 2000EP-0203810.

XX XX (TEWE-) STICHTING TECH WETENSCHAPPEN.

XX XX

XX XX Smit AB, Sixma TK;

XX XX

XX XX WPI; 2001-497071/54.

XX XX

XX XX Water-soluble ligand-binding proteins derived from molluscs and analogues

XX XX of ligand-gated ion channels, useful in drug screening assay, where the

XX XX drugs identified can be used in the treatment of Alzheimer's disease or

XX XX schizophrenia -

XX XX

XX XX Disclosure; Page 252-254; 260pp; English.

XX XX

XX XX The present sequence is that of the alpha subunit of human

XX XX nicotinic acetylcholine receptor (nAChR). The sequence includes

XX XX regions that are conserved throughout the various nAChR alpha

XX XX subunits and which are essential for ligand binding. The invention

XX XX relates to water-soluble ligand-binding proteins derived from

XX XX molluscs, especially acetylcholine-binding proteins (AChBPs) and

XX XX analogues of ligand-gated ion channels, their crystals, and their

XX XX use for screening ligands of ligand-gated ion channels. The

XX XX water-soluble ligand-binding proteins are capable of forming

XX XX multimers and are amenable to crystallization. The crystal

XX XX structure of AChBP is provided, and can be used to generate 3D

XX XX models of the extracellular ligand-binding domain of ligand-gated

XX XX ion channels and thus for screening of drugs that act on these

XX XX ion channels. Chimeric proteins are provided that are capable of

XX XX binding a ligand of a ligand-gated receptor, and comprise at

XX XX least the amino acids of the AChBP determining solubility of the

XX XX AChBP, in the same positions as in the AChBP, and also comprising

XX XX amino acids determining binding to the ligand. In the chimeric

XX XX proteins, at least the essential amino acids of at least 1 of the

XX XX conserved regions of an nAChR have been substituted for the

XX XX corresponding amino acids, and preferably entire stretches have

XX XX been substituted. New drugs can be developed that selectively

XX XX intervene in neuronal signalling pathways, especially where the

XX XX ligand-gated ion channel is the nAChR, and the related disorder is

XX XX Tourette's syndrome, Alzheimer's disease, addiction to nicotine

XX XX or schizophrenia.

XX SQ Sequence 502 AA;

Query Match 47.7%; Score 1258.5; DB 22; Length 502;

Best Local Similarity 48.6%; Pred. No. 9e-124;

Matches 250; Conservative 75; Mismatches 138; Indels 51; Gaps 7;

QY 8 LALLA-LLPVSEQSPHEKRLNALLANNTLRLPVRANSEPLEVRLTQIIVDEKN 66

DB 10 LALAALLHVSLSQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSLQLQIMDVDEKN 69

QY 67 QLLITNINLSLEWYNDYNLRWNSSEYGGVKDLRITPNKLPKDVLMNSADEGFDGTQYN 126

DB 70 QVLTTNINLQMSWTQHYLQWNYSEYPGVKTVFPDQIWKPDILLYNSADERDATFTFN 129

QY 127 VVVRSGGCLYVPPGIFKSTCKMDIAWPFDDQCHDMKFGSWTYDGNQLDLVLKDEAGD 186

DB 130 VLVNSGHCQYLPDGGIFKSSCYIDRWPFVQHKLKFGSGSYGGWSLDLQOE---AD 186

QY 187 LSDFITNGEWYLLIGMPGKKNITYACCPPEYVDVTFITMIRRTLYYFNLIVPCVLISS 246

DB 187 ISGYIPNGEWDLVGIPGRSERFECCKEPYPDVTFVTMRRRTLYYGLNLLIPCVLISA 246

QY 247 MALLGETLPDPSGEKLTIGVTLLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMPWVAS 306

DB 247 LALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIVGL 306

QY 307 SVVLTVVVLNYHRTADITHMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTMRREL 366

DB 307 SVVTVIVLQYHHHDPDGGKMPKTRVILLNWCANFLMKRPGEDKVRPACQHKQRCSL 366

QY 367 ELKERSKSLANVLIDDDFRHPPPPNSTASTGNL-----GPGC 407

DB 367 ASVEMSAVA-----PPP---ASGNLLYIGFRGLDGVHCVPTPDGVCVC 407

QY 408 STFTDFRFRSFRPSTMEDV---GGGLGSHHRELHLILRELQITARMKKADEAEELISDW 465

DB 408 G-----RMACSPTHDEHLHGQPPGPDPLAKILEVRYIANFRQDESEAVCSEW 460

QY 466 KFAAMVDRFCVFTFTFTIATVALLSAPHII 499

DB 461 KFAACVWDRLCLMAFSVFTICTIGILMSAPNFV 494

RESULT 10

AAB50012

ID AAB50012 standard; Protein; 502 AA.

XX AC AAB50012;

DT 14-MAR-2001 (first entry)

XX DE Wild-type human alpha7 ligand gated ion channel.

XX KW Human; alpha7 nicotinic acetylcholine gated ion channel;

XX KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance.

XX OS Homo sapiens.

XX XX WO200073431-A2.

XX XX 07-DEC-2000.

XX XX 25-MAY-2000; 2000WO-US11862.

XX XX 27-MAY-1999; 99US-0136174.

XX XX (PHAA) PHARMACIA & UPJOHN CO.

XX XX Groppi VE, Wolfe ML, Berkenpas MB;

XX XX WPI; 2001-061524/07.

XX XX N-PSDB; AAC90380.

QY 466 KFAAMVVDRECLFVFTLTIIATVAVLLSAPHII 499
 Db 461 KFAACVVDRLCLMAFSVFTIICITIGILMSAPNFV 494

RESULT 12

ABG70492
 ID ABG70492 standard; Protein; 502 AA.

XX AC ABG70492;
 XX 06-DEC-2002 (first entry)
 XX DE Human neuronal nicotinic acetylcholine receptor alpha 7 subunit.
 XX KW Human; neuronal nicotinic acetylcholine receptor; nAChR; receptor;
 XX KW ion flux; alpha 7 subunit.
 XX OS Homo sapiens.
 XX US6440681-B1.
 XX PN 27-AUG-2002.
 XX PF 07-JUN-1995; 95US-0487596.
 XX PR 03-APR-1990; 90US-0504455.
 XX PR 30-NOV-1992; 92US-0938154.
 XX PR 08-MAR-1993; 93US-0028031.
 XX PR 08-NOV-1993; 93US-0149503.
 XX PA (MERI) MERCK & CO INC.

XX PI Elliott KJ, Ellis SB, Harpold MM;
 XX DR WPI: 2002-711528/77.
 XX DR N-PSDB; ABS54875.
 XX PT Identifying antagonists or agonists of human neuronal nicotinic
 PT acetylcholine receptors, by contacting recombinant cells with test
 PT compound, and measuring ion flux of cells or binding of compound to
 PT nAChR
 XX PS Claim 101; Column 59-64; 56pp; English.
 XX CC The invention relates to a method for identifying compounds that are
 CC antagonists or agonists of human neuronal nicotinic acetylcholine
 CC receptors (nAChRs), by contacting recombinant cells with a test
 CC compound and measuring ion flux, the electrophysiological response of the
 CC cells or binding of the test compound to the nAChR. The recombinant
 CC cells are produced by transfection with a nucleic acid encoding at least
 CC one human nAChR (alpha or beta) subunit, such that the cells express an
 CC nAChR comprising one human subunit encoded by the transfected nucleic
 CC acid. This sequence represents the alpha 7 subunit of the human nAChR
 XX polypeptide.

SQ Sequence 502 AA;

Query Match 47.7%; Score 1258.5; DB 23; Length 502;
 Best Local Similarity 48.6%; Pred. No: 9e-124;
 Matches 250; Conservative 75; Mismatches 138; Indels 51; Gaps 7;

QY 8 LALLA-LLPVSQGPHEKRLNALLANYNTLRPVANSEPLEVRFGTLTQIIVDDEKN 66
 Db 10 LALAASLLHVSLLQGEFQRLKLYKYNPLRPVANDSOPLTVYFSLSLQIMDVDEKN 69
 QY 67 QLLITNIWLSLEWDYNIWRNDSEYGGVKDLRITPNKWLKPDVLYMNSADEGFGDTYQTN 126
 Db 70 QVLTNIWLMQSWTDHYLQWNVSEYPGVKTFRPDGIWKPDILLYNSADERFDFATFTN 129
 QY 127 VVVRSGGCLLYPPGIFKSTCKMDIAWPFDDQCHDMKFGSWTYDGNLDLVKDEAGD 186
 Db 130 VLVNSSGHCQYLPPIGIFKSSCYIDVRWPFDDVQHCKLKFGSWSYGLDQMQE---AD 186

QY 187 LSDFITNGEWYILGMPGKKNITTYACCPYVDVTFTIMRRRLTYFFNLIVPCVLSS 246
 Db 187 ISGYIPNGEWDLVIGPKRSERYECKEPYDPVTFTVTRRTLYYGLNLLIPCVLISA 246
 QY 247 MALLGFTLPDPGSEKLTGLVTLLSTVFLNVAETLPQVSDAIPLLGTYFNCIMFVWAS 306
 Db 247 LALLVFLPADSGEKISLGTIVLLSTVFLNVAETLPATSDSVPLIAQYFASTMIIVGL 306
 QY 307 SVVLTVVVNLNYHRTADIHEMPQWIKSVFLOLWLPWILRMSRPGCKKITRKTMMNTMRREL 366
 Db 307 SVVTVIVLYQHHDDPGGKMPKRWVILLNMCWFLMRKRPGEKVRPACQHKQRCSL 366
 QY 367 ELKRSKSLLANVLIDDDFRHGPPPPNSTAGNL-----GPGC 407
 Db 367 ASVMSAVA-----PPP--ASGNLLYIGRGLDGVHCVPTPDGSGVVC 407
 QY 408 SIFRTDFRRSVRPSTMEDV--GGGLGSHHRELHLILRELQFITARKKADEAELISDW 465
 Db 408 G-----RMACSPTHDEHLHGQPPGPDPLAKILEEVRYTIANRFRQDESEAVCSEW 460
 QY 466 KFAAMVVDRECLFVFTLTIIATVAVLLSAPHII 499
 Db 461 KFAACVVDRLCLMAFSVFTIICITIGILMSAPNFV 494

RESULT 13

AAW69216
 ID AAW69216 standard; Protein; 502 AA.

XX AC AAW69216;
 XX 09-OCT-1998 (first entry)
 XX DE V274T variant human alpha7 nAChR protein.

XX KW Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cancer;
 KW neurodegeneration; enzyme dysfunction; affective disorder; therapy;
 KW immune dysfunction; diabetic neuropathy; Alzheimer's disease;
 KW schizophrenia.

XX OS Homo sapiens.

XX PN WO9828331-A2.

XX PD 02-JUL-1998.

XX PF 22-DEC-1997; 97WO-US23405.

XX PR 20-DEC-1996; 96US-0771737.

XX PA (ABBO) ABBOTT LAB.

XX PI Briggs CA, Gopalakrishnan M, McKenna DG, Monteggia LM;

XX PI Roch J, Sullivan JP, Touma E;

XX DR WPI: 1998-377593/32.

XX DR N-PSDB; AAV44687.

XX PT Nucleic acid encoding variant of human alpha7 nicotinic
 PT acetylcholine receptor sub-unit - used to identify modulators of
 PT the receptor, potentially useful for treating neuro-degeneration,
 PT cancer, affective disorders etc.

XX PS Claim 15; Fig 2; 44pp; English.

XX CC This sequence is the V274T variant of human alpha7 nicotinic
 CC acetylcholine receptor (nAChR) subunit of the invention. Cells containing
 CC the DNA are used to express the protein and to identify modulators of
 CC alpha7 nAChR activity or cytoprotective agents, e.g. antisense
 CC compounds or antagonists that are potentially useful for treating
 CC neurodegeneration, enzyme dysfunction, affective disorders and immune
 CC dysfunction, such as cancer, post-herpetic neuralgia, diabetic

CC neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,
 CC psychosis and schizophrenia. Probes based on the DNA are used to detect
 CC the DNA in usual hybridisation or amplification tests, while monoclonal
 CC antibodies are used to detect the protein for diagnosis (in vitro or by
 CC in situ immuno-fluorescent assay). Compared with wild-type alpha7 nACHR,
 CC the protein has about 100-fold greater sensitivity to cholinergic
 CC receptor agonists (nicotine or acetylcholine) and response to these
 CC agonists decays more slowly, but the wild-type inward rectification is
 CC retained.

XX SQ Sequence 502 AA;

Query Match 47.5%; Score 1254.5; DB 19; Length 502;
 Best Local Similarity 48.4%; Pred. No. 2.4e-123;
 Matches 249; Conservative 75; Mismatches 139; Indels 51; Gaps 7;

Qy 8 LALLA-LLPVSEQPHKRLNALLANYNTLERPVANSEPLEVRFGLTILQIIVDDEKN 66
 Db 10 LALAASLLHVSLOGEFORKLYKELVKNPLERPVANDSQPLTVYFSLSLQIMDVDEKN 69
 Qy 67 QLLITNIWLSLEWNDYLNLRWNSYGGVKDLRITPNKLRKPDVLMYNSADEGFGDTYQTN 126
 Db 70 QVLTNIWLSQSWTDHYLQNNVSEYPGVKTVRFDPGOIKWKPDIILYNSADERFATHTN 129
 Qy 127 VVVRSGSCLYVPGIFKSTCKMDIAWPPDDQHCMDKFGSWTYDGNQLDLVLKDEAGD 186
 Db 130 VLVNSSGHGQVLPPIGFKSCYIDVRWFPDQVHCKLFGSWSYGGWSLDLQMOE---AD 186
 Qy 187 LSDFITNGEYWLIGMPGKKNITVACCPYVDVTFIMIRRTLYFFNLIIVPCVLIS 246
 Db 187 ISGYPNGEYWLIGMPGKKNITVACCPYVDVTFIMIRRTLYFFNLIIVPCVLIS 246
 Qy 247 MALLGFTLPDPSGEKLTGLVILLSTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306
 Db 247 LALLVFLPADSGEKISGITVLLSTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306
 Qy 307 SVLTVVVLNHHRTADIEHMPQIKSVFLQWLPIILRMSRPGKTIKTKIMTMRREL 366
 Db 307 SVVTVVIVLQVHHDPDGGKMPKTRVILLNWCALFMRKRGDKVRPACQHKRCSL 366
 Qy 367 ELKRSKSLANLVIDDDDFRHGPPPPNPNSTAGNL-----GPGC 407
 Db 367 ASVMSAVA-----PPP--ASNGNLLYIGRGLDGVHCVPTDGSVVC 407
 Qy 408 SIFRTDFRRSRVPSMEDV--GGGLGSHHRELHLILRELQFITARMKKADEAEELISDW 465
 Db 408 G-----RMACSPTHDEHLLHGQPPGEGDPLAKILEEVRYIANFRCDQSEAVCSEW 460
 Qy 466 KFAAVVDRCFLVFTLTITATVAVLLSAPHII 499
 Db 461 KFAACVVDRLCLMAFSVFTICTIGILMSAPNFV 494

RESULT 14

ID AAW12368 standard; Protein; 502 AA.

XX AC AAW12368;

XX DT 17-JUN-1997 (first entry)

DE Neuron alpha-bungarotoxin binding protein alpha subunit.

XX Neuron alpha-bungarotoxin binding protein alpha 1; cholinergic;
 KW ligand binding; ion channel.

XX Gallus sp.

XX Key Location/Qualifiers
 FH Peptide 1..22
 FT Peptide /label= Sig_peptide
 FT Protein 23..502
 FT Protein /label= Mat_protein

XX US5599709-A.
 PN 04-FEB-1997.
 PD 28-SEP-1989; 89US-0413947.
 PF 28-SEP-1989; 89US-0413947.
 XX 28-SEP-1989; 89US-0413947.
 PR (SALK) SALK INST BIOLOGICAL STUDIES.
 XX Lindstrom JM, Schoepfer RD;
 PI WPI; 1997-118297/11.
 DR N-PSDB; AAT59196.

XX New isolated neuronal alpha-bungarotoxin-binding protein DNA - used
 PT to screen cholinergic agents and other drugs which may affect ligand
 PT binding, ion channel or other activities of the protein.
 XX Example; Fig 2A-B; 18pp; English.

XX The alpha subunit (AAW12368) and alpha2 subunit (AAW12369) amino acid
 CC sequences of chick neuronal alpha-bungarotoxin binding protein
 CC (ABBP) were deduced from newly isolated DNA molecules (AAT59196-97)
 CC obtd. from an 18-day chick embryo cDNA library. ABBP subunits can
 CC be produced in recombinant host cells, pref. a bacterium, and used
 CC in the screening of cholinergic agents and other drugs that may
 CC affect the ligand binding, ion channel or other activity of intact
 CC ABBP subtypes. The ABBP alpha1 and alpha2 subunits can also be
 CC used to produce subunit peptides for use as immunogens for
 CC preparing antibodies to permit affinity purification of subtypes
 CC and their histological location.

XX SQ Sequence 502 AA;

Query Match 47.5%; Score 1253; DB 18; Length 502;
 Best Local Similarity 48.8%; Pred. No. 3.5e-123;
 Matches 250; Conservative 81; Mismatches 145; Indels 36; Gaps 8;

Qy 2 APLAALALALLSPQSGHEKRLNALLANYNTLERPVANSEPLEVRFGLTILQIIVD 61
 Db 5 ALMLWLLAAAGLVRESLOGEFORKLYKELNKNPLERPVANDSQPLTVYFSLSLQIMD 64
 Qy 62 VDEKQQLITNIWLSLEWNDYLNLRWNSYGGVKDLRITPNKLRKPDVLMYNSADEGFGD 121
 Db 65 VDEKQVLTITNIWLTQWYTDHYLQNNVSEYPGVKTVRFDPGOIKWKPDIILYNSADERF 124
 Qy 122 TYQTNVVRSGSCLYVPGIFKSTCKMDIAWPPDDQHCMDKFGSWTYDGNQLDLVLK 181
 Db 125 TFHTNVLNNSGHGQVLPPIGFKSCYIDVRWFPDQVHCKLFGSWSYGGWSLDLQMOE 184
 Qy 182 EAGDGLSDFITNGEYWLIGMPGKKNITVACCPYVDVTFIMIRRTLYFFNLIIVPC 241
 Db 185 ---ADISGYSNGEYWLIGMPGKKNITVACCPYVDVTFIMIRRTLYFFNLIIVPC 241
 Qy 242 VLISSMALLGFTLPDPSGEKLTGLVILLSTVFLNLVAETLPQVSDAIPLLGTYFNCIM 301
 Db 242 VLISALALLVFLPADSGEKISGITVLLSTVFLNLVAETLPQVSDAIPLLGTYFNCIM 301
 Qy 302 FWAVSSVVLTVVNLNHHRTADIEHMPQIKSVFLQWLPIILRMSRPGKTIKTKIMT 361
 Db 302 IIVGLSVVTVVIVLQVHHDPDGGKMPKTRVILLNWCALFMRKRGDKVRPACQHK 361
 Qy 362 RMRELELKERSSKS-----LLANVLIDIDDDF-----HGPPPPNPNSTAGNLGPGC 412
 Db 362 RRCSSWEMTVSGQCSNGLMYI--GFRGLDGVHCTPTTDSVIGRM--TCS----- 413
 Qy 413 DFRRSFVRPSMEDVGGGLGSHH-----RELHLILRELQFITARMKKADEAEELISDW 467
 Db 414 -----PTEENL---LHSGHPSEGDPLAKILEEVRYIANFRCDQSEAEICNENK 462
 Qy 468 AAVVDRCFLVFTLTITATVAVLLSAPHII 499

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OM nucleic - nucleic search, using sw model

Run on: August 21, 2003, 03:48:31 ; Search time 3282.73 Seconds
(without alignments)
11127.831 Million cell updates/sec

Title: US-09-303-232-5_COPY_95_1597

Perfect score: 1503

Sequence: 1 atggccctatgttggcgc.....cacgcgcatcatcgtgcaa 1503

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	423.8	28.2	885	10	BG632919	BG632919 GH16126.3
2	331.2	22.0	607	9	AI292581	AI292581 GH15518.5
3	301.2	20.0	1201	9	AL530299	AL530299 AL530299
4	293.2	19.5	2940	11	AK034228	AK034228 Mus muscu

5	293.2	19.5	3230	11	AK083157	AK083157 Mus muscu
6	281.6	18.7	3483	11	AK081254	AK081254 Mus muscu
7	281.6	18.7	4037	11	AK049722	AK049722 Mus muscu
8	281.6	18.7	4046	11	AK051742	AK051742 Mus muscu
9	275.6	18.3	1864	11	AK053497	AK053497 Mus muscu
10	275.6	18.3	2316	11	AK051730	AK051730 Mus muscu
11	275.6	18.3	3126	11	AK080415	AK080415 Mus muscu
12	258.8	17.2	2010	11	AK080475	AK080475 Mus muscu
13	256.6	17.1	833	14	CB245337	CB245337 UI-M-FY0-
14	246.2	16.4	4290	11	AK029177	AK029177 Mus muscu
15	240	16.0	908	13	BUI49265	BUI49265 AGENCOURT
16	239.2	15.9	922	13	BUI15857	BUI15857 AGENCOURT
17	236.8	15.8	1036	13	BX437801	BX437801 BX437801
18	234.8	15.6	755	13	B0702422	B0702422 UI-M-FY0-
19	228.2	15.2	615	14	CB149460	CB149460 K-EST0205
20	220.4	14.7	2513	11	AK033068	AK033068 Mus muscu
21	212.6	14.1	1034	13	BX403124	BX403124 BX403124
22	210.8	14.0	755	10	AK914206	AK914206 EST345510
23	210.4	14.0	658	12	BW711715	BW711715 UI-E-CL1-
24	210.4	14.0	797	14	CA326954	CA326954 UI-M-FY0-
25	202.2	13.5	939	13	BQ720344	BQ720344 AGENCOURT
26	202	13.4	607	14	CA751482	CA751482 UI-M-FY0-
27	201.8	13.4	4589	11	AK030464	AK030464 Mus muscu
28	199.2	13.3	720	14	CA373069	CA373069 647093 NC
29	198	13.2	763	14	CA374163	CA374163 648474 NC
30	194.8	13.0	411	12	BI516733	BI516733 BB160023A
31	193.8	12.9	410	12	BI516843	BI516843 BB160023B
32	193.6	12.9	640	14	CB244439	CB244439 UI-M-FY0-
33	192.8	12.8	2074	11	AK087554	AK087554 Mus muscu
34	192.2	12.8	932	29	CNS02DCP	AL192274 Tetraodon
35	190.6	12.7	1001	29	CNS03RTG	AL257677 Tetraodon
36	188.4	12.5	882	12	BI195149	BI195149 602944157
37	188.2	12.5	1101	29	CNS000IF	AL058211 Drosophil
38	187.2	12.5	1007	29	CNS00HJU	AL073676 Drosophil
39	186.8	12.4	3827	11	AK041217	AK041217 Mus muscu
40	183.8	12.2	1835	11	AK010496	AK010496 Mus muscu
41	182.8	12.2	586	13	BX299163	BX299163 BX299163
42	179.8	12.0	978	29	CNS006F9	AL064281 Drosophil
43	179.6	11.9	830	10	BG190899	BG190899 RST9980 A
44	177.8	11.8	809	10	BG404575	BG404575 602420721
45	176.6	11.7	672	10	BB637693	BB637693 BB637693

ALIGNMENTS

RESULT 1	BG632919/c	BG632919	885 bp	mRNA	linear	EST 23-APR-2001
LOCUS	GH16126.3	prime GH Drosophila melanogaster head	POT2	Drosophila		
DEFINITION	melanogaster cdna clone GH16126.3 similar to CG4128: FBan0004128					
	'ion channel', located on: 2L 30D1-30E1:: 04/10/2001, mRNA sequence.					
ACCESSION	BG632919					
VERSION	BG632919.1	GI:13758409				
KEYWORDS	EST.					
SOURCE	Drosophila melanogaster (fruit fly)					
ORGANISM	Drosophila melanogaster					
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;					
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;					
	Ephydroidea; Drosophilidae; Drosophila.					
REFERENCE	1 (bases 1 to 885)					
AUTHORS	Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,					
	Lewis,S. and Rubin,G.M.					
TITLE	BDGP/HMI Drosophila EST Project					
JOURNAL	Unpublished					
COMMENT	Other_ESTs: GH16126.5prime					
	Contact: Stapleton, M.					
	BDGP					
	Lawrence Berkeley National Lab					
	One Cyclotron Rd, Berkeley, CA 94720, USA					
	Fax: 510 486 6798					
	Email: http://www.fruitfly.org/EST , est@fruitfly.berkeley.edu					
	Based upon the presence of a XhoI site followed by a run of 14 or					

QY 131 AGAGCGAAGCGGTAGAGGTTCGGCTTGACCTTGACGAGCAAAATCATTTGACGTGGACG 190
D 195 AATCGGAGCCCTGGAGGTTAAGTTCGGACTGACGCTGCAGCAGATCATCGACGTGGACG 254
QY 191 AGAAGAAATCAACTATATATAACCAATATATGCTGCTGGAGTGAATGACTACAACC 250
D 255 AGAAGAAATCAGCTTCTATACCAATATATGCTGCTGGAGTGAATGACTACAATC 314
QY 251 TGAGGTGGAAACGACGAGTATGCGGGGTCAAGGACCTCAGGATCAGCGCCCAACAAGT 310
D 315 TGGCTGGAATGAACGGAATACGCGGGGTCAAGGATCTACGAATCAGCGCCCAACAAGC 374
QY 311 TGTGGAGCGGAGCTCTTATATATATAGTCTGACGAGGTTTGGAGGACCTAC 370
D 375 TGTGGAGCGGAGCTCTTATATATAGTCTGACGAGGTTTGGAGGACCTAC 434
QY 371 AGACCAAGCTGTGGTTCAGAGCGGCGGAGTTCCTGTACGTCGACCTGGCATATCA 430
D 435 ACACGAGCTGTGGTTCAGAGCGGCGGAGTTCCTGTACGTCGACCTGGCATATCA 494
QY 431 AGACCAATGCAAGATGACATCGCTGCTTCCCTTCGACGACCAACACTGTGATATGA 490
D 495 AGACCAATGCAAGATGACATCGCTGCTTCCCTTCGACGACCAACACTGTGATATGA 554
QY 491 AGTTCGCTAGCTGACATGACGCGCAATCAGTTGGATCTGGTGCTAA 538
D 555 AATTCGCTAGTTCGACTTACGATGGAATCAGTTGGATTTGGA 602

RESULT 3

AL530299

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL530299 1201 bp mRNA linear EST 23-MAY-2003
AL530299 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
cDNA clone CS0DD007YP05 5-PRIME, mRNA sequence.

AL530299

AL530299

EST.

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

On Feb 13, 2001 this sequence version replaced gi:12793792.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

7646.r For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DD007CH03QPL&cluster=7646.r. Contact :

Feng Liang Email : fliang@life.com

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DD007CH03QPL.

Location/Qualifiers

1. 1201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

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/clone.lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

258 a 326 c 319 g 273 t 25 others

BASE COUNT

ORIGIN

RESULT 4

AK034228

LOCUS

DEFINITION

ACCESSION

VERSION

AK034228

Mus musculus adult male diencephalon cDNA, RIKEN full-length

enriched library, clone:933016516 product:cholinergic receptor,

nicotinic, alpha polypeptide 4, full insert sequence.

AK034228

AK034228.1

GI:26329798

2940 bp

mRNA

linear

HTC 05-DEC-2002

mus musculus adult male diencephalon cDNA, RIKEN full-length

enriched library, clone:933016516 product:cholinergic receptor,

nicotinic, alpha polypeptide 4, full insert sequence.

AK034228

Mus musculus adult male diencephalon cDNA, RIKEN full-length

enriched library, clone:933016516 product:cholinergic receptor,

nicotinic, alpha polypeptide 4, full insert sequence.

AK034228

AK034228.1

GI:26329798

Query Match 20.0%; Score 301.2; DB 9; Length 1201;
Best Local Similarity 60.2%; Pred. No. 3e-72;
Matches 537; Conservative 10; Mismatches 333; Indels 12; Gaps 3;

QY 65 ACCAGAGAGACTCCCTGAACGGCTTCTGCGGCACTACACACCCCTGGAGCGACCGGTGG 124
D 197 WCCAGAGAGAGCTTTCACAGGAGCTGGTCAAGAACTACAATCCCTTTGGAGAGCGCGGTGG 256
QY 125 CCAACAGAGAGCGACCGCTAGAGGTCAGGTTTCCGGCTTGCACCTTGCAGCAAAATCATTTGACG 184
D 257 CCANTGACTCGCAACCACTCACCGTCTACTTCTCCCTGAGCCCTCTGCAGATCATCGACG 316
QY 185 TGGACGAGAGAAATCAACTACTTATTAACCAATATATGGCTGTGGTGGAGTGAATGACT 244
D 317 TGGATGAGAAGAACCAAGTTTAAACCAACCAATTTGGCTGCAAAATGTCTTGGACAGATC 376
QY 245 ACAACCTGAGGTGGAGACGACGAGTATGGCGGGGTCAAGGACCTCAGGATCAACCCCA 304
D 377 ACTATTACAGTGAATGTGTCAAGATATCCAGGGGTGAAGACTGTTCGTTCCTCCAGATG 436
QY 305 ACAAGTTGTGGAGCGGACGCTCTTATGTATAATAGTGTGACGAGGGTTTGTGACGGGA 364
D 437 GCCAGATTTGGAAACCAAGACATCTTCTCTATAACAGTGTGATGAGCGCTTTGACGCCA 496
QY 365 CTTACAGACCAACGTTGGTGTGAGAGCGGGGAGTTGCCCTGTACGTGCTGCCACCTGGCA 424
D 497 CATTCACACTAACGTTGTTGGTGAATTTCTTGGGCAATGCCAGTWCCTGCCCTCCAGGCA 556
QY 425 TATTCAGAGACATCAAGATGGACATCGCTGGTGTTCCTTCGACGACCAACACTGTG 484
D 557 TATTCAGAGATTCCTCTACATCGATGATGCTGGTTCCTTTGATGTCAGACATGCA 616
QY 485 ATATGAAGTTCCGTAGCTGACATATGACGCGCAATCAGTTGGATCTGCTGCTAAAAGATG 544
D 617 AACTGAAGTTGGTCTCTGCTTACGAGGCTGGTCTTGGATCTGCAGATGCAGGA -- 674
QY 545 AGCAGGCGGGGATCTATCGGACTTCATTAACAAATGGGAGTGGTATCTAATAGGAATGC 604
D 675 -----GGCAGATATCAGTGGCTATATCCCAATGGAGATGGGACCTAGTGGGAATCC 727
QY 605 CAGGCAAAAGAACACAATAACATACGCTGCTGCCCGCCGACCTACGTGGAGTCACT 664
D 728 CCGGCAAGAGGAGTGAAGGTTCTATGAGTCTGCAAGAGCCCTACCCCGATGTACCT 787
QY 665 TCACCATCATGATAAGAAGACGAACTGTACTACTTCTTCAACCTGATGCTGCCGTGG 724
D 788 TCACAGTACCATGCGCGCCGACGACCTCTACTATGGCTCAACCTGCTGATCCCTGTG 847
QY 725 TGTGATCATCGATGGACCTCTCGGCTTCACATGCGCAGACACTCGGAG -- AGAA 782
D 848 TGTCTATCTCCGCCCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 907
QY 783 ACTCACACTTGGAGTCACTATCTTCTATCGCTGACGGTGTTCCTCAACCTGTAGCCGA 842
D 908 ATTTCCTTGGGATTAACAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 967
QY 843 GACCTTGCACAGGCTCCGACGCTATCCCTCTTGTAGGAGACGCTACTTCAATTTGATCAT 902
D 968 GATATGCCCGCAACATCCGATTCGGTACCATTTGAWAGCCAGTCTTCTCGCCAGACCAT 1027
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D 1028 GATCATCGT - GGGCTTTGGGTGTTGKRMGGTGTATCGTGTCTGCTGCTGCTGCTGCTG 1078

RESULT 4

AK034228

LOCUS

DEFINITION

ACCESSION

VERSION

AK034228

Mus musculus adult male diencephalon cDNA, RIKEN full-length

enriched library, clone:933016516 product:cholinergic receptor,

nicotinic, alpha polypeptide 4, full insert sequence.

AK034228

AK034228.1

GI:26329798

2940 bp

mRNA

linear

HTC 05-DEC-2002

mus musculus adult male diencephalon cDNA, RIKEN full-length

enriched library, clone:933016516 product:cholinergic receptor,

nicotinic, alpha polypeptide 4, full insert sequence.

AK034228

Mus musculus adult male diencephalon cDNA, RIKEN full-length

enriched library, clone:933016516 product:cholinergic receptor,

nicotinic, alpha polypeptide 4, full insert sequence.

AK034228

AK034228.1

GI:26329798

KEYWORDS

SOURCE

ORGANISM

HTC; CAP trapper.
Mus musculus
Mus musculus

REFERENCE

AUTHORS

Ukariyotia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

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AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
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Shibata, K., Itoh, M., Aizawa, K., Nagao, K., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multipillar sequencer
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Arakawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
Saito, T., Okazaki, Y., Gojohori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,
Quackenbush, J., Schriml, L.M., Stauber, J., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Canciani, P., de Bonaldo, M., Brownstein, M.J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D.A., Kaniya, M., Lee, N.H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombauts, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L.,
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Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851

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AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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6 (bases 1 to 2940)

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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,

TITLE

JOURNAL

Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES

source

Location/Qualifiers
1. 2940
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116. 2005
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CDS

BASE COUNT 630 a 903 c 755 g 652 t
ORIGIN
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Best Local Similarity 55.9%; Pred. No. 7.4e-70;
Matches 578; Conservative 0; Mismatches 453; Indels 3; Gaps 1;
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Qy 131 AGAGCGAACCGCTAGAGTTCAGGTTTCGGCTTGTGACCTTGCAGCAAAATCATTCACGTGACG 190
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Qy 191 AGAAGATCAACTACTTATATACCAATATATGGCTGTGCTGTGGAGTGAATGACTACAC 250
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Db 414 TGGCGCTGGGACCCCTGGTGTACGAGATGTCACCTCCATCGCGATCCCATCTGAACCTCA 473
QY 311 TGTGGAAGCGGACGCTCTATGTAATAGTGTCTGACGAGGCTTTGACGGGACCTACC 370
Db 474 TGTGGAAGCGGACGCTCTATGTAATAGTGTCTGACGAGGCTTTGACGGGACCTACC 533
QY 371 AGACCAACGCTGTGTGTGAGAAAGCGGCGAGTTGCTGTACGCTGCGACCTGGCATATTC 430
Db 534 TAACCAAGGCCACCTGTTCTATGATGGCGGTGTGCGAGTGGACACCCCGGCCATCTATA 593
QY 431 AGAGCACATGCAAGATGGACATCGGTGGTGTTCCTTCGACGACCAACACTGTGATGTA 490
Db 594 AGAGCTCTGCGACATGCGACGTCACCTTCTTCCCTTCGACGACCAAGACTGTACCATGA 653
QY 491 AGTTCGGTGTGCTGACATATGACGCAATGCTGTGATGCTGTGCTGTGAAAGATGAGCGAG 550
Db 654 AGTTTGGTCTGGACCTAGCAGACAGGCAAGTTCATGCTGTGAGCATGCACAGCCGTG 713
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QY 611 AAAGAACACATAATACGCTGCTGCGCGAGCCCTACGTTGGAGCTCACTTCACCA 670
Db 771 CCTACACACACAGGAATGATGCTGTGCGGAGATCTATCTGACATCACTAGCCCT 830
QY 671 TCATGATAAGAACGACCACTTGTACTACTTCTTCAACCTGATCGTCCGCTGGTCTCA 730
Db 831 TCATGATCGCGGACTGCGACCTGTCTACACCATCAACCTTATCATCTCCGCTGCTCA 890
QY 731 TCTATCATGTCGACCTCTCGGCTTCACACTGCGACGACTCGGAGAGAACTCACAC 790
Db 891 TCTCTGCTCTACCGTGGTCTTCTATCTGCGCTCGAGTGGCGGAGAGGTCACGC 950
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Db 951 TGTGCTATCGGTGCTTCTTCTACCGCTTCTTCTGCTGCTCACTCACTGCTGCTATCC 1010
QY 851 CACAGCTCTCCGACGCTATCCCTCTTAGGAGCTGCTTCAATTCATCTGTTTCATGG 910
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QY 1031 GAATGTCGAGGCA 1044
Db 1191 TCATGAGCGGCCA 1204

AK083157 3230 bp mRNA linear HTC 05-DEC-2002
Mus musculus adult male hippocampus cDNA, RIKEN full-length
enriched library, clone:C630019M18 product:cholinergic receptor,
nicotinic, alpha polypeptide 4, full insert sequence.
AK083157
AK083157 1 GI:26350296
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kusunagi, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Aizawa, K., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G.,
Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
Mancinelli, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
Ring, B., Rinchald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,
Toyo-oka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S.
and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3230)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koyu, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp,

URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.go.jp/>
URL: <http://fantom.gsc.riken.go.jp/>.

FEATURES

Location/Qualifiers

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/strain="C57BL/6J"

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/tissue_type="hippocampus"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="adult"

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putative"

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/db_xref="GI:26350297"

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SSCSDYVTFPQDQCTMRFGSWTYDKAKIDLVMSHRVDOLDWFSGEWIIVDAVG
TYNPKYECCEALVPDIYAFILRLPLFTINLIIPCLILSCLTVLFFVLPSCGPK
VTLGISVLSITVLLIETIIPSTSLVPLIGELYLLFTMIFVTLISIVIVFLNVHH
RSPHTPMVAWRVFLDIIVRLFLMRKPVVNDNRRLIESMHKMANAPRFWPEPES
EPGLIDICNOGLSPAFTFCNMDTAVETQTCRSPHKYDPDLKTSVDEKASCPSPG
SCHPNSSGAPLIVKARLSVQHVPSQEAEGSIRCRSRIQYCVSDQAASLTESK
TVGSPASLKTRPSLPVSDQTSCKCTCKPSPVPTVLKAGTKAPPOHLLSPAL
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LAGNI"

BASE COUNT 699 a 992 c 816 g 723 t

ORIGIN

Query Match 19.5%; Score 293.2; DB 11; Length 3230;
Best Local Similarity 55.9%; Pred. No. 7.8e-70;
Matches 578; Conservative 0; Mismatches 453; Indels 3; Gaps 1;

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Db 94 TCTTAGGACCGGCTTGTGCTGCTAGCAGCCACATAGAGACCCGGGCCCATCGGAGG 153
Qy 71 AGACATCTTGAACCGTGTGTCGCGAATACACACCCCTGGACCGACCGGTGCCACAG 130
Db 154 AGCGGCTCTGAAGAGACTCTTCTTGCTGCTACAAAGAGTGTCTCGGCCAGTAGCCAA 213
Qy 131 AGACGCAACCGCTAGAGGTGAGTTCGGCTTGCCTTGCAGCAAAATCATTTGACGTGAGC 190
Db 214 TCTCAGATGTGCTTGTGCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 273
Qy 191 AGAAGATCAACTACTTATACCAATATATATGCTGTGCTGTGCTGTGCTGTGCTGTGCT 250
Db 274 AGAAAAACCATGATGACGACCAACGTTGGTGGTGAAGCAGGAGTGCATGACTACAAAC 333
Qy 251 TGAGTGAACGACGACGATGATGGGGGTCAAGGACCTCAGGATCAGCCCAACAAAGT 310
Db 334 TGCCTGGGACCCCTGGTGACTACAGAAATGTCACTCCATCCGATCCCATCTCAACTCA 393
Qy 311 TGTGAAGCCGCGCTCTTATGATATATAGTGTGCTGACGAGGGTGTGACGGGACCTACC 370
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Qy 371 AGACCAACAGTGGTGGTTCAGAGGGCGGAGTGGCTGTACGTGCGCCACCTGGGCATATCA 430
Db 454 TAACCAAAAGCCACCTGTTATGATGGCGTGTGACAGTGCACACCCCGCCATCTATA 513
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Qy 491 AGTTCGGTAGCTGGACATATGAGGCAATCAGTTGGATCTGGTCTAAAAGATGAGGAG 550
Db 574 AGTTGGTCTCGACCTAGCAGCAAGGCCAAGATTGACTTGGTGGAGCATGCACAGCCGTG 633
Qy 551 GCGCGCATATCGGACTTTCATAACAAATGGGAGTGGTATCTAATAGGAATGCCAGCA 610
Db 634 TGGACCAACT--GGACTTCTGGGAAAGTGGGAGTGGTCAATGTGTGATGCTGGCGCA 690
Qy 611 AAAAGAACAAATACATACGCGTGTGCCCCGAGCCCTACGTGGAGCTCACCTTCACCA 670
Db 691 CCTACAACACCAAGAGTGAATGCTGTCGCGAGATCTATCTTGACATCACCTACGCT 750
Qy 671 TCATGATAAGAAAGACGAACCTTGTACTTCTTCAACCTGATCGTCCCGTGGCTGCTGA 730
Db 751 TCATCATCCCGGACTGCCACTGTCTACACCATCAACCTATCATCCCGTGGCTGCTCA 810
Qy 731 TCTCATGATGGCACTCTCGGTTACACTGCCACGAGCTCGGAGAGAACTCACAC 790
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Qy 851 CACAGGTCTCCGACGCTATCCCCCTGTAGGAGCTACTTCAATTCATGCTCATGTTTCAT 910
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Db 991 TCACCCCTCCATTTGCTATCAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1050
Qy 971 TACATGAATGCCACGCTGATGAATAAATCAGTATTCCTTACAAATGTTGCTGCTGCTGCT 1030
Db 1051 CACACACCTGCGCGCTGGTGGCAGAGTCTTCTGCGACATGTGCTGCTGCTGCTGCT 1110
Qy 1031 GAATGCTGAGGCCA 1044
Db 1111 TCATGAAGCGCCCA 1124

RESULT 6
AK081254
LOCUS
DEFINITION
AK081254
Mus musculus adult male corpus striatum cDNA, RIKEN full-length
enriched library, clone: C030030P04 product: cholinergic receptor,
nicotinic, beta polypeptide 2 (neuronal), full insert sequence.
AK081254
ACCESSION
AK081254.1 GI:26099790
VERSION
HTC; CAP trapper.
KEYWORDS
Mus musculus (house mouse)
SOURCE
ORGANISM
Mus musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1
REFERENCE
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636
2
REFERENCE
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes

QY	819	GGTGTTCCTCAACCTGGTAGCGAGACCTGCCACAGAGTCTCTCGAGAGCTATCCCTCGT	878
DB	1034	GGTGTTCCTGGCTGCTCATCTCCAAGATTGTGGCTCCACACTCCTCTCGAGACTACCGCTGGT	1093
QY	879	AGGAGAGTACTTCAATGGTGCATCATGTTCATGTGTAGTGGTGGTCTGTGGTACTGACTGGT	938
DB	1094	GGGAAGTAGTACCTCATGTTCCACATGGTGTAGTCACCTTCTCCATCGTCACTAGCGGTG	1153
QY	939	GGTACTCAATTAACCACTGCGAACACGTGATACATGAAATGCCACAGTGGGATAAAATC	998
DB	1154	TGTGCTCATGTGCACACCGCTTCGCTACCAGGCACACCATGGCGCCCTGGGTCAAGGT	1213
QY	999	AGTATTCCTACAAATGTTGCCATGGTACTGCGAATGTGAGGCCAGG	1046
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RESULT 7			
LOCUS	AK049722	4037 bp	linear
DEFINITION	Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library; clone:c530044p16 product:cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal), full insert sequence.		
ACCESSION	AK049722	GI:26340459	
VERSION	AK049722.1		
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Ueda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequeencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schram, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Cariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,		

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Best Local Similarity		57.7%	Pred.	No. 1.4e-66				
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						Gaps		2
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DB	970	CTTGCCCTCAGACTGTGGTGAAGAAGTGAACACTTTGTTCTGTGTGTGGCGCTCAC	1029					
QY	819	GGTGTTCCTCAACCTGGTAGCCGAGACCTTCCACAGGCTCTCCGACGCTATCCCCCTGTT	878					
DB	1030	GGTGTTCCTGCTGCTCATCTCCAAGATTGTGCTCCCACTCCCTCGACGTACCGCTGGT	1089					
QY	879	AGGAGCTACTTCAATTTGCAATCATGTTTCATGGTAGCTGCTGTGTGTACTGACTGTGGT	938					
DB	1090	GGGAAGTACCTCATGTTTTCACCATGGTGTGTAGTCAACCTTCTCCATCTGCTACTAGCGTGTG	1149					
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DB	1150	TGTGCTCAATGTGCACACCGTTCGCCCTACCGACACCATGCGGCCCTGGGTCAAAGT	1209					
QY	999	AGTATTCTACAATGTTTGGCATGATGATGCGAATGTGAGGCGCAGG	1046					
DB	1210	GGTCTTCTGGAGAGCTGCCACCTCTCTTCTTCTCCAGCAGCCACG	1257					
RESULT 8								
AK051742								
LOCUS								
AK051742 4046 bp mRNA linear HTC 05-DEC-2002								

RESULT 8
AK051742
LOCUS

DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

REFERENCE
AUTHORS

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REFERENCE
AUTHORS

TITLE
JOURNAL
MEDLINE
PUBMED

Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone: D130070121 product: cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal), full insert sequence.

AK051742 GI:26342173

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

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2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

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Genome Res. 10 (10), 1617-1630 (2000)

20499374

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3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,

Yamamoto, R., Matsumoto, H., Sakeguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multiplexed capillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

4

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,

Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,

Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamakata, I.,

Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,

Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,

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Carninci, P., de Bona, M. F., Brownstein, M. J., Bult, C.,

Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,

Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,

Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,

Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,

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Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L.,

Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S.

and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

21085660

11217851

5

The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 4046)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,

Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kouda, M.,

Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES

Location/Qualifiers

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Matches 547; Conservative 0; Mismatches 389; Indels 12; Gaps 2;

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Qy 219 ATGCTGTCTGTTGAGTGGATGACTACACCTGAGTGGAGCAGACAGGATGCGG 278

Db 451 CTGCTGACCCAGAGTGGGAGGATTTATCGCCTCACATGGAAGCCTGAGGATTTGCAAA 510

Qy 279 GGTCAAGACCTCAGGATCAGCCCAACAAAGTCTTGGAGCGGACGCTCTATGTATAA 338

Db 511 TATGAAGAAGTCCGACCTCCCTTCAAGCACATCTGCTCCGATGTGGTCTTATACAA 570

Qy 339 TAGTGTGACAGAGGTTTTTACGGGAGCTACCAAGCAACGCTGGTGTGACAGAGGGGG 398

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Qy 399 CAGTTGCTGTACGTGCGACCTGCATATTAACAGCAGCATGCAAGATGGACATCGCGTG 458

Db 631 CAGATCTTTTGGTACCGCTGCCATCTACAGAGGCGATAGAGATTGAGGTGAAGCA 690

Qy 459 GTTTCCTTCGACCAACCAACTGTGATATGAAGTTCGGTACGTCGACATATGACGGCAA 518

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DEFINITION
Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:EL30103E14 product:NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
ACCESSION
AK053497
VERSION
AK053497.1 GI:26343494
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to


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DEFINITION	Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730007P14 product:NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.		
ACCESSION	AK080415		
VERSION	AK080415.1	GI:26348538	
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ORGANISM	Mus musculus		
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AUTHORS	Carninci,P. and Hayashizaki,Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
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AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakauchi,S., Ikegami,T., Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	20530913		

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PUBMED
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AUTHORS

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Caldarelli, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Hofmann, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kaniya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Noirone, P., Ring, B., Ringwald, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

21085660

PUBMED
REFERENCE
AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 3126)

JOURNAL

REFERENCE

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/.

Location/Qualifiers

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Matches 570; Conservative 0; Mismatches 469; Indels 3; Gaps 1;
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Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bujung, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Maccioni, L., Mashima, A., Mazzarelli, J., Mombaerts, P., Nordone, P., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y.

TITLE
Functional annotation of a full-length mouse cDNA collection

JOURNAL
Nature 409 (6821), 685-690 (2001)

REFERENCE
21085660

PUBMED
11217851

REFERENCE
5

AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL
Nature 420, 563-573 (2002)

REFERENCE
6 (bases 1 to 2010)

AUTHORS
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
Direct Submission

JOURNAL
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES
Location/Qualifiers

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17.2%; Score 258.8; DB 11; Length 2010;
Query Match 55.0%; Pred. No. 2.3e-60;
Best Local Similarity

BASE COUNT	489 a	536 c	465 g	520 t
ORIGIN				
Query Match		17.2%	Score 258.8;	DB 11; Length 2010;
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RESULT 13
CB245337

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 AK029177
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 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
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 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
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 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384 format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
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 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yananaka, I., Saito, T., Okazaki, Y., Gojohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Glissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nkaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Mombauts, P., Nordone, P., Ring, B., Rongwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)
 21085660
 11217851
 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 4290)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
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College of Medicine); available through Life
Technologies.

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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SUMMARIES

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24	302.8	20.1	1808	24	AAT59528	Alpha4 subunit of
25	302.2	20.1	1908	18	AAT48236	Neuronal nicotinic
26	302.2	20.1	2277	15	AAV12199	Human neuronal nic
27	302.2	20.1	2277	16	AAQ09387	Alpha 2 subunit of
28	302.2	20.1	2277	24	ABV73243	Human neuronal NAC
29	302.2	20.1	2277	24	ABS54870	Human neuronal nic
30	302.2	20.1	2664	18	AAT48235	Neuronal nicotinic
31	302.2	20.1	2664	24	ABK92165	Prostate cancer-as
32	295.2	19.6	1896	24	ABL45870	Modified acetylcho
33	295.2	19.6	1896	24	ABL54791	Modified hen ACR s
34	292.4	19.5	1869	24	ABL45864	Modified acetylcho
35	292.4	19.5	1869	24	ABL54788	Insect nicotinic A
36	292	19.4	1896	24	ABL45867	Modified acetylcho
37	290.6	19.3	1854	24	ABV73244	Human neuronal NAC
38	290.6	19.3	1854	24	ABS54871	Human neuronal nic
39	290.6	19.3	1757	15	AAV12200	Human neuronal nic
40	290	19.3	2363	15	AAV12196	Human neuronal nic
41	290	19.3	2363	24	ABV73245	Human neuronal NAC
42	290	19.3	2363	24	ABS54872	Human neuronal nic
43	279	18.6	1416	22	AAC90382	Chimeric alpha7/5-
44	274.4	18.3	1915	18	AAT48241	Neuronal nicotinic
45	274.4	18.3	1915	24	ABV73251	Human neuronal NAC

ALIGNMENTS

RESULT 1
AAZ224477
ID AAZ224477 standard; cDNA to mRNA; 3109 BP.

XX AC AAZ224477;

XX DT 17-FEB-2000 (first entry)

XX DE H. virescens acetyl-choline receptor DNA from clone Hva7-2.

XX DE Acetyl-choline receptor; nicotinic; insect; insecticide; screening;

XX KW neurotransmission; plant protection agent; conductance; AChR; ds.

XX OS Heliothis virescens.

XX PN DE19819829-A1.

XX PD 11-NOV-1999.

XX PF 04-MAY-1998; 98DE-1019829.

XX PR 04-MAY-1998; 98DE-1019829.

XX PA (FARB) BAYER AG.

XX PI Adamczewski M, Oellers N, Schulte T;

XX DR WPI; 2000-014207/02.

XX DR P-PSDB; AAV50816.

XX PT New nucleic acid encoding a nicotinic acetylcholine receptor from

XX 17-FEB-2000 (first entry)
 XX DE H. virescens acetyl-choline receptor DNA from clone Hva7-1.
 XX KW Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
 XX KW neurotransmission; plant protection agent; conductance; ACHR; ds.
 XX OS Heliothis virescens.
 XX PH Key Location/Qualifiers
 XX CDS 335..1825
 XX FT /*tag= a
 XX FT /product= "acetyl-choline receptor"
 XX PN DEL19819829-AL.
 XX PD 11-NOV-1999.
 XX PF 04-MAY-1998; 98DE-1019829.
 XX PR 04-MAY-1998; 98DE-1019829.
 XX PA (PARB) BAYER AG.
 XX PI Adamczewski M, Oellers N, Schulte T;
 XX DR P-PSDB: AAY50815.
 XX WPI: 2000-014207/02.
 XX PT New nucleic acid encoding a nicotinic acetylcholine receptor from
 XX PT insects, used to identify potential insecticides -
 XX PS Claim 1a; Page 14-17; 26pp; German.
 XX CC This invention describes a novel nucleic acid (NA) encoding a nicotinic
 XX CC acetyl-choline receptor (I) from insects which can be used as an
 XX CC insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
 XX CC (also vectors containing it, its regulatory regions, and antibodies
 XX CC directed against (I)-encoded proteins) are used to screen for: (a) plant
 XX CC protection agents that alter conductance of ACHR, potentially useful as
 XX CC insecticides; or (b) genes which encode polypeptides that are involved in
 XX CC formation of functionally related ACHR in insects. (I) are also used to
 XX CC isolate and characterize the specified regulatory regions and for
 XX CC recombinant production of (II). This sequence encodes an acetyl-choline
 XX CC receptor isolated from *Heliothis virescens*.
 XX SQ Sequence 3700 BP; 893 A; 953 C; 944 G; 910 T; 0 other;
 Query Match 38.38; Score 575; DB 21; Length 3700;
 Best Local Similarity 64.6%; Pred. No. 1.9e-150;
 Matches 929; Conservative 0; Mismatches 460; Indels 48; Gaps 3;
 QY 64 CACGAGAAGAGACTCCCTGAACGGCTGCTGCGGAACCTACAAACCCCTGGAGCGACCGGTG 123
 DB 431 CACGAGAAGCGGTACTGACACCACTATTGGACCACTACAACTGAGAGAGCGCCGTC 490
 QY 124 GCCAACGAGAGCGAAGCGGTAGAGTCAGGTTCGGCTTGACCTTGCAGCAAAATCATTTGAC 183
 DB 491 GTCAACGAGAGCGACCGCTGCACCTCTCCTTCGGCTCAGCTCATCGATCATCGAC 550
 QY 184 GTGACGAGAGAATCACTACTTATTAACCAATATATGGCTGTGCTGGAGTGAATGAC 243
 DB 551 GTGACGAGAGAAGACCAAGCTTTTAAACAAACATCTGGCTTAAACATAGAGTGAATGAT 610
 QY 244 TACAACCTGAGTGAACGAGAGATGCGCGGTCAAGGACCTCAGATCAACGCC 303
 DB 611 ATGAACCTGAGTGAACACTTCAATTTTCGGCGGGGTCAAAGATTAAAGAGTCCCAACC 670
 QY 304 AACAAAGTTGTGAAGCGGAGCTCCTTATGTATTAATAGTGTACGAGGGTTTTGACGGG 363
 DB 671 CACAGACTATGGAACCAAGAGCTCTTATGTATCAACAGCGCGGACGAAGGGTTGCACAGC 730

QY 364 ACCTACAGACACACGCTGGTGGTTCAGAAAGCGCGGCGAGTTCCTGTAGCTGCCACCTGGC 423
 DB 731 ACCTATCCAAAGAACGCTGGTGGTGGCGGAACAACGGCTCGTGTGTAGTGGCCGCCCGGC 790
 QY 424 ATATTCAGAGACACATCAAGATGACATCGCGTGGTTTCCCTTCGACGACCAACACTGT 483
 DB 791 ATCTTCAAGAGACCTCGAGATCGACATCACTGGTTCCTTCGACGACCAACGATGC 850
 QY 484 GATATGAAGTTCGGTAGCTGGACATATGACGGCAATCAGTTGGATCTGGTCTAAAGAT 543
 DB 851 GAGATGAAGTTTGGCAGCTGACCTTATGATGGTTATCAGTTGGATCTACAACTACAGAT 910
 QY 544 GAGCAGCGCGGATCTATCGGACTTCATACAAATGGGAGTGGTATCTAATAGGATG 603
 DB 911 GAAGGGGGCGGAGATATAAGCAGTTTGTACGAATGGCAATGGGAGTTAATAGGATC 970
 QY 604 CCAGGCAAAAAGAACACAATAACATACGCGTGTGCCCCGAGCGCTACGTGAGCTCAC 663
 DB 971 CCCGGCAAGCGCAACGAGATCTACTACAAGTTGTCCGGAGCCATACATGACATCAG 1030
 QY 664 TTCACCATCATGATGAAGAAGACGAACTTGTACTACTTCTTCAACCTGATCGTCCGTC 723
 DB 1031 TTTGCGGTGGTATCCGGAGGAAAACGCTCTACTACTTCTTCAATCTGATCGTCCCTGC 1090
 QY 724 GTGCTGATCTCATCGATGGCAGCTCTCGGCTTCACACTGCCACGAGACTCCGGAGAGAA 783
 DB 1091 GTGCTCATCGCTCCATGGCTTATGGGGTTCACTTGGCTCCAGACTCCGGAGAAAG 1150
 QY 784 CTCACACTTGGAGTCACTATTCTTATCGGTGACGGTGTTCCTCAACCTGGTAGCCGAG 843
 DB 1151 TTGCTTTAGTGTGACGATATTAATGCTGTGAGCGTGTTCCTCAACATGGTGGCGAG 1210
 QY 844 ACCCTGCCACAGCTCCGACGCTATCCCTGTTAGGAGCTACTTCAATTTGATCATG 903
 DB 1211 ACGATGCCAGCGAGCTCGGCGCTGCTTGTCTGCGCACTACTTCAACTGCATCATG 1270
 QY 904 TTCATGTAGCGTCTGTGGTACTGACTGTGGTGGTACTCAATACCACCATCGRACA 963
 DB 1271 TTCATGTGGCTTCCCTCCGCTCTCCACCATATGATTCCTCAACTACCACCGGAC 1330
 QY 964 GCTGATATACATAAATGCCACAGTGGATAAATCAGTATTCTTCAATGGTGGCTG 1023
 DB 1331 GCACACTCACGAATGAGTGAATGCTGTTGCGGTGTTCCTTTATTGGCTCCGCTG 1390
 QY 1024 ATACTGGAATGTGAGCGCAGGGAAGAATACACGAGAGACTATAATGATGAACAG 1093
 DB 1391 GTGCTGCGCATGTACGCGCGGCTCGGCG---ACGACGCGCGCGCGCGCTACCT 1447
 QY 1084 AGGATGAGGAGCTGGAACCTGAAGGAGAGGTGCTGGAAGTCTTCTGGCGCAATGTTCTA 1143
 DB 1448 CCGCGCGGACCTGGAGCTGCGGAGCGCTCTCCAAAGTCTCTTAGCAAGCTGCTC 1507
 QY 1144 GATATTGATGATGATTCAGACACGCGCTCCGCTCTCTAAACAGTACTGCTCGACCGGG 1203
 DB 1508 GACATCATGACGACTTCCGCCACCCGCAAGCGCAGCAG-----CGCAATGTCGCG 1560
 QY 1204 AATTGGGACCTGGTGTCAATATCCGACAGGATTTCCGTCGGTGTGCTGCTGCTGCG 1263
 DB 1561 ATACTACAGGGGGGTGAGGAGAATGCGCGGGGTGGCGGCGCAGAGTTGCTTCG---- 1616
 QY 1264 TCCACGATGGAAGAGCTGGGCGGGGCTGGGTAGCCACCATCGGAGCTCACCTCAT 1323
 DB 1617 -----GTGTCGACTACGAGCTCTCCCTCAT 1642
 QY 1324 CTGAGAGAGCTGCAATTCATCACCGCCAGGATGAAGAGGCTGATGAGAAAGCGGAGCTG 1383
 DB 1643 CTGAGAGATAGAGTATCATACAGATCAGATGCGAAGGACGAGAGATGCGACATT 1702
 QY 1384 ATCAGCAGCTGAAGATTTGCTGCGATGTTGATAGGTTTTGCTGTTGCTGTTTAC 1443
 DB 1703 TCGCGCAGCTGAAGATTCGCGCCATGCTGTCGACAGACTGTGCTCTATTATCTTACC 1762
 QY 1444 CTTTTCACATCATCGCGACAGTAGTCTCTCTGTTATCGGCAACCGCATATCATCGT 1500

Db	1763	CGTTTCAAAATCATGCCACGCTAGCCGCTGCTGTCTCCGCCACACATCATGGTG	1819
RESULT 4			
ABLI13733			
ID	ABLI13733	standard; cDNA; 936 BP.	
XX	AC	ABLI13733;	
XX	DT	26-MAR-2002 (first entry)	
XX			
DE		Drosophila melanogaster expressed polynucleotide SEQ ID NO 35681.	
XX		Drosophila; developmental biology; cell signalling; insecticide;	
KW		pharmaceutical; gene; ss.	
XX		Drosophila melanogaster.	
OS			
XX			
PN	WO200171042-A2.		
XX			
PD	27-SEP-2001.		
XX			
PF	23-MAR-2001; 2001WO-US09231.		
XX			
PR	23-MAR-2000; 2000US-191637P.		
PR	11-JUL-2000; 2000US-0614150.		
XX	(PEKE) PE CORP NY.		
PA			
PI	Venter JC, Adams M, Li PWD, Myers EW;		
XX			
DR	WPI; 2001-656860/75.		
DR	P-PSDB; ABB69630.		
XX			
PT		New isolated nucleic acid detection reagent for detecting 1000 or more	
PT		genes from Drosophila and for elucidating cell signalling and cell-cell	
PT		interactions -	
XX			
PS	Claim 1; SEQ ID NO 35681; 21pp + Sequence Listing; English.		
XX			
CC	The invention relates to an isolated nucleic acid detection reagent		
CC	capable of detecting 1000 or more genes from Drosophila. The invention is		
CC	useful in developmental biology and in elucidating cell signalling and		
CC	cell-cell interactions in higher eukaryotes for the development of		
CC	insecticides, therapeutics and pharmaceutical drugs. The invention		
CC	discloses genomic DNA sequences (ABLI16176-ABLI30511), expressed DNA		
CC	sequences (ABLI01840-ABLI16175) and the encoded proteins		
CC	(ABBS7737-ABB72072).		
CC	The sequence data for this patent did not form part of the printed		
CC	specification, but was obtained in electronic format directly from WIPO		
CC	at ftp.wipo.int/pub/published_pct_sequences.		
XX			
SQ	Sequence 936 BP; 238 A; 213 C; 239 G; 246 T; 0 other;		
Query Match	28.6%;	Score 430.6; DB 23; Length 936;	
Best Local Similarity	68.5%;	Pred. No. 3.1e-110;	
Matches 595;	Conservative 0;	Mismatches 274; Indels 0; Gaps 0;	
QY	19	GCCTTGGCGCTGCTGGCTTTGCTGCTCCCGTATCGGAGCAAGGTCTCTCAGGAAAGAGACTC	78
Db	67	GGCCTGGGACTTTTAATTATGATACCGGCTGTGCGGCTGGACCCCATGAGAAGCGGCTA	126
QY	79	CTGACAGCGTGTGCTGGGGAACATAACACCCCTGAGCGACCGGTGCCAACGAGACGAA	138
Db	127	CTCCACGGCCCTCTGGACACTACAGACGCTGGAGCGTCGGGTGTCATGAATCCGAT	186
QY	139	CCGCTAGAGGTTCAGGTTTCGGCTTGACCTTCACGACAAATCATTCAGCTGGACGAGAAAT	198
Db	187	CCATTGCAACTGACCTTCGGNCACTAACACTCATCGAGTATCGATGTGACCAAGAAAT	246
QY	199	CAACTACTTATTAACCAATATATGCTGCTGCTTGGAGTGGAAATGACTATACACCTGAGGTG	258

247	CAACTGCTTATAACAGATATTTGGCTCAAAATTTGGAATGGAACGATATGAATCTTCGATGG	300
259	AACGACACGCGAGTAGTATGGCGGGGTCAAGGACCTCAGGATCAGCCCAACAAAGTTGTGGAG	318
307	AATTCGATGAGTTTCGGTGTGCGGGATCTGCGAAATTCGCCACATCGCCTATGGAAA	366
319	CCGACGCTCTTATATAGTATAGTCTGACGAGGGTTTTCAGCGGACCTACACAGACCAAC	378
367	CCGATGCTACTGATGTACAACAGTCCCGACGAGGGCTTCGATGGAACGCTACGCCACAAT	426
379	GTGCTGTGTCAAGACGGCGGCGAGTTGCCTGTACGTGCCACCTGGCATATTCGAAGGCACA	438
427	GTGCTGTGTTCGATATATGAGGAGCTGTCTGTACGTACCGCAGGATATATTTAAGTCAACG	486
439	TGCAAGATGACATCGCGTGTGTTCCCTTCGACGACCAACACTGTGCATATGAAGTTTCGT	498
487	TGTAAGATCGACATTACGTGCTTCCATTTCGACGATCAGAGATGTGAAATGAAATTTGCT	546
499	AGCTGGACATATGACGGCAATCAGTTGGATCTGTGTCTTAAAGATGAGCGAGCGGCGAT	558
547	TCGTGGACCTACGATGGGTTTTCAGTTGGACCTGCAGTTGCAGGACGAAGCTGTGGCGAC	606
559	CTATCGGACTTCATAACAAATGGGGAGTGTATCTAATAGGAATGCCAGGCAAAAAGAAC	618
607	ATTTCCTAGCTTTATACCAATGGGGAATGGGACTTTGTAGGTGTGCCCGTAAACGAAT	666
619	ACAATAACATACGCGTGTGCTCCCGAGGCGCTACGTGGACGTCAACCTTCACCATCATGATA	678
667	GAAATCTACTATAATTGCTGCGCCAGAACCTTATATTGACATAACATTCGCCATTTTGATA	726
679	AGAAGACGACCTTGTAAGTCTTCTTCAACCTGATCGTCCGCTGGCTGTGATCTCATCG	738
727	AGGCGCAAAACGGTTGTACTATTTTCAATCTGATTTGTCCGCTGGCTACTGATCGCTCC	786
739	ATGCACTCTCTCGCTTCACACTGCCACCGACTCCGAGAGAACTCACACTTCGGATC	798
787	ATGCACTGTGTAGGTTTACACTGCCACAGATCTGTGTGAAAGCTTTTCGTTTGAGTT	846
799	ACTATTCCTCTATCGCTGACGGTGTCTCAACCTGGTAGCGGAGACCTGCCACAGATC	858
847	ACAATCTATATATCGCTTACAGTCTTCTCAACATGGTGGCGGAACAATGCCGCGAC	906
859	TCCGACGCTATCCCGCTGTTAGGACGTA	887
907	TCCGATCGGTACCGCTGCTCGTAAAGTA	935
RESULT 5		
AAZ24475		
ID	AAZ24475 standard; cDNA to mRNA; 2886 BP.	
XX	AAZ24475;	
AC		
XX		
DT	17-FEB-2000 (first entry)	
XX		
XX	D. melanogaster acetyl-choline receptor DNA from clone Da7.	
XX		
KW	Acetyl-choline receptor; nicotinic; insect; insecticide; screening;	
KW	neurotransmission; plant protection agent; conductance; AChr; ds.	
XX		
OS	Drosophila melanogaster.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	372..2684
FT	/*tag= a	
FT	/product= "acetyl choline receptor."	
XX		
XX	DE19819829-A1.	
PD	11-NOV-1999.	
XX		
XX	04-MAY-1998; 98DE-1019829.	
XX		

PR 04-MAY-1998; 98DE-1019829.
XX PA (FARB) BAYER AG.
XX Adamczewski M, Oellers N, Schulte T;
XX WPI; 2000-014207/02.
DR P-PSDB; AAY50814.
PT New nucleic acid encoding a nicotinic acetylcholine receptor from
PT insects, used to identify potential insecticides
XX Claim 1a; Page 8-12; 26pp; German.
XX This invention describes a novel nucleic acid (NA) encoding a nicotinic
CC acetyl-choline receptor (I) from insects which can be used as an
CC insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
CC (also vectors containing it, its regulatory regions, and antibodies
CC directed against (I)-encoded proteins) are used to screen for: (a) plant
CC protection agents that alter conductance of AChR, potentially useful as
CC insecticides, or (b) genes which encode polypeptides that are involved in
CC formation of functionally related AChR in insects. (I) are also used to
CC isolate and characterize the specified regulatory regions and for
CC recombinant production of (II). This sequence encodes an acetyl-choline
CC receptor isolated from *Drosophila melanogaster*.
XX SQ Sequence 2886 BP; 942 A; 687 C; 640 G; 617 T; 0 other;
Query Match 27.4%; Score 411.4; DB 21; Length 2886;
Best Local Similarity 68.8%; Pred. No. 1.3e-104;
Matches 565; Conservative 0; Mismatches 256; Indels 0; Gaps 0;
QY 57 AGGTCTCCACGAGAGAGACTCTCGAAGCGCTTCTGCGCAACTACACACCTCTGGAGCG 116
DB 1295 AGGATATCATGAAAGAGACTGTTACACGATCTTTTGGATCTTATAATACACTAGAACG 1354
QY 117 ACCGGTGGCCAAACGAGCGGACCGCTAGAGGTGAGGTTCGGCTTGACCTTGACGAAAT 176
DB 1355 TCCCGTTCTCAATGAATCGGACCGCTTACAAATTAAGCTTTGGTTTAACTTTAATGCAAT 1414
QY 177 CATTTGACGTGACGAGAGAAATCAACTACTTATACCAATATATGCTGCTGGTAGTG 236
DB 1415 TATCGATGTGGACGAGAAATCAATTCCTAGTCACTAATGTGGTTAAACCTGGAGTG 1474
QY 237 GAATGACTACAACTGAGGTGGACGACGAGGAGGTGCGGGGTCAAGGACCTCAGAT 296
DB 1475 GAACGACATGAATCTCCGCTGGAACACCTCGGACTATGCGGAGTTAAGGATCTGCGAAT 1534
QY 297 CACGCCCAACAAGTTGTGGAAGCGGACGCTCTTATGATATATAGTCTGACGAGGTTT 356
DB 1535 ACCGCGGATCGCATCTGGAAGCGGACGCTGCTGATGATACACAGTGGGATGGGATT 1594
QY 357 TGACGGGACCTACACGACCAACGTGGTGGTGCAGAGCGGCGGAGTTCCTGTACGTGCC 416
DB 1595 TGACGGGACCTACACGACGACGTGGTGGTGGGACGACGCTCGTCTCTATACGTTC 1654
QY 417 ACCTGGCATATTAAGAGACACATGCAAGATGACATCGGTGGTTCCTCTTCGACGACCA 476
DB 1655 GCCGGGATCTTCAAGTCGAGTGCAGATGCAAGATGACATCGGTGGTTCCTCTTCGATGACCA 1714
QY 477 ACATCTGTATATGAATTCGCTAGCTGCACATATGACGCAATCAGTTGGATCTGGTCT 536
DB 1715 CGGTGGGATGAATTCGCGAGTTCGACCTACGAGGATTCAGCTGGATTTACAAT 1774
QY 537 AAAAGATGAGGACGCGGATCTATCGGACTTCATACAAATGGGAGTGGTATCTAAT 596
DB 1775 ACAAGATGAACCTGCGGTGATATACAGCAGTTACGTCTCAACGCGGAGTGGGAATCT 1834
QY 597 AGGAATGCCAGGAAAAGACACATACATACATGCGGTGCTGCGCCCGGAGCCCTACGTGGA 656
DB 1835 GGGTGTGCGCGCAACGTAACGAGATCTATTACAACTGCTGCTCCCGGAAACCTATAGA 1894
QY 657 CGTCACCTTCACCATCATGATGAAGAAGACGAACCTTGTACTTCTTCAACCTGATCGT 716

DB 1895 CATCACCTTCGCGCATCATATCCGCGACGAACTACTATTTCTTCAACCTGATCAT 1954
QY 717 CCGTGTGGTCTGATCTCATCTCATCTCGGCTTCGACCTTCACACTGCCACGACTCCGG 776
DB 1955 ACCTTGTGACTGATTCCTCCATGCGCTTCTCGGATTCACCTGCGCGGAGATTCGG 2014
QY 777 AGAGAAACTCACACTTGGAGTCACTATTTCTATCTGCTGACGGTGTTCCTCAACCTGGT 836
DB 2015 TGAATAATTATCGCTGGTGTGTACCATCTTGTCTGCTGACCGTGTTCCTGAATATGGT 2074
QY 837 AGCGGAGACCTGCGCACAGGTCTCCGACGCTATCCCTCTGT 877
DB 2075 TGCCGAGACATGCCGCTACTTCCGATCGGTGCTCATTTGT 2115
RESULT 6
AAC58395
ID AAC58395 standard; cDNA; 1509 BP.
XX AAC58395;
AC AAC58395;
XX 29-JAN-2001 (first entry)
DT Human PRO2145 nucleotide sequence SEQ ID NO:76.
DE Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumorigenesis; identification; cancer; cytostatic;
KW neotropic; neuroprotective; antiinflammatory; immunosuppressive;
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; stromal disorder; blastocoelec disorder;
KW inflammatory disorder; immunologic disorder; ss.
XX Homo sapiens.
OS
XX WO200053755-A2.
FN
XX 14-SEP-2000.
PD
XX 06-JAN-2000; 2000WO-US00376.
PF
XX 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 26-JUL-1999; 99US-0143048.
PR 26-JUL-1999; 99US-0145698.
PR 30-NOV-1999; 99WO-US28313.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
XX (GETH) GENENTECH INC.
PA Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
PI Watanabe CK, Wood WI;
XX WPI; 2000-572270/53.
DR P-PSDB; AAB24088.
XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT treatment, diagnosis and prevention of cancer -
XX Claim 50; Fig 57; 286pp; English.
XX The present invention describes an isolated antibody that binds to
CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,
CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
CC growth. The PRO polypeptides and nucleotides are useful in the
CC treatment, diagnosis and prevention of cancer. The antibodies and other

(PHAA) PHARMACIA & UPTJOHN CO.

Groppi VE, Wolfe ML, Berkenpas MB;
WPI: 2001-061524/07.
P-PSDB; AAB50012.

Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH

Example 5; Pages 60-61; 77pp; English.

The present sequence is the coding sequence for wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells.

Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 other;

Query Match 24.9%; Score 374; DB 22; Length 1509;
Best Local Similarity 55.1%; Pred. No. 2.9e-94;
Matches 809; Conservative 0; Mismatches 635; Indels 24; Gaps 3

QY 33 GCCTTTGTCGCCGTATCGGAGCAAGTCTCAGGACAAGACTCCTGAACGGTGCT 92
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 42 GTCCGCTCTGCAGCTGTCCCTGCAAGCGAGATTCCAGAGGAAGCTTTACAAGGAGCTGGT 101
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 93 GCGCAACTACAAACACCCTGGAGCGCACCGGTGGCCAACGAGAGGAAACCGTAGAGGTGAC 152
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 102 CAAGAATACAACTCCCTTGGAGAGCCCGTGGCCATGACTCCCAACCATCACCGTCTA 161
QY 153 GTTCGGCTTGACCTTGCAGCAAATCATGTAGCTGGAGGAGAGAAATCAACTACTTATAAC 212
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 162 CTTCCTCCCTGAGCCCTCTGCAGATCATGGAGCTGGATGAGAAGAACCAAGTTTTAACCA 221
QY 213 CAATATATGGCTGCTGTGGAGTGGATGGAATGACTACAACTGAGTGGAAACGACAGCGAGTA 272
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 222 CAACATTTGGCTTGCAAATGCTTGGACAGATCACTATTTACATGTGGAATGTGTGCAAGAATA 281
QY 273 TGCGGGGTCAAGGACCTCAGGATCAGCGCCCAACAAGTTGTGGAAGCCGGAGCTCCTTAT 332
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 282 TCCAGGGTGAAGACTGTTCTGTTCCCAGATGGCCAGATTGGAACACAGACATCTCTCT 341
QY 333 GTATTAATAGTGTGACGAGGCTTTTGACGGGACCTACGACACAACGCTGGTGGTGCAGAA 392
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 342 CTATAACAGTGTGATGAGCGCTTTGACGCCACATTCACACATTAACGTTGTGGTGAATTC 401
QY 393 CGCGGGCAGTTGCCTGTACGTGCCACCTGGCCATATTCAGAGCACATGCAAGATGGACAT 452
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 402 TTCTGGGCATTTCCGAGTACCTTCGCTCCAGGCATATTCAGAGATTCCTGTGTACATCGATG 461
QY 453 CGCGTGGTTTCCCTTCGACGACCAACACTGTGATATGAAGTTCGGTAGCTGGACATATGA 512
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 462 AGCTGGTTTCCCTTTGATGTGCAGCACTGCAACTGAAAGTTTGGGTCTCTGGTCTTACGG 521
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 513 CGGCAATCAGTTGGATCTGGTGTCTAAAAGATGAGCGAGCGCGGATCTATCGGACTTTCAT 572
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 522 AGGCTGGTCTTGGATCTGCAGATGCAGGA-----GGCAGATATCAGTGGCTATAT 572
QY 573 ACAAAATGGGAGTGGTATCTAATAGGAATGCCAGGCAAAAAAGACACAATACATACGC 632
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 573 CCCCCAATGGAAATGGGACCTAGTGTGGAATCCCGGCAAGAGAGGTGAAGGTTCTATGA 632
QY 633 GTGCTGCCCGGAGCCCTACGTGGAGCTCACCTTCACCATCATGATAAGAAGACGACCTT 692
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 633 GTGCTGCAAGAGCCCTACCCCGATGTACCTTTCACAGTGACCATCGGCCGAGCGCT 692
QY 693 GTACTACTTCTTCAACCTGATGTCGCGGTGCTGCTATCTCATCATGGCACTCTCTGG 752

FT XX /*tag= a
 PN WO9641876-A1.
 XX 27-DEC-1996.
 XX 07-JUN-1996; 96WO-US09775.
 XX 07-JUN-1995; 95US-0484722.
 XX (SIBI-) SIBIA NEUROSCIENCES INC.
 XX Elliott KJ, Harpold MM;
 PI WPI; 1997-065463/06.
 DR P-PSDB; AAW09025.
 XX Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
 PT used in screening to determine the effect of drugs on the receptor
 XX Disclosure; Page 71-73; 108pp; English.
 PS A DNA sequence (AA748239) codes for the alpha-7 subunit (AAW09025) of
 CC the human neuronal nicotinic acetylcholine receptor (nAChR). Host
 CC cells, esp. mammalian cells or amphibian oocytes, carrying alpha-7
 CC nucleic acids, opt. in combination with other alpha and/or beta
 CC subunit nucleic acids (see also AA748232-38, AA748240-41), express
 CC recombinant nAChR subunits useful for identifying opds. that
 CC modulate the activity of human nAChRs.
 XX Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T; 0 other;
 SQ Query Match 24.9%; Score 374; DB 18; Length 1876;
 Best Local Similarity 55.1%; Pred. No. 3.2e-94;
 Matches 809; Conservative 0; Mismatches 635; Indels 24; Gaps 3;

QY 33 GGCTTTGCTGCGGATGAGGAGGAGGCTCTCAGAGAGAGAGACTCCTGAACGCGTGTCT 92
 DB 114 GTCGCTCTCTGACGCTGCTCCGCAAGGCGAGTTCCAGAGGAGGCTTTACAGGAGCTGT 173
 QY 93 GGGGAACTACAACACCCTGGAGGACCGGTGGCCACGAGAGGAGGAGGAGGAGGAGGAG 152
 DB 174 CAGAAGTACATCCCTTGGAGGAGGCGGTGGCCAAATGATCTGCAACCACTCAGCTCTA 233
 QY 153 GTTGGCTTGACCTTGACGAAATCATTTGACGTGGAGGAGGAGGAGGAGGAGGAGGAGGAG 212
 DB 234 CTTCTCCCTGAGGCTCTGAGATCATGACGCTGGATGAGAGGAGGAGGAGGAGGAGGAGGAG 293
 QY 213 CAATATATGCTGCTGCTGGAGTGAATGACTACACCTGAGGTGGAACGAGGAGGAGGAGGAG 272
 DB 294 CAACATTTGGCTGCAAAATGCTTGGAGAGATCACTATTTACAGTGGAAATGCTGCAAGATA 353
 QY 273 TGGCGGGGTCAAGGAGCTCAGGATACGCCCAAGTTGTGGAAGCGGAGGAGGAGGAGGAGGAG 332
 DB 354 TCCAGGGGTGAGAGCTGTCGTTCCAGATGGCCAGATTTGGAACCAAGAGATCTCTCT 413
 QY 333 GTATAATAGTGTGACGAGGTTTGGACGGGACCTACAGAGCAAGGAGGAGGAGGAGGAGGAGGAG 392
 DB 414 CTATAACAGTGTGATGAGGCTTTGACGCCACATTTCCACACTTAACGCTTGTGTAATTC 473
 QY 393 CGCGGCGAGTGGCTGCTGAGTGGCCACCTGGCATATTTCAAGAGACATGCAAGATGAGAT 452
 DB 474 TTCTGGGCAATGGCCAGTACTGCTCCAGGCAATTTCAAGAGTTCTGCTACATGATGATG 533
 QY 453 CGCGTGTCTTCCCTTCGAGGAGCAACACACTGTGATGAGTTGCGTGTGAGGAGGAGGAGGAGGAG 512
 DB 534 ACGCTGGTTCCCTTTGATGTGAGCACTGCAAACTGAAGTTTGGGTCTGCTGTCTTACGG 593
 QY 513 CGGCAATAGTGTGATGCTGCTAAAGATGAGGAGGCGGAGTCTATCGGAGCTTCAAT 572
 DB 594 AGGCTGGTCTTGGATCTCAGATGCAGGAG-----GGCAGATATCAGTGGCTATAT 644
 QY 573 ACAAAATGGGAGTGTATCTAATAGGAATGCCAGGCAAAAAGAACAAATACATACGC 632

Db 645 CCCCAATGGAGAAATGGGACCTAGTGGAAATCCCGCAAGAGAGAGTGAAGGTTCTATGA 704
 QY 633 GTGTGCTGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 692
 Db 705 GTGTGCTGCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 764
 QY 693 GTACTACTTCTTCAACCTGATGCTCCCGTGGCTGCTGATCTCATCATGATGGCAGTCTCTCGG 752
 Db 765 CTACTATGGCTCAACCTGCTGATCCCTGTGTGCTCATCTCCGCTCTCGCTCTGCTGTGTGT 824
 QY 753 CTTTACACTGGCCACAGAGACTCCGGAGAGAACTCACACTTTGGAGTGCATTTCTTCTATTC 812
 Db 825 GTTCTGTCTTCTGTCAGATTCGGGGAGAGATTTCCCTGGGAGATAACAGTCTTACTCTC 884
 QY 813 GCTGACGGTGTCTTCAACCTGATGCTCCAGAGACCTGCGCACAGGCTCTCCGAGCTATATCC 872
 Db 885 TCTTACCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 944
 QY 873 CTTGTAGGAGGAGTACTTCAATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 932
 Db 945 ATTGATAGCCAGTACTTCCGAGCAGCACCATGATCATCTGCTGGCTCTCTGCTGCTGCTGCTGCT 1004
 QY 933 TGTGTGTGCTTCAATTTACACCATTCGACAGCTGATATACATGATGAATGCCACAGTGGAT 992
 Db 1005 GGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1064
 QY 993 AAAATCAGTATTCCTTACAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1052
 Db 1065 CAGAGTATCTTCTGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1124
 QY 1053 GATCACAGGAGAGACTTAAATGATGAACAGGAGGATGAGGAGCTGGAATCAATGAAGAGAG 1112
 Db 1125 CAAGGTGCGCCGCGCTGCGCAGCACAAGCAGCGGCTGCGAGCTTGGCCAGTGTGGAGAT 1184
 QY 1113 GTCGTGGAAGTCTTGTCTGGCGAATGTTCTAGATATTGATGATGATGATGATGATGATGATGATGAT 1172
 Db 1185 GAGCGCGGTGGCG 1244
 QY 1173 TCCGCTCTCTAACAGTACTGCTCGACCGGGAATTTGGGACCTGGGTGCTCAATATTCG 1232
 Db 1245 CTTGGAGCGGTGCACTGTGCTCCGACCCCGGCTGCTGGGTGATGATGATGATGATGATGATGATGAT 1302
 QY 1233 CACGATTTCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1292
 Db 1303 GCTGCTGCTCCCGCAGCAGTATGAGCACTCTCTGCGCGGCGGCAACCCCGCGAGGGG-- 1360
 QY 1293 GGGTAGCCACCATCGGAGCTGCACCTCATACTGAGAGAGCTGCACTTTCATCAGGCGCAG 1352
 Db 1361 -----ACCGGAGCTTGGCCAAAGATCTGGAGGAGGTCCTGCTACATTTGCCAATCG 1409
 QY 1353 GATGAAGAGGCTGATGAGGAAGCGGAGCTGATCAGCGAGTGAAGTTTGGTTCGCTGCTGCTGCT 1412
 Db 1410 CTTCCGCTGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1469
 QY 1413 TCTTATAGGTTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1472
 Db 1470 GGTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1529
 QY 1473 CTTGTTATCGGACCGCATATCATCTGTG 1500
 Db 1530 CTTGATGTGCGCTCCCACTTCGTGGAG 1557

RESULT 9
 AAV44687

ID AAV44687 standard; cDNA; 1590 BP.

XX AAV44687;

XX 09-OCT-1998 (first entry)

DE V274T variant human alpha7 nAChR coding sequence.

XX Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cancer;
 KW neurodegeneration; enzyme dysfunction; affective disorder; therapy;
 KW immune dysfunction; diabetic neuropathy; Alzheimer's disease;
 KW schizophrenia; ss.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 9..1517
 FT /*tag= a
 XX
 PN W09828331-A2.
 XX
 PD 02-JUL-1998.
 XX
 PF 22-DEC-1997; 97WO-US23405.
 XX
 PR 20-DEC-1996; 96US-0771737.
 XX
 XX (ABBO) ABBOTT LAB.
 XX
 XX Briggs CA, Gopalakrishnan M, McKenna DG, Monteggia LM;
 PI Roch J, Sullivan JP, Touma E;
 XX
 DR WPI; 1998-377593/32.
 XX
 XX Nucleic acid encoding variant of human alpha7 nicotinic
 PT acetyl-choline receptor sub-unit - used to identify modulators of
 PT the receptor, potentially useful for treating neuro-degeneration,
 PT cancer, affective disorders etc.
 XX
 PS Claim 14; Fig 2; 44pp; English.
 XX
 CC This sequence encodes the V247T variant of human alpha7 nicotinic
 CC acetylcholine receptor (nAChR) subunit of the invention. Cells containing
 CC the DNA are used to express the protein and to identify modulators of
 CC alpha7 nAChR activity or cytoprotective agents, e.g. antisense
 CC compounds or antagonists that are potentially useful for treating
 CC neurodegeneration, enzyme dysfunction, affective disorders and immune
 CC dysfunction, such as cancer, post-herpetic neuralgia, diabetic
 CC neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,
 CC psychosis and schizophrenia. Probes based on the DNA are used to detect
 CC the DNA in usual hybridisation or amplification tests, while monoclonal
 CC antibodies are used to detect the protein for diagnosis (in vitro or by
 CC in situ immuno-fluorescent assay). Compared with wild-type alpha7 nAChR,
 CC the protein has about 100-fold greater sensitivity to cholinergic
 CC receptor agonists (nicotine or acetylcholine) and response to these
 CC agonists decays more slowly, but the wild-type inward rectification is
 CC retained.
 XX
 XX Sequence 1590 BP; 322 A; 471 C; 449 G; 348 T; 0 other;
 SQ
 Query Match 24.9%; Score 373.6; DB 19; Length 1590;
 Best Local Similarity 55.1%; Pred. No. 3.8e-94;
 Matches 808; Conservative 0; Mismatches 634; Indels 24; Gaps 3;
 QY 35 CTTTCCTCCGCTATCGAGCAAGTCTCTCAGGAGAGAGACTCTGAAACGGTGTGCTGG 94
 DB 52 CTCTCCTGCAGCTGTCCCTCGAAGCGGAGATTCCAGGAGAGCTTTACAAAGAGCTGGTCA 111
 QY 95 CGAACTACAACACCTCGGAGGACCGGTGGCCACGACGAGAGGAAACCGCTAGAGGTCAAGT 154
 DB 112 AGAATCAATCCCTTGGAGAGGCGCGTGGCAATGACTCGCAACCACTCAACCTACTACT 171
 QY 155 TCGGCTTGACCTTCGAGCAATCATATGCTGGAGGAGAAATCACTACTTTAAACCA 214
 DB 172 TCTCCCTGAGCCTCTCGAGATCATGGAGCTGGATGAGAAGAACCAAGTTTTTAACCA 231
 QY 215 ATATATGCTGTGCTGGATGGAATGACTACAACCTCAGGTGGAGACGACGAGTATG 274
 DB 232 ACATTGTGCTGCAATGCTTGGACAGATCACTATTTACGTGGAATGTGTGACAAATATC 291

QY 275 GCGGGGTCAAGGACCTCAGGATACGCCCCAACAAAGTTGTGGAGCCCGGACGCTCCTTATGT 334
 DB 292 CAGGGGTGAAGACTGTTTCGTTTCCAGATGGCCAGATTGGAAACACAGACATTTCTCTCT 351
 QY 335 ATAATAGTCTGACGAGGGTTTTCACGGGACCTACCAGACCAACGTTGGTGTGTCAGAGCG 394
 DB 352 ATAACAGTGTGATGAGCGCTTTTACGCCCATTTCCACACTTAACGTTGTGTGAATCTTT 411
 QY 395 GCGCAGTGTGCTGACGTGCGACCTGCGCATATTAAGAGACACATGCAAGATGACATCG 454
 DB 412 CTGGGCATTTGCCAGTACTGCTCCAGGCATATTAAGAGATTCCTGCTACATCATGATGAC 471
 QY 455 CGTGGTTTCCCTTCGACGACCAACACTGTGTGATATGAAGTTGCGTGGAGTGGACATATGACG 514
 DB 472 GCTGGTTTCCCTTTGATGTGCAGCACTGCAAACTGAAGTTTGGGTCTCTGCTTACGGAG 531
 QY 515 GCAATCAGTTGGATCTGCTTAAAGATGAGGAGCGGGCGGATCTATCGACACTTCATAA 574
 DB 532 GCTGGTCTTTGGATCTGCAGATGCAGGA-----GGCAGATATCAGTGGCTATATACC 582
 QY 575 CAAATGGGAGTGTATCTAATAGGAATGCCAGGCAAAAGAACACATAACATACACGCT 634
 DB 583 CCAATGGAGATGGGACCTAGTGGGAATCCCGGCAAGAGAGTGAAGGTTCTTATGAGT 642
 QY 635 GCTCCCCGAGCCCTACGTGACGCTCACCTTTCACCATCATGATGAAGAGACGAACCTTGT 694
 DB 643 GCTGCAAGAGCCCTACCCGATGTCACTTTCACAGTGACCATGCGCGCAGGACACTCT 702
 QY 695 ACTACTTCTCAACCTGATCGTCCGTCGCTGCTGATCTCATCTCATCGACACTCTCTCGCT 754
 DB 703 ACTATGGCTCAACCTGCTGATCCCTGTGTGCTCATCTCCGCTCTCGCTCTGCTGGT 762
 QY 755 TCACACTGCCACCAGACTCCGAGAGAAACTCACACTTTGGAGTCACTATTCTTCTATCGC 814
 DB 763 TCCTGCTCTCGAGATTCGSGGAGAGATTTCCTCTGGGATTAACAGTCTTACTCTCTC 822
 QY 815 TGACGGGTTCCTCAACCTGTTAGCGAGACCCCTGCGCACAGAGTCTCGACGCTATFCCCC 874
 DB 823 TTACCACTTCTCATGCTGCTGCTGAGATCATGCCCGCAACATCCGATTCTGGTACCAT 882
 QY 875 TGTTAGGACGCTACTTCAATTTGCATCATGTTTCATGTTAGCTGCTGTGTGCTACTGACTG 934
 DB 883 TGATAGCCACGACTTCTGCGCACACCATGATCATCTGTTGGGCTCTCTGGTGTGGTGAAGG 942
 QY 935 TGTGGTACTCAATTAACCACTCGACAGCTGATATACATGAATGCCACAGTGGATGA 994
 DB 943 TGATCGTCTCAGTACCACCCAGACCCCGGCGGCGGCAAGATGCCCAAGTGGACCA 1002
 QY 995 AATCAGTATTCCTCAATGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1054
 DB 1003 GAGTCATCTCTTGAACCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1062
 QY 1055 TCACCAGGAAGACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1114
 DB 1063 AGGTGCGCGCGCTGCGCAGCAAGCAGCGCGCTGCGCCTGCGCCTGCGCCTGCGCCTGCGC 1122
 QY 1115 CGTGAAGTCTCTGCTGCGGAATGTTCTAGATATTTGATGATGATGATGATGATGATGATGATG 1174
 DB 1123 GCGCGTGGCG 1182
 QY 1175 GCGCTCTTAACAGTACTGCTCGACCGGGGAATTTGGGACCTTGGGTGCTGCTCAATATTTCCGCA 1234
 DB 1183 TGGACGGCGTCACTGTCTCCGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1240
 QY 1235 CGGATTTCCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1294
 DB 1241 CTGCTCCCCCGACGACGATGAGCACTCTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1296
 QY 1295 GTAGCCACCATCGGAGCTGCACCTCTACTACTGAGAGAGCTGACGTTCATCATCGGCCAGGA 1354
 DB 1297 -----ACCCGACTTGGCCAAAGATCCTTGAGGAGGTCCGCTACATATGCAACCGCT 1347

QY 1355 TGAAGAGGCTGATGAGGAAGCCGAGCTGATCAGCGACTGGAAGTTTGTGCGATGTTG 1414
 Db 1348 TCCGCTGCCAGGACGAAGAGCGCGGTCTGCGAGGAGTGGAAAGTTGCGCGCTGTGTGG 1407
 QY 1415 TTGATAGTTTTCGCTTTCGCTGTCACACTTTTCAAAATCAGCGGACAGTAGCTGTCC 1474
 Db 1408 TGAACCGCTGTGCTCATGGCTTCTGCGTCTTCACCATCATCTGCACCATCGGCATCC 1467
 QY 1475 TGTATGCGACCGCATATCATCGTG 1500
 Db 1468 TGATGTGCGCTCCCAACTTCGTGGAG 1493

RESULT 10

AAV12197
 ID AAV12197 standard; cDNA; 1876 BP.

XX AC AAV12197;
 XX AC AAV12197;
 XX DT 14-MAY-1998 (first entry)

Human neuronal nicotinic acetylcholine receptor alpha-7 subunit cDNA.

Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
 brain tissue; screening; NACHR; antibody; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX FT 73..1581
 XX FT /*tag= a
 XX FT /product= "neuronal nicotinic acetylcholine receptor
 alpha-7 subunit"

XX PN W09420617-A2.

XX XX 15-SEP-1994.

XX PF 08-MAR-1994; 94WO-US02447.

XX PR 08-MAR-1993; 93US-0028031.

XX PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.

XX PI (SIBI-) SIBIA NEUROSCIENCES INC.

XX DR Elliott KJ, Ellis SB, Harpold MM;

XX DR WPI; 1994-303024/37.

XX DR P-PSDB; AAW44153.

XX PT Human neuronal nicotinic acetylcholine receptor subunits and DNA -
 also transformed cells useful for screening cpds. which modulate
 activity of the receptor

XX PS Claim 8; Page 78-79; 99pp; English.

XX CC The present sequence encodes a human neuronal nicotinic acetylcholine
 CC receptor (NACHR) subunit. The cells expressing the alpha and/or beta
 CC NACHR subunits may be used in a method of screening compounds to
 CC identify any which modulate the activity of human neuronal NACHR.
 CC Subunit specific antibodies may be used to monitor the distribution
 CC and expression density of various subunits in normal vs diseased brain
 CC tissues. Testing of single receptor subunits or specific receptor
 CC subunit combinations with a variety of potential agonists or antagonists
 CC provides information with respect to the function and activity of the
 CC individual subunits and should lead to the identification and design of
 CC compounds that are capable of very specific interaction with one or
 CC more receptor subtypes. The resulting drugs should exhibit fewer
 CC unwanted side effects than drugs identified e.g. screening with cells
 CC that express a variety of subtypes.

XX SQ Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T; 1 other;

Query Match 24.9%; Score 373.6; DB 15; Length 1876;
 Best Local Similarity 55.0%; Pred. No. 4.1e-94;
 Matches 808; Conservative 1; Mismatches 635; Indels 24; Gaps 3;

QY 33 GGCTTTTGGTCCCGTATCGGAGCAAGGTCTCTACGAGAGAAGAGACTCTCTGAACGGTGGCT 92
 Db 114 GTCGCTCCCTGACGTGCTCCCTGCAAGCGAGTTCAGAGGAAGCTTTTACAAAGAGCTGGT 173
 QY 93 GCGAACTACAACACACCTTGAGCGAGCGGTGGCCAAACGAGAGGGAAGCTAGAGGTCTAG 152
 Db 174 CAAGAACTACAATCCCTTGAGAGAGCGCGTGGCCAACTGACTCCGACCACTCACCCTCTA 233
 QY 153 GTTCGGCTTGACCTTGAGCAAAATCATGTACGTGGAGAGGAAGAACTAACTATTAAAC 212
 Db 234 CTTCTCCCTGAGCCTCTGAGATCATGGAGCTGGATGAGAAGAACCAAGTTTTTAACAC 293
 QY 213 CAATATATGGCTGCTGTTGGAGTGAATGACTACAACCTGAGGTGAACACACAGCGAGTA 272
 Db 294 CAACATTTGGCTGCAAAATGCTTTGGACAGATCACTATTTACAGTGAATGTGCAGAAATA 353
 QY 273 TGGCGGGGTCAAGGACTCAGGATCACGCCCAACAAGTTGTGGAAGCGGACGTCCTTAT 332
 Db 354 TCAGGGGTGAAGACTGTTCTCCAGATGGCCAGATTTGAAACACACACATCTTCT 413
 QY 333 GTATAATAGTGTGACGAGGGTTTTGACGGGACCTACAGACCAACAGTGGTGTCAAGAG 392
 Db 414 CTATAACAGTGTGATGAGCGCTTTGACGCCACATTTCCACACTAACGTGTGTGTAATTC 473
 QY 393 CGCGCGAGTTGCTGTACGTGCCACCTGGCCATATTTCAAGAGACACATGCAAGATGACAT 452
 Db 474 TTTGGGCAATGGCAGTACTGCTCCAGGCATATTTCAAGAGTTCCTGCTACATCGATGT 533
 QY 453 CGCGTGGTTTCCCTTCGAGCAACACACTGTGTATATGAAGTTCGGTAGCTGGACATATGA 512
 Db 534 ACCTGGTTTCCCTTTGATGTGAGCACTGCAAACTGAAAGTTTGGGTCTGGTCTTACGG 593
 QY 513 CGGCAATCAGTTGGATCTGTGCTAAAAGATGAGCGAGCGCGGATCTATTCGAGCTTCAT 572
 Db 594 AGGCTGGTCTTGGATCTGCAGATGCAGGA-----GGCAGATATCATAGTGGCTATAT 644
 QY 573 AACAAATGGGAGTGTATCTAATAGGAATGCCAGCAACAAAGAAACACATATACATACGC 632
 Db 645 CCCCAATGGAGAATGGGACCTAGTGGAAATCCCGGCAAGAGAGTGAAGGTTCATATGA 704
 QY 633 GTCTGCCCCGAGCCCTAGTGGACGTCACTTTCCACCATCATATGAAGAGAGCAACCTT 692
 Db 705 GTCTGCAAGAGCCCTACCCCGATGTCACTTTCACAGTACCATCGCCGCGAGAGGCT 764
 QY 693 GTACTACTTCTCAACCTGATCGTCCGCTGCTGATGATCTATCATGATGGCACTCTCTGG 752
 Db 765 CTACTATGGCTCAACCTGCTGATCCCTGTGTGCTCATCTCCGCCCTCGCCCTGTGCTGT 824
 QY 753 CTTACACTGCCACAGACTCCGGAGAGAAACTCACACTTGGAGTCACTATTTCTTCTATC 812
 Db 825 GTTCTCTCTCTCGAGATTCGCGGAGAGATTTCCCTGGGATACAGTCTTACTCTC 884
 QY 813 GCTGACGGTGTCTCTCAACCTGGTAGCGAGCCCTGCCACAGCTCTCCGACGCTATPCC 872
 Db 885 TCTTACCGCTTCTATGCTGCTGCTGATGATCATGCCGCAACATCCGATTCGATACC 944
 QY 873 CTTGTTAGGACGCTACTTCAATTTGCATCATGTTTCATGGTAGCGTCTGTGTGTTACTGAC 932
 Db 945 ATTGATAGCCCACTACTTCCGCAAGCACTGATCATCTCGTGGGCTCTCGGTGGTGGTAC 1004
 QY 933 TGTGGTGGTACTCAATTAACCATCGACAGCTGATATACATGAATGCCACAGTGGAT 992
 Db 1005 GGTGATGTGCTGCTAGTACCAACCCAGCCGCGGAGGAGAGTGCCTCAAGTGGAG 1064
 QY 993 AAAATCAGTATTCTTCAATGTTCATGCTGCAATGTGCGAGTCTGCGAGCGCAGGAGAA 1052
 Db 1065 CAGAGTCATCTTCTCAACTGGTGGGTTCCTSCGAATGAAGAGCCCGGGAGGA 1124
 QY 1053 GATCACCGAGAGACTATAATGATGAACACAGGAGTGAAGAGCTGGAACATGAAGAGAG 1112

Qy	1413	TGTTGATAGT	TTTGGCTGTTGCTGTTTTCACACATTCATCGCGACATGAGTGT	1477
Db	1398	GGTGGACCGCTG	CTGCTCATGGCCTTCTCGGCTTTACCATCATCTGCACCATCGGCAT	1457
Qy	1473	CCCTGTTATCGC	ACCGCATATCATCGTG	1500
Db	1458	CCTGATCTCGCT	CCCACTTCGTGGAG	1485
RESULT 15				
AAC90387				
ID	AAC90387 standard; cDNA; 1509 BP.			
XX	AAC90387;			
XX	14-MAR-2001 (first entry)			
XX	Mutant human alpha7 ligand gated ion channel coding sequence #3.			
XX	Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;			
KW	5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.			
KW	Homo sapiens.			
OS	WO200073431-A2.			
XX	07-DEC-2000.			
XX	25-MAY-2000; 2000WO-US11862.			
XX	27-MAY-1999; 99US-0136174.			
XX	(PHAA) PHARMACIA & UPJOHN CO.			
XX	Groppi VE, Wolfe ML, Berkenpas MB;			
PI	WPI; 2001-061524/07.			
DR	P-PSDB; AAB50017.			
XX	Special cell culture medium for treating cells and for inducing			
PT	mammalian cell lines to conduct calcium ions, comprising specified			
PT	concentrations of ions of sodium, calcium and potassium at specified pH			
PT	Claim 64; Page 75; 77pp; English.			
XX	The present sequence is the coding sequence for a mutant human alpha7			
CC	nicotinic acetylcholine gated ion channel. The human alpha7 ion channel			
CC	was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3)			
CC	chimeric ligand gated ion channel (see AAC90382 and AAB50014). The			
CC	alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells			
CC	in the present invention, resulting in preferential calcium ion			
CC	conductance by the cells. The protein encoded by this sequence has the			
CC	wild-type threonine residue at position 230 substituted by a proline			
CC	residue and the wild-type cysteine residue at position 241 substituted			
XX	by a serine residue.			
XX	Sequence 1509 BP; 297 A; 452 C; 429 G; 331 T; 0 other;			
SQ	Query Match 24.7%; Score 370.8; DB 22; Length 1509;			
	Best Local Similarity 55.0%; Pred. No. 2.3e-93;			
	Matches 807; Conservative 0; Mismatches 637; Indels 24; Gaps 3;			
Qy	33	GGCTTTTCTGCC	TATCGGACGAAGTCTCCAGGACGAGACTCCTGAACGGTTGCT	92
Db	42	GTCCTCTCTGC	ACCTGTGCTCCGACGAGAGCTTTTACAAAGGAGCTGT	101
Qy	93	GGCGAACTACA	CAACACCTGGAGCCGCGTGGCCCAACGAGAGCGCAACCGCTAGAGGTCAG	152
Db	102	CAAGAAGTACA	NTCCCTTGGAGAGCCGCGTGGCCCAATGACTCGCAACCACTACCCGCTCA	161
Qy	153	GTTCCGGTGTG	ACCTTGCAGCAAAATCATTTGACGTGGACGAGGAAGTAACACTACTATTATAC	212

Db 162 CTTCTCCTGAGCCTCTGCAGATCATGAGAGTGGATGAGAGAACCAAGTTTTTAACCCAC 221
Qy 213 CAATATATGCTGCTGCTGAGTGGAAATGACTACAACCTGAGTGGAAACGACAGCGAGTA 272
Db 222 CAACATTTGGCTGCAATGCTTTGGACAGATCACTATTTACAGTGGAAATGTCAGANATA 281
Qy 273 TGGCGGGGTCAAGACCTCAGGATCAGCCCAACAAGTTGTGGAAGCCGACGCTCCCTTAT 332
Db 282 TCCAGGGGTGAAGACTTTCCTTCCAGATGGCCAGATTGGAACCCAGACATCTCTCT 341
Qy 333 GTATATAGTCTGACGAGGTTTTCAGCGGACTTACCAGACCAACGCTGCTGCTCAGAAG 392
Db 342 CTATAACAGTGTGATGAGCGCTTTGACGCCAATTCACACATTAACGCTGTTGTGAAATC 401
Qy 393 CGCGCGCAGTTGCTGTACCTGACCTGACCTGACATATCAAGAGCACATGCAAGATGGACAT 452
Db 402 TTCTGGSCATTGCCAGTACCTGCCAGGCATATCAAGAGTTCCTGCTACATCATGT 461
Qy 453 CGCGTGGTTTCCCTTTCAGCACCAACACTGTGATATGAAGTTTCGGTAGCTGGACATANGA 512
Db 462 ACCTGTGTTTCCCTTTGATGTGACGACTGCAAACTGAAGTTTGGGTCTCTGCTTACGG 521
Qy 513 CGCAATCACTTGGATGCTGCTAAAGATGAGGAGCGCGGATCTATCGGACTTCAT 572
Db 522 AGCTGTGCTTGGATCTGCAGATGCAGGA-----GGCAGATATCAGTGGCTATAT 572
Qy 573 AACAAATGGGAGTGTATCTAATAGGAATGCCAGGCAAAAGAACAAATAACATACGC 632
Db 573 CCCAATGGAGATGGGACCTAGTGGAAATCCCGGCAAGAGAGTCAAGGTTCTATGA 632
Qy 633 GTGCTCCCGGAGCCCTPACGTGACGCTCACCTTACCATCATGATAGAAGACGAACTT 692
Db 633 GTGCTGCAAGAGCCCTTACCCCGATGTCACCTTTCACAGTGACCATGCGCGGAGCGCT 692
Qy 693 GTACTACTTCTTCAACTGATCTCCGCTGCTGCTGATCTCATCGATGGCACTCTCCG 752
Db 693 CTACTATGGCTCAACTGCTGATCTCCGCTGCTGCTGATCTCCGCTCTCCGCTGCTGCT 752
Qy 753 CTTACACTGCCACAGACTCCGGAGAAACTCACACTTGGAGTCACTATTCTCTATC 812
Db 753 GTTCTCTCTTCCAGATTCCGGGAGAGATTTCCTGGGATACAGTCTTACTCTC 812
Qy 813 GCTGACGGTGTCTCAACTGGTAGCCGAGACCTGCCACAGGCTTCCGACGCTATCC 872
Db 813 TCTTACCGCTTCTATGCTGCTGCTGCTGATCATGCCCGCAACATCCGATTCCGTAOC 872
Qy 873 CTTGTTAGGACGCTACTTCAATGCTATCATGTTGATGCTAGCTGCTGCTGCTGCTGAC 932
Db 873 ATTGATAGCCAGTACTTCCGACGACCATGATCATGCTGGGCTCTCGGTGGTGGGAC 932
Qy 933 TGTGGTGTACTCAATTTACCACTCGAACAGCTGATATACATGAATGCCACAGTGGAT 992
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Qy 993 AATATAGTATTCATAGATGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1052
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Qy 1053 GATCACCAGGAAGACTATATGATGAACAGAGATGAGGAGTGGAACTGAAGGAGAG 1112
Db 1053 CAAGTGGCGCGGCTGCGAGCAGCAAGAGCGGCGCTGAGCTGGCCAGTGTGGAGAT 1112
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Db 1113 GAGCGCGTGGCG 1172
Qy 1173 TCCGCTCTCTAAGAGTACTGCTCGACCGGAAATTTGGGACCTTGGTGTCTCAATATTCG 1232
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Db 1398 GGTGGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1457
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Db 1458 CCTGATGCTCGCTCCCAACTTCGTGGAG 1485

Search completed: August 21, 2003, 04:24:43
Job time : 409.032 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2003, 00:04:15 ; Search time 5602.3 Seconds
(without alignments)
10975.350 Million cell updates/sec

Title: US-09-303-232-5_COPY_95_1597

Perfect score: 1503

Sequence: 1 atggccctatgttggcgc.....caccgcatacatcgtgcaa 1503

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Result No.	Score	Query Match	Length	DB ID	Description
1	1503	100.0	3029	3	AF143847 Heliothis
2	1503	100.0	3109	6	AX009614 Sequence
3	1503	100.0	3109	6	E58348 Nucleic aci
4	770.2	51.2	2023	3	AF321447 Drosophil
5	751	50.0	2023	3	AF321445 Drosophil
6	751	50.0	2023	3	AF321446 Drosophil
7	747.8	49.8	1665	3	AF321448 Drosophil
8	715.2	47.6	2068	3	AF321449 Drosophil
9	654	43.5	2110	3	AF321449 Drosophil
10	575	38.3	3629	3	AF143846 Heliothis
11	575	38.3	3700	6	AX009612 Sequence
12	575	38.3	3701	6	E58347 Nucleic aci
13	535	35.6	1683	3	DME554210 Drosophil
14	521.6	34.7	2907	3	AF272778 Drosophil
15	412.4	27.4	2834	3	AY036613 Drosophil
16	411.4	27.4	2886	6	AX009610 Sequence
17	411.4	27.4	2886	6	E58346 Nucleic aci
18	378.8	25.2	2107	9	AF486623 Macaca mu
19	377.2	25.1	1509	9	HSNACHRA7 H.sapiens m
20	377.2	25.1	1916	9	AF385585 Homo sapi
21	377.2	25.1	1977	9	HSU40583 Human alpha
22	376.8	25.1	1551	4	BT47 B.taurus mr
23	376.4	25.0	2106	10	RATNARAD L31619 Rattus ratt
24	376.4	25.0	3030	10	S53987 nicotinic r
25	375.6	25.0	2087	9	HSARA7A H.sapiens m
26	375	25.0	1559	9	HUMA7NAR L25827 Human a7 ni
27	374	24.9	1509	6	AX054567 Sequence
28	374	24.9	1876	6	AR282833 Sequence
29	374	24.9	1876	6	AX719088 Sequence
30	374	24.9	1876	9	HSUG2436 Human nicot
31	374	24.9	2088	10	AF225980 Mus muscu
32	373.6	24.9	1590	6	AR261850 Sequence
33	373.6	24.9	1590	6	BD023656 Variant h
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35	373.6	24.9	1876	6	AR071403 Sequence
36	373.6	24.9	1876	6	AR173187 Sequence
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41	370.8	24.7	1509	6	AX054579 Sequence
42	365	24.3	1555	9	HSCHRNA7A H.sapiens C
43	342.4	22.8	2037	5	GGNARA7A X68586 G.gallus mR
44	342.4	22.8	2696	5	GGY7NAREC X52295 Chicken alp
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ALIGNMENTS

RESULT 1
AF143847

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AF143847 3029 bp mRNA linear INV 27-MAY-1999
Heliothis virescens putative nicotinic acetylcholine receptor alpha
7-2 subunit mRNA, complete cds.

AF143847 GI:4895006

Heliothis virescens (tobacco budworm)

Heliothis virescens

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

Noctuoidea; Noctuidae; Heliothinae; Heliothis.

1 (bases 1 to 3029)

Schulte,T., Oellers,N. and Adamczewski,M.

Pred. No. is the number of results predicted by chance to have a

TITLE Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than to other insect nicotinic acetylcholine receptor alpha subunits

JOURNAL

Unpublished

2 (bases 1 to 3029)

Schulte, T., Oellers, N. and Adamczewski, M.

Direct Submission

Submitted (19-APR-1999) 2F-BTB, Bayer AG, Bldg. Q 18., Leverkusen

51368, Germany

FEATURES

Location/Qualifiers

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7-2 subunit"

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FLWETPLMTSRPQKTKTRKTIMNTRMRELEKERSKSLANVDIDDDFRHGP

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BASE COUNT 908 a 586 c 718 g 817 t

ORIGIN

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 Matches 1503; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 95 ATGGCCCCATATGTTGGCGCCCTTGGCGCTGCTGGCTTGTGCTGCCGCTATCGGAGCAAGT 154
 DB |
 QY 61 CCTACGAGAGAGACTCTCTGAACGCGTGTGCTGGGAACTACACACCCCTGGAGCGCG 120
 DB |
 QY 155 CCTACGAGAGAGACTCTCTGAACGCGTGTGCTGGGAACTACACACCCCTGGAGCGCG 214
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 QY 121 GTGGCCAAAGAGAGCAACCGCTAGAGGTCAAGTTCAGGTTGCGCTTGACCTTCAGCAAAATCAT 180
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 QY 215 GTGGCCAAAGAGAGCAACCGCTAGAGGTCAAGTTCAGGTTGCGCTTGACCTTCAGCAAAATCAT 274
 DB |
 QY 181 GACGTGGACGAGAGAAATCAACTACTTATAACCAATATATGCTGTGCTGGAGTGGAA 240
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 QY 275 GACGTGGACGAGAGAAATCAACTACTTATAACCAATATATGCTGTGCTGGAGTGGAA 334
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 QY 241 GACTACACACCTGAGGTGAACGACGAGTATGCGGGGTCAAGGACCTCAGATCAG 300
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 QY 335 GACTACACACCTGAGGTGAACGACGAGTATGCGGGGTCAAGGACCTCAGATCAG 394
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 QY 395 CCCAACAAAGTTGTGAACCGGACGCTCTTATATATAGTGTGCTGACGAGGGTTTGTAC 454
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 QY 361 GGGACCTACGACCAACGTTGGTGTGAGAGCGGCGCAGTGTGCTGTAGTCCACCT 420
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 QY 481 TGTGATATGAAGTTGCGGTAGCTGGACATATGACGGCAATCAGTTGGATCTGGTCTAAAA 540
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 QY 575 TGTGATATGAAGTTGCGGTAGCTGGACATATGACGGCAATCAGTTGGATCTGGTCTAAAA 634
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RESULT 2

AX009614

LOCUS

AX009614

3109 bp

DNA

linear

PAT 06-SEP-2000

RESULT 4

AF321447 2023 bp mRNA linear INV 29-APR-2002
 LOCUS Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6
 DEFINITION subunit variant type III (nAcRalpha-30D) mRNA, complete cds,
 alternatively spliced.
 AF321447
 ACCESSION AF321447.1 GI:20152848
 KEYWORDS
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 2023)
 GRAUO,M., REENAN,R.A., CULETTO,E. and SATTELLE,D.B.
 Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
 Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
 New and Highly Conserved Target of Adenosine Deaminase Acting on
 RNA-Mediated A-to-I Pre-mRNA Editing
 Genetics 160 (4), 1519-1533 (2002)
 21969411
 PUBMED 11973307
 REFERENCE 2 (bases 1 to 2023)
 GRAUO,M. and SATTELLE,D.B.
 Direct Submission
 Submitted (15-Nov-2000) Human Anatomy and Genetics-Functional
 Genetics Unit, University of Oxford, South Park Road, Oxford OX1
 30X, UK
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 variation 846
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 Best Local Similarity 70.9%; Pred. No. 1.le-193;

Matches 1058; Conservative 0; Mismatches 393; Indels 42; Gaps 1;
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 Db 530 AATCGGAGCGCCCTGGAGGTTAAGTTCGGACTCAGCTGACGCTGAGGAGATCATCGAGCTGGAGC 589
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Db 1310 TCGCTG 1369
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QY 1151 ATGATGACTTACAGACGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1210
Db 1550 AGGAGTGGAACTGAAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1576
QY 1211 GACCTGGGTGCTCAATATTTCCGACGGATTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1270
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LOCUS Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6
DEFINITION subunit variant type II (nAcRalpha-30D) mRNA, complete cds,
alternatively spliced.
ACCESSION AF321446
VERSION AF321446
KEYWORDS AF321446.1 GI:20152846.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 2023)
AUTHORS Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
TITLE Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
JOURNAL Genetics 160 (4), 1519-1533 (2002)
MEDLINE 21969411
PUBMED 11973307
REFERENCE 2 (bases 1 to 2023)
AUTHORS Grauso,M. and Sattelle,D.B.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
3QX, UK
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JOURNAL Submitted (31-MAR-2003) Millar N.S., Department of Pharmacology,
University College London, Gower Street, London, WC1E 6BT, UNITED
KINGDOM

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QY 491 AGTTCCGTAGCTGGACATATGACGCAATCAGTGTGATCTGTGTTAAAGATGAGGAG 550
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RESULT 8

AF321448

LOCUS

DEFINITION Drosophila melanogaster nicotinic acetylcholine receptor Dalphab6
subunit variant type IV (nAcRalpha-30D) mRNA, complete cds,
alternatively spliced.

AF321448

2068 bp

mRNA

linear

INV 29-APR-2002

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ACCESSION      AF321448
VERSION        AF321448.1  GI:20152850
KEYWORDS
SOURCE
ORGANISM      Drosophila melanogaster (fruit fly)
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               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
               Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
               Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
AUTHORS        Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
TITLE          Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
               Dalpna5, Dalpna6 and Dalpna7, in Drosophila melanogaster Identify a
               New and Highly Conserved Target of Adenosine Deaminase Acting on
               RNA-Mediated A-to-I Pre-mRNA Editing
               Genetics 160 (4), 1519-1533 (2002)
JOURNAL        1. (bases 1 to 2068)
MEDLINE        Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
PUBMED        11973307
REFERENCE      2 (bases 1 to 2068)
AUTHORS        Grauso,M. and Sattelle,D.B.
TITLE          Direct Submission
JOURNAL        Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
               Genetics Unit, University of Oxford, South Park Road, Oxford OX1
               3QX, UK
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VERSION	AX009612.1	GI:9996844	
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	Heliothis virescens (tobacco budworm)		
REFERENCE			
AUTHORS	Adamczewski, M.D., Schulte, T.D. and Oellers, N.D.		
TITLE	Nucleic acids encoding acetylcholin-receptor subunits from insects		
JOURNAL	Patent: EP 0962528-A 3 08-DEC-1999;		
	BAYER AG (DE)		
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DEFINITION
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ACCESSION
VERSION
AJ554210.1 GI:29466436
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Drosophila melanogaster
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REFERENCE
1. (bases 1 to 1683)
Millar, N.S.
AUTHORS
Direct Submission
TITLE
Submitted (31-MAR-2003) Millar N.S., Department of Pharmacology, University College London, Gower Street, London, WC1E 6BT, UNITED KINGDOM
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LOCUS	2907 bp	mRNA	linear
DEFINITION	Drosophila melanogaster nicotinic acetylcholine receptor Dalpha5 subunit (nAcRalpha-34E)	mRNA, nAcRalpha-34E-A allele, complete cds.	INV 29-APR-2002
ACCESSION	AF272778		
VERSION	AF272778.1	GI:20152839	
KEYWORDS			
SOURCE	Drosophila melanogaster (fruit fly)		
ORGANISM	Drosophila melanogaster		
REFERENCE			
AUTHORS	Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.		
TITLE	Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing		
JOURNAL	Genetics 160 (4), 1519-1533 (2002)		
MEDLINE	21969411		
PUBMED	11973307		
REFERENCE	2 (bases 1 to 2907)		
AUTHORS	Grauso,M. and Sattelle,D.B.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-MAY-2000) Human Anatomy and Genetics, MRC-FGU, University of Oxford, South Park Road, Oxford OX1 3QX, UK		
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          subunit (nAcRalpha34E) mRNA, nAcRalpha34E-B allele, complete cds,
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ACCESSION AY036613
VERSION   1
KEYWORDS  AY036613.1 GI:20340268
SOURCE   Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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          1 (bases 1 to 2834)
          Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
          Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
          Dalphea5, Dalphea6 and Dalphea7, in Drosophila melanogaster Identify a
          New and Highly Conserved Target of Adenosine Deaminase Acting on
          RNA-Mediated A-to-I Pre-mRNA Editing
          Genetics 160 (4), 1519-1533 (2002)
JOURNAL  21969411
MEDLINE  11973307
PUBMED   11973307
REFERENCE 2 (bases 1 to 2834)
          Grauso, M. and Sattelle, D.B.
          Direct Submission
          Submitted (26-MAY-2001) MRC-FGU Human Anatomy and Genetics,
          University of Oxford, South Parks Road, Oxford OX1 3QX, UK
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:21:20 ; Search time 47.4386 Seconds
(without alignments)
2698.100 Million cell updates/sec

Title: US-09-303-232-4

Perfect score: 2665

Sequence: 1 MGRARRSHLAAPAGLLLLL.....LFTTIATLAVLLSAPHIMVS 496

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mnc:*
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9: sp_phage:*
10: sp_plant:*
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12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2046.5	76.8	545	5 Q9WV19	Q9WV19 drosophila
4	1803.5	67.7	501	5 Q9XZ14	Q9XZ14 heliothis v
5	1795.5	67.4	494	5 Q8T7S2	Q8T7S2 drosophila
6	1792.5	67.3	494	5 Q8T7S1	Q8T7S1 drosophila
7	1790.5	67.2	494	5 Q8T7S3	Q8T7S3 drosophila
8	1774	66.6	509	5 Q8T7S0	Q8T7S0 drosophila
9	1769	66.4	523	5 Q8T7R9	Q8T7R9 drosophila
10	1484.5	55.7	534	5 Q9VL79	Q9VL79 drosophila
11	1371	51.4	525	5 Q8TPE2	Q8TPE2 drosophila
12	1279	48.0	273	5 Q9VJT9	Q9VJT9 drosophila
13	1242	46.6	502	11 Q9JHD6	Q9JHD6 mus musculus
14	1219.5	45.8	511	13 Q03481	Q03481 gallus gall
15	1141	42.8	461	5 P91197	P91197 caenorhabdi
16	1113	41.8	480	5 Q81932	Q81932 caenorhabdi

17	1106.5	41.5	335	5 Q9NKD1	Q9NKD1 drosophila
18	1058.5	39.7	554	5 Q62083	Q62083 caenorhabdi
19	1055.5	39.6	542	5 Q18556	Q18556 caenorhabdi
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21	975.5	36.6	537	5 Q9U941	Q9U941 myzus persi
22	972	36.5	515	5 Q46133	Q46133 locusta mig
23	962	36.1	537	5 Q8MUR0	Q8MUR0 apis mellif
24	960	36.0	536	5 Q8T0Y9	Q8T0Y9 aplysia cal
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26	956.5	35.9	567	5 Q9VC74	Q9VC74 drosophila
27	951	35.7	536	5 Q8T9S0	Q8T9S0 aplysia cal
28	949.5	35.6	509	5 Q9NFX8	Q9NFX8 myzus persi
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ALIGNMENTS

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DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Putative nicotinic acetylcholine receptor alpha 7-1 subunit.
OS Heliothis virescens (Noctuid moth) (Owlet moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Noctuoidea;
OC Noctuidae; Heliothinae; Heliothis.
OX NCBI_TaxID=7102;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte T., Oellers N., Adamczewski M.;
RT "Putative alpha subunits of insect nicotinic acetylcholine receptors
more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than
to other insect nicotinic acetylcholine receptor alpha subunits.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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DR TIGRfams; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
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KW Transmembrane.
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DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DE 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor Dalpha5 subunit.
GN NACR-ALPHA-34E OR NACRALPHA-34E OR BG:DS05899.4 OR BG:DS05899.5 OR
  CG4498 OR CG16878.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21969411; PubMed=11973307;
RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
RT Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
RT Mediated A-to-I Pre-mRNA Editing.";
RL Genetics 160:1519-1533(2002).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF272778; AAM13390.1;
DR FlyBase; FBgn0028875; nACR-alpha-34E.
DR InterPro; IPR006201; Neur_channel.
DR InterPro; IPR006202; Neur_channel_LBD.
DR InterPro; IPR006029; Neur_channel_memb.
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DR TIGRfam; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
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QY 197 DISSVFTNGEWELIGVPGKRNIIYNCPEPIDITFAVIRKTLTYFFNLIVPCVLIA 256
Db 197 DISSVFTNGEWELIGVPGKRNIIYNCPEPIDITFAVIRKTLTYFFNLIVPCVLIA 256
QY 475 DISSVFTNGEWELIGVPGKRNIIYNCPEPIDITFAVIRKTLTYFFNLIVPCVLIA 534
Db 475 DISSVFTNGEWELIGVPGKRNIIYNCPEPIDITFAVIRKTLTYFFNLIVPCVLIA 534
QY 257 SMALLGFTLPDPSGKLSLGVITLLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFVA 316
Db 257 SMALLGFTLPDPSGKLSLGVITLLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFVA 316
QY 535 SMALLGFTLPDPSGKLSLGVITLLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFVA 594
Db 535 SMALLGFTLPDPSGKLSLGVITLLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFVA 594
QY 317 SSVVSTILILNYHHRHDTHEMSDWIRCVFLYWLPLVLRMSRPGSATPPPARVPPPP 374
Db 317 SSVVSTILILNYHHRHDTHEMSDWIRCVFLYWLPLVLRMSRPGSATPPPARVPPPP 374
QY 595 SSVVSTILILNYHHRHDTHEMSDWIRCVFLYWLPLVLRMSRPGSATPPPARVPPPP 651
Db 595 SSVVSTILILNYHHRHDTHEMSDWIRCVFLYWLPLVLRMSRPGSATPPPARVPPPP 651
QY 375 -----DLELRSSKSLANVLIDDDFRH-----PQAQOQCCRYR----- 412
Db 375 -----DLELRSSKSLANVLIDDDFRH-----PQAQOQCCRYR----- 412
QY 652 DTSSERKHQILSDVELKERSKSLANVLIDDDFRHNCRPMTGGTLPHPNPAFYRTYVG 711
Db 652 DTSSERKHQILSDVELKERSKSLANVLIDDDFRHNCRPMTGGTLPHPNPAFYRTYVG 711
QY 413 GGEENGAG-----LAHSCF--GVDELSLILKEIRVITDOMRKDDDEDADISRDW 460
Db 413 GGEENGAG-----LAHSCF--GVDELSLILKEIRVITDOMRKDDDEDADISRDW 460
QY 712 QGDDGSGIGSTRMPDAVTHHTCTKSTSEYELGLILKEIRFITDQLRKDDCEDANDW 771
Db 712 QGDDGSGIGSTRMPDAVTHHTCTKSTSEYELGLILKEIRFITDQLRKDDCEDANDW 771
QY 461 KFAAMVVDRLCLLIIFTFTIATLAVLSAPHIMVS 496
Db 461 KFAAMVVDRLCLLIIFTFTIATLAVLSAPHIMVS 496
QY 772 KFAAMVVDRLCLLIIFTFTIATLAVLSAPHIMVS 807
Db 772 KFAAMVVDRLCLLIIFTFTIATLAVLSAPHIMVS 807

RESULT 3
Q9VWI9 PRELIMINARY; PRT; 545 AA.
AC Q9VWI9;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE CG32538 protein.
GN NACR-ALPHA-18C OR CG8082 OR CG8109 OR CG32538.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkley;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.N., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
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QY	31	GYHEKRLHLHLLDHYNVLERPVVNESDPLQLSFGTLTLMQIIIDVDEKNQLLTINWLKLEW	90
Dd	39	GPHEKRLHALLDNYSLERPVVNESDPLQLSFGTLTLMQIIDVDEKNQLLTINWLKLEW	98
QY	91	NDMNLRWNTSDFGVGKDLRVPPHRLKRPDVLMYNSADEGFDSTPTNVVVRNGSCLYVP	150
Dd	99	NDMNLRWSSEFGVGRLRIPPPRLKRPDVLMYNSADEGFDGTATNVVVRNGSCLYVP	158
QY	151	PGIFKSTCKIDITWFPPDDORCEMKFGSWTYDGQLDLQLODEGGDISSFVTNGEWELI	210
Dd	159	PGIFKSTCKIDITWFPPDDORCEMKFGSWTYDGQLDLQLODEAGGDISSFITNGEWDL	218
QY	211	GVPGRNEIYYNCPEPYIDITFAVIRRKRTLYFFNFNLIVPCVLIASMALLGFTLPDPDSG	270
Dd	219	GVPGRNEIYYNCPEPYIDITFAILIRRKRTLYFFNFNLIVPCVLIASMALLGFTLPDPDSG	278
QY	271	EKLISLGVTTILLSTVFNLMAETMPATSDAVPLLGTYFNCIMFMVASSVSVSTILLNYHH	330
Dd	279	EKLISLGVTTILLSTVFNLMAETMPATSDAVPLLGTYFNCIMFMVASSVSVSTILLNYHH	338
QY	331	RHADTHEMSDWIRCFLYWLPMVLRMGRSPGSATTTPPARVPPPP-----	374
Dd	339	RNPDTHEMSWIRVIFYLWLPCLIRMQRPGOV----GYECPPPPSSSSSSASGEKKQIQ	394
QY	375	DLELRSSKSLLANVLIDDDFR--HPQA-----QQPCCCR-YRGGEEAG--	420
Dd	395	NVELKERSSKSLLANVLIDDDFCNRHCASATLPHQPTYRYTMYROGDCSGVPGVPAG	454
QY	421	-----LAANSCEF--GYDYELSLLKEIRVITDQMRKDDEDADISRDKFKFAMVVDR	469
Dd	455	PVMDGRGLHEAISHTCLSAYEALAILKELRWITEQLKKEDETSDITRDWKFKFAMVVDR	514
QY	470	LCLLIIFTLTIIATLAVLLSAPHIMVS	496
Dd	515	LCLLIIFTLTIIATLAVLFSAHFIVS	541
 RESULT 4			
ID	QXZXIA	PRELIMINARY;	PRT; 501 AA.
AC	QXZXIA;		
DT	01-NOV-1999	(TrEMBLrel. 12, Created)	
DT	01-NOV-1999	(TrEMBLrel. 12, Last sequence update)	
DT	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)	
DE		Putative nicotinic acetylcholine receptor alpha 7-2 subunit..	
OS		Heliolithis virescens (Noctuid moth) (Owlet moth)..	
OC		Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	
OC		Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;	
OX		Noctuidae; Heliiothinae; Heliothis.	
OX		NCBI_TaxId=7102;	
RN	[1]		
SEQUENCE FROM N.A.			
RA	Schulte T., Oellers N., Adamczewski M.;		
RT	"Putative alpha subunits of insect nicotinic acetylcholine receptors		
RT	more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than		
RT	to other insect nicotinic acetylcholine receptor alpha subunits.";		
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.		
DR	EMBL; AF143847; AAD32698.1;		
DR	InterPro; IPR006201; Neur_channel.		
DR	InterPro; IPR006202; Neur_chan_LBD.		
DR	InterPro; IPR006029; Neu_channel_memb.		
DR	Pfam; PF02931; Neur_chan_LBD; 1.		
DR	Pfam; PF02932; Neur_chan_memb; 1.		
DR	PRINTS; PR00252; NRIONCHANNEL.		
DR	TIGRFAMS; TIGR00860; LIC; 1.		

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DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 501 AA; 56704 MW; 43CB0DC3960C78AB CRC64;

Query Match 67.7%; Score 1803.5; DB 5; Length 501;
Best Local Similarity 68.7%; Pred. No. 1.le-162;
Matches 347; Conservative 53; Mismatches 78; Indels 27; Gaps 7;

Qy 12 APAGLLLLCLLWPRGARGYHEKRLHLLHLDHYNVLRPVVNESDPLQSFGLTLMQII 71
Db 2 APLAALALLALLVSEQ-GPHEKRLNALLANTTLERPVANSEPLEVRFGLTLMQII 60
Qy 72 DVDEKNOLLITNIWLKLEWDMNLRWNTSDPGVKDLRVPPHRLWKPDVLMYNSADGFD 131
Db 61 DVDEKNOLLITNIWLSLEWMDYLRWNSDSEYGVKDLRITPNKLRKPDVLMYNSADGFD 120
Qy 132 STYTNNVVRNGSCLYVPPGIFKSTCKIDITWFPDDORCEMKGFSWTYDGLDLOLQ 191
Db 121 GYTQTNVVRNGSCLYVPPGIFKSTCKMDIANFPDDQCHDMKFGSWTYDGNOLDVLK 180
Qy 192 DEGGDISSTWNGEWELIGVPGKRNIEYVNCPEPIDITFAVIRKRLTYEFNLIVP 251
Db 181 DEAGDLSDFITNGEWELIGMPGKNTITYACCEPVVDVFTIMIRRLTYEFNLIVP 240
Qy 252 CVLIASALLGFTLPPDSGEKLSGLVITLLSLVFLNMVAETPATSDAVPLLTGFNCI 311
Db 241 CVLISSALLGFTLPPDSGEKLTLCVITLLSLVFLNLVAETLPQVSDAIPLLTGFNCI 300
Qy 312 MFWVASSVSTILLINLHRRHADTHEMSDWIRCVFLWPLVLRMSRPGSATPPPARV- 370
Db 301 MFWVASSVFLVNLVHRRHADTHEMPQWIKSVFLQWLPLVLRMSRPGKTKRTIMN 360
Qy 371 PPPDLELRSSKSLANVLIDIDDFRH-----PQACQ-----PQCCRY---YRGG--- 414
Db 361 TRMELEKRSKSLANVLIDIDDFRHGPPPNSTASTGNLPGCSIRTFDERRSFVR 420
Qy 415 -----EENGAGLAHSCFVDYELSLILKEIRVITDQMRKDEDEDADISRWKFAAMVVDRL 470
Db 421 PSTMEDVGGGLSH-----HRELHLILRELQFITARMKADDEAEELISDKFAAMVVDRE 475
Qy 471 CLIFTFTIATLAVLLSAPHIMV 495
Db 476 CLFVFTLTIATVAVLLSAPHIIV 500

RESULT 5
Q8T7S2 PRELIMINARY; PRT; 494 AA.
AC Q8T7S2
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor Dalpha6 subunit variant type II.
GN NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21969411; PubMed=11973307;
RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
RT Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
RT Mediated A-to-I Pre-mRNA Editing.";
RL Genetics 160:1519-1533(2002).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL: AF321446; AAML3393.1;
DR FlyBase; FBgn0032151; nacr-alpha-30D.

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DR InterPro; IPR006201; Neur_channel.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006209; Neur_channel_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 494 AA; 56048 MW; 6EE711810EDE7BBB CRC64;

Query Match 67.4%; Score 1795.5; DB 5; Length 494;
Best Local Similarity 68.1%; Pred. No. 6.le-162;
Matches 342; Conservative 54; Mismatches 81; Indels 25; Gaps 5;

Qy 8 SHLAAPAGLLLLCLLWPRGARG-YHEKRLHLLHLDHYNVLRPVVNESDPLQSFGLT 66
Db 3 SPLPASLSLVLLIFLAIIESCOGPEHKKLLNLLSTYNTLERPVANSEPLEVRFGLT 62
Qy 67 LMQIIDVDEKNOLLITNIWLKLEWDMNLRWNTSDFGVKDLRVPPHRLWKPDVLMYNSA 126
Db 63 LQIIDVDEKNOLLITNIWLSLEWMDYLRWNETEYGVKDLRITPNKLRKPDVLMYNSA 122
Qy 127 DEGFDSYTPNNVVRNGSCLYVPPGIFKSTCKIDITWFPDDORCEMKGFSWTYDGLQ 186
Db 123 DEGFDSYTPNNVVRNGSCLYVPPGIFKSTCKMDITWFPDDQCHCKFGSWTYDGNQL 182
Qy 187 DLQLODGGDISSTWNGEWELIGVPGKRNIEYVNCPEPIDITFAVIRKRLTYEFF 246
Db 183 DLVNSDGGDISSTWNGEWELIGVPGKRNIEYVNCPEPIDITFAVIRKRLTYEFF 242
Qy 247 NLIVPCVLIASALLGFTLPPDSGEKLSGLVITLLSLVFLNMVAETPATSDAVPLLT 306
Db 243 NLIVPCVLISSALLGFTLPPDSGEKLTLCVITLLSLVFLNLVAESMPTSDAVPLLT 302
Qy 307 YFCIMPMVASSVSTILLINLHRRHADTHEMSDWIRCVFLWPLVLRMSRPGSATPP 366
Db 303 YFCIMPMVASSVSTILLINLHRRHADTHEMSDWIRCVFLWPLVLRMSRPGSATPP 362
Qy 367 PARPV-PPPDLELRSSKSLANVLIDIDDFRHPPQACQPPCCRYRGGEENGAGLAA-- 423
Db 363 TILLSNEMKELEKRSKSLANVLIDIDDFRHITIS-----GSAIGSSASF 411
Qy 424 -----HSCFVDY-ELSLILKEIRVITDQMRKDEDEDADISRWKFAAMVVDRLCL 473
Db 412 GRPTTVEEHTAIGCNHKLHLILKELOFITARMKADDEAEELIGDKFAAMVVDRECLI 471
Qy 474 IFTLFTIATLAVLLSAPHIMV 495
Db 472 VFTLFTIATVAVLLSAPHIIV 493

RESULT 6
Q8T7S1 PRELIMINARY; PRT; 494 AA.
AC Q8T7S1
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor Dalpha6 subunit variant type
DE III.
GN NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21969411; PubMed=11973307;
RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
RT Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
RT Mediated A-to-I Pre-mRNA Editing.";
RL Genetics 160:1519-1533(2002).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL: AF321446; AAML3393.1;
DR FlyBase; FBgn0032151; nacr-alpha-30D.

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GN NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21969411; PubMed=11973307;
RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
RT Dalphas5, Dalphas6 and Dalphas7, in Drosophila melanogaster Identify a
RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
RT Mediated A-to-I Pre-mRNA Editing.";
RL Genetics 160:1519-1533(2002).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF321448; AM13395.1; -;
DR FlyBase; FBgn0032151; nacr-alpha-30D.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neu_channel_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
KW SEQUENCE 509 AA; 57887 MW; B8D8E0198E0C2BD CRC64;

Query Match 66.6%; Score 1774; DB 5; Length 509;
Best Local Similarity 66.0%; Pred. No. 7.1e-160;
Matches 341; Conservative 54; Mismatches 82; Indels 40; Gaps 6;

QY 8 SHLAAPAGLLLLCLLPRGARC-GYHEKRLHLLHLLDHYNVLPRPVNVEDPLQSLFGLT 66
DB 3 SPLPASLSLVLLIFLAIKESCGPHEKRLNLLSTYNTLERPVANESPELVKFGLT 62
QY 67 LMQIIDVDEKNOQLITNWLKLEWDMNLRNWTSDFGVGDRLRVP 111
DB 63 LQIIDVDEKNOQLITNWLKLEWDMNLRNWTSDFGVGDRLRVP 122
QY 112 PHLWKPDVLYNSADGFDSTYTNVVRNNGSLYVPPGIFKSTCKIDITWFPDDQR 171
DB 123 PNLWKPDVLYNSADGFDSTYTNVVRNNGSLYVPPGIFKSTCKIDITWFPDDQR 182
QY 172 CEMFGSWTYDGYQLDQDEGGDISFFVTNGEWELIGVPGKRNIEYVACCEPYIDI 231
DB 183 CEMFGSWTYDGNLDVNSDGGDLSDFTNGEWILLAMPKKNIVYACCEPYIDI 242
QY 232 TFVAVIRKTYLFFNLIVPCVLIASMALLGFTLPDPSGKSLGVTILLSLTVFLNWA 291
DB 243 TFTIQRRTLYYFNILVPCVLISLMSALLGFTLPDPSGKSLGVTILLSLTVFLNVA 302
QY 292 ETMPATSDAVPLLTGTYNCIMFVASSVSPILLINLHRRADTHMSDMTRCVFLYWL 351
DB 303 ETLFQVSDAIPLLGTGTYNCIMFVASSVSPILLINLHRRADTHMSDMTRCVFLYWL 362
QY 352 WILRMSRPGSATPPPARVP-PPDLELRSSKSLANVLIDDDDFRHPQAOQPCCRY 410
DB 363 WILRMSRPGSATPPPARVP-PPDLELRSSKSLANVLIDDDDFRHTIS----- 414
QY 411 YRGEENGAGLAA-----HSCFVDY-ELSLILKEIRVITOMRKDEADISR 458
DB 415 ---GSQTAIGSSASFGPRTTVEEHTAIGCNHKLHLKELQITARMRKADAEALIG 471
QY 459 DWKFAAMVVDRLCLIFLFTIATLAVLLSAPHIMV 495
DB 472 DWKFAAMVVDRLCLIFLFTIATLAVLLSAPHIMV 508

RESULT 9
Q8T7R9

ID Q8T7R9 PRELIMINARY; PRT; 523 AA.
AC Q8T7R9;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor Dalphas6 subunit variant type V.
GN NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21969411; PubMed=11973307;
RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
RT Dalphas5, Dalphas6 and Dalphas7, in Drosophila melanogaster Identify a
RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
RT Mediated A-to-I Pre-mRNA Editing.";
RL Genetics 160:1519-1533(2002).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF321448; AM13395.1; -;
DR FlyBase; FBgn0032151; nacr-alpha-30D.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neu_channel_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
KW SEQUENCE 523 AA; 59110 MW; 1C200AF74F87F841 CRC64;

Query Match 66.4%; Score 1769; DB 5; Length 523;
Best Local Similarity 64.4%; Pred. No. 2.2e-159;
Matches 342; Conservative 53; Mismatches 82; Indels 54; Gaps 6;

QY 8 SHLAAPAGLLLLCLLPRGARC-GYHEKRLHLLHLLDHYNVLPRPVNVEDPLQSLFGLT 66
DB 3 SPLPASLSLVLLIFLAIKESCGPHEKRLNLLSTYNTLERPVANESPELVKFGLT 62
QY 67 LMQIIDVDEKNOQLITNWLKLEWDMNLRNWTSDFGVGDRLRVP 126
DB 63 LQIIDVDEKNOQLITNWLKLEWDMNLRNWTSDFGVGDRLRVP 122
QY 127 DEGFDSYPTNVVVRNNGSLYVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGYQL 186
DB 123 DEGFDSYPTNVVVRNNGSLYVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGYQL 182
QY 187 DLQIQDEGGDISFFVTNGEWELIGVPGKRNIEYVACCEPYIDI 246
DB 183 DLVNSDGGDLSDFTNGEWILLAMPKKNIVYACCEPYIDI 242
QY 247 NLIYPCVLIASMALLGFTLPDPSGKSLGVTILLSLTVFLNVAETMPATSDAV----- 301
DB 243 NLIYPCVLISLMSALLGFTLPDPSGKSLGVTILLSLTVFLNVAESPTTSDAVPLIGV 302
QY 302 -----PLLTGTYNCIMFVASSVSPILLINLHRRADTHMSDMTRCVFLYWL 337
DB 303 TILLSLTVFLNVAETLPDPSGKSLGVTILLSLTVFLNVAESPTTSDAVPLIGV 362
QY 338 MSDWIRCVFLYWLPMWLRMSRPGSATPPPARVP-PPDLELRSSKSLANVLIDDD 396
DB 363 MPPWIKSVFLQWLPMWLRMSRPGSATPPPARVP-PPDLELRSSKSLANVLIDDD 422
QY 397 FRHPQAOQPCCRYRGEENGAGLAA-----HSCFVDY-ELSLILKEIRVIT 444
DB 423 FRHTIS-----GSQTAIGSSASFGPRTTVEEHTAIGCNHKLHLKELQIT 471
QY 445 DQMRKDEDEDISRDKFAAMVVDRLCLIFLFTIATLAVLLSAPHIMV 495

ID Q9VJT9 PRELIMINARY; PRT; 273 AA.
AC Q9VJT9;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE CG498 protein.
GN NACR-ALPHA-34E OR NACRALPHA-34E OR BG:DS05899.4 OR BG:DS05899.5 OR
GN CG498 OR CG16878.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Abayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Fabios B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flossler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hoston D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kamei B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hoston D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]

RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Klomp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003642; AAF53374.2; -;
DR HSSP; P58154; 119B.
DR FlyBase; FBgn0028875; nACR-alpha-34E.
DR InterPro; IPR006201; Neur_channel.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_channel_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
SQ SEQUENCE 273 AA; 31655 MW; CA95F19953E37248 CRC64;
Query Match 48.0%; Score 1279; DB 5; Length 273;
Best Local Similarity 57.6%; Pred. No. 3.7e-113;
Matches 247; Conservative 19; Mismatches 7; Indels 156; Gaps 4;
QY 68 MQIDVDEKNOLLITNINLKLWNNLWNTSDFGVYKDLRPPHRLWKPDLVLYNSAD 127
DB 1 MQIDVDEKNOLLITNINLKLWNNLWNTSDFGVYKDLRPPHRLWKPDLVLYNSAD 60
QY 128 EGFDSYTYTNVVRNNGSLVYVPGIFKSTCKIDITWFPDDQRCMEKFGSWTYDGYQLD 187
DB 61 EGFDSYTYTNVVRNNGSLVYVPGIFKSTCKIDITWFPDDQRCMEKFGSWTYDGYQLD 119
QY 188 LQLQDEGGDISFVYNGEWELIGVGRNEIYVNCCEPYIDITFAVIRKTKTYYPFN 247
DB 120 -----W--FSVPGKRNEIYVNCCEPYIDITFAIIRRTLYYPFN 158
QY 248 LIVPCVLIASMALLGFTLPPDSGKLSGLVITLLSLTVFLNVAETMPATSDAVPLLCGY 307
DB 159 LIIPCVLIASMALLGFTLPPDSGKLS-----LGTY 189
QY 308 FNCIMFVASSVSVSTILLNLYHHRHADTHEMSDWIRCVFLYWLWVLRMSRPGSATTPPP 367
DB 190 FNCIMFVASSVSVSTILLNLYHHRNADTHEMSEW----- 223
QY 368 ARVPPPPDLERERSKSLANLVLDIDDFRHPQAPQCCRYRGGEENGAGLAHSCF 427
DB 224 ----- 223
QY 428 GVDYELSLILKEIRVITDQMRKDEDDADISRDWKAAMVVDRLCLIIETLETIATLAVL 487
DB 224 -----LRKDDCNDIANDWKAAMVVDRLCLIIETLETIATLAVL 264
QY 488 LSAPHIMVS 496
DB 265 LSAPHIIVS 273
RESULT 13
Q9JHD6
ID Q9JHD6 PRELIMINARY; PRT; 502 AA.
AC Q9JHD6;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)

Db 370 PK-----HPSLKNTEMNVL-----PGHPSNGNMIYSHYTMENPCPCQ-----NNDLG 413
Qy 419 AGLAAHSC-FGVDEY-----LSLILKEIRVITDOMKDDDEDADISRDWFAA 464
Db 414 SKSKINCPLSENEHVOKKALMDTIPVIVKILIEVOFIAMFRKQDEGEICSEWFAA 473
Qy 465 MVVDRCLIIITFTTIATLAVLSAPHIM 494
Db 474 AVIDRLCLVAFTLFAICTTILMSADNFI 503

RESULT 15

P91197 ID P91197 PRELIMINARY; PRT; 461 AA.
AC P91197;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 52.7 kDa protein.
GN D2092.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Gattung S., Maggi L.;
RT "The sequence of C. elegans cosmid D2092.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL: U88167; AAB42223.1; -
DR WormPep; D2092.3; CE03102.
DR InterPro; IPR006201; Neur_channel.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neu_channel_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Hypothetical protein; Glycoprotein; Ionic channel;
KW Postsynaptic membrane; Transmembrane.
SQ SEQUENCE 461 AA; 52718 MW; 6182A7F827357B92 CRC64;

Query Match 42.8%; Score 1141; DB 5; Length 461;
Best Local Similarity 46.2%; Pred. No. 9.8e-100;
Matches 218; Conservative 85; Mismatches 121; Indels 48; Gaps 7;
Qy 34 EKRLHLLDHYNVLEPVPVNESDPLQLSEGLTLMQIIDVDKKNOLLITNIWKLKLENDM 93
Db 26 ETKLFTDLKGYNPLERPVONSQPLEVKIKLFQQLLDVDKKNQIVSNAWLSYTFWDH 85
Qy 94 NLRWNTSDFGKVDLRVP--PHRLWKPDVLNMSADEGFDSTYPTNVVNRNNGSCLYVPP 151
Db 86 KLQWEPKKGIGIQDIRPFGSDHIWKPDVLLYNAAEDFDSTFKSNLLIYHTGTVVWIPP 145

Qy 152 GIFKSTCKIDITWFPDDQRCMKFGSWTYDGYQLDLQDEGG-----DISSFTVNGEW 207
Db 146 GVLKFCQLDVTWFPDDQRCMKFGSWTFHGYAIDLQIDDDTNGTQSMDLSTVYVNGEW 205
Qy 208 ELICVPCKRNEIYNNCCPEYIDITFAVVRRTKLYFFNLIVPCVLIASMAILGFTLPP 267
Db 206 QVISTNAKRVVSYKCCPEYPTVNYLYLHRRRTLYYGFNLIIIPSLIISMAILGFMFP 265
Qy 268 DSGEKLSLGVITILLSLTFLNVAETMPATSDAVPLIGTYFNCFIMFVASSVSTILN 327
Db 266 DAGEKITLEVITLLAIVFLLSMVSETPPTSEAVPLIGVFESCCMLVVSASVFTIVLN 325
Qy 328 YHHRHADTHEMSDWIRCVFLYWLPLWLRMSRPGSATPPPARVPPPPDLELRERSSKLL 387
Db 326 LHFRSADSHENMPLVRRVLLLEFLPWLIFMSRPG-----YKFKV 363
Qy 388 ANVLIDIDDDFRHPQAOQPCCRYRGGEENGAGLAHSCFCGVDELSLIL-----KEIRV 442
Db 364 ANVIDSTDKM-PKKPKNPLDCNL-----PSNHAG-----YEAQILLHSHVHTELRR 408
Qy 443 ITDQMRKDDDEDADISRDWFAAMVVDRLCLIIITFTTIATLAVLSAPHIM 494
Db 409 VVAFYKKEEHDRIQTDWRFAAMVVDRACLLLFTVFIVISILAIMMSAPHII 460

Search completed: August 13, 2003, 15:29:09
Job time : 49.4386 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:14:55 ; Search time 10.386 Seconds
(without alignments)
2245.843 Million cell updates/sec

Title: US-09-303-232-4

Perfect score: 2665

Sequence: 1 MGGRRSHLAAPAGLLLLL.....LFTIATLAVLLSAPHIMVS 496

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	DB ID	Description
1	1267	47.5	502	1	ACH7_CHICK
2	1246	46.8	502	1	ACH7_HUMAN
3	1241	46.6	502	1	ACH7_MOUSE
4	1232.5	46.2	502	1	ACH7_RAT
5	1218.5	45.7	499	1	ACH7_BOVIN
6	1201	45.1	498	1	ACH1_CABEL
7	980.5	36.8	516	1	ACH1_MANSE
8	979	36.7	557	1	ACH1_SCHGR
9	960	36.0	503	1	ACH3_HUMAN
10	960	36.0	529	1	ACH3_HUMAN
11	959	36.0	528	1	ACH2_CHICK
12	956.5	35.9	567	1	ACH1_DROME
13	951	35.7	511	1	ACH2_RAT
14	936.5	35.1	495	1	ACH3_BOVIN
15	930	34.9	499	1	ACH3_RAT
16	926	34.7	576	1	ACH2_DROME
17	918.5	34.5	456	1	ACHA_CHICK
18	918	34.4	494	1	ACH6_HUMAN
19	917	34.4	496	1	ACH3_CHICK
20	908.5	34.1	491	1	ACHN_CHICK
21	906	34.0	461	1	ACHA_TORCA
22	904	33.9	622	1	ACHA_CHICK
23	903.5	33.9	498	1	ACHP_HUMAN
24	902.5	33.9	502	1	ACHN_HUMAN
25	902	33.8	495	1	ACHP_RAT
26	899	33.7	461	1	ACHA_TORCA
27	898.5	33.7	512	1	ACH3_CARAU
28	898	33.7	500	1	ACHN_RAT
29	896.5	33.6	457	1	ACHA_BOVIN
30	896.5	33.6	493	1	ACH6_RAT
31	893.5	33.5	519	1	ACHA_DROME
32	890	33.4	457	1	ACHA_RAT
33	889	33.4	457	1	ACHA_MOUSE

ALIGNMENTS

RESULT 1

ID	ACH7_CHICK	STANDARD;	PRT;	502 AA.
AC	P22770;			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Neuronal acetylcholine receptor protein, alpha-7 chain precursor.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=91097796; PubMed=1702646;			
RA	Couturier S., Bertrand D., Matter J.M., Hernandez M.C., Bertrand S., Millar N., Valera S., Barkas F., Ballivet M.;			
RA	"A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is developmentally regulated and forms a homo-oligomeric channel blocked by alpha-BTX."			
RL	Neuron 5:847-856(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=90311518; PubMed=2369519;			
RA	Schoeffer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.;			
RA	"Brain alpha-bungarotoxin binding protein cDNAs and MABs reveal subtypes of this branch of the ligand-gated ion channel gene superfamily."			
RL	Neuron 5:335-48(1990).			
RN	[3]			
RP	SEQUENCE OF 1-18 FROM N.A.			
RC	STRAIN=White leghorn; TISSUE=Erythrocyte;			
RX	MEDLINE=93049204; PubMed=1425587;			
RA	Matter-Sadzinski L., Hernandez M.C., Roztocil T., Ballivet M., Matter J.M.;			
RA	"Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor promoter develops during morphogenesis of the central nervous system."			
RL	EMBO J. 11:4529-4538(1992).			
RN	[4]			
RP	SEQUENCE OF 24-47.			
RC	TISSUE=Brain;			
RX	MEDLINE=85270494; PubMed=3860855;			
RA	Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A., Ray N., Raftery M.A.;			
RA	"Brain and muscle nicotinic acetylcholine receptors are different but homologous proteins."			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).			
RN	[5]			
RP	MUTAGENESIS OF LEU-270.			
RX	MEDLINE=92049732; PubMed=1719423;			
RA	Recan F., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C., Hussy N., Bertrand S., Ballivet M., Changeux J.-P.;			

P26153 gallus gall
P49581 gallus gall
P19370 carassius a
O98880 brachydanio
P43681 homo sapien
P05377 xenopus lae
P04755 drosophila
P45963 caenorhabdi
P09483 rattus norv
P02708 homo sapien
P20430 rattus norv
Q05901 homo sapien

34 888 33.3 470 1 ACHP_CHICK
35 886.5 33.3 494 1 ACHN_CHICK
36 885.5 33.2 459 1 ACHN_CARAU
37 880 33.0 456 1 ACHA_BRARE
38 879.5 33.0 627 1 ACHA_HUMAN
39 876.5 32.9 457 1 ACH2_XENLA
40 874 32.8 521 1 ACH3_DROME
41 872 32.7 538 1 ACH8_CABEL
42 867.5 32.6 630 1 ACHA_RAT
43 866.5 32.5 482 1 ACHA_HUMAN
44 858.5 32.2 452 1 ACH5_RAT
45 855.5 32.1 458 1 ACHO_HUMAN


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452 EDADISRDWKFAAMVDRCLIIFTLTIIATLAVILSAPHIM 494
1 : : : : : : : : : : : : : : : : : : : : : : : : :
449 ESEAVCSEWKFAACVVDRLCLMAFSVFTILCTIGILMSAPNFV 491

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ACH1_CAEEL					
ID	ACH1_CAEEL	STANDARD;	PRT;	498 AA.	
AC	P48180;				
DT	01-FEB-1996	(Rel. 33, Created)			
DT	01-FEB-1996	(Rel. 33, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DE	Acetylcholine receptor like protein, alpha-type chain precursor.				
GN	F25G6.3.				
OS	Caenorhabditis elegans.				
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;				
OC	Rhabditiidae; Peloderinae; Caenorhabditis.				
OX	NCBI_TaxId=6239;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Bristol N2;				
RX	MEDLINE=96196478; PubMed=8627624;				
RA	Ballivet M., Alliod C., Bertrand S., Bertrand D.;				
RT	"Nicotinic acetylcholine receptors in the nematode Caenorhabditis				
RT	elegans.";				
RL	J. Mol. Biol. 258:261-269(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Bristol N2;				
RA	Nelson J., Wohldmann P.;				
RL	Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.				
CC	-!- FUNCTION: POSSIBLE ACETYLCHOLINE RECEPTOR.				
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.				
CC	-- CC --				
CC	This SWISS-PROT entry is copyright It is produced through a collaboration				

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CC	-----
CC	EMBL; X83887; CAA58764.1; ..
DR	EMBL; AF022973; AAC25796.1; ..
DR	PIR; S68588; S68588.
DR	HSSP; PS8154; 1I9B.
DR	WormPep; F25G6.3; CE09639.
DR	InterPro; IPR006029; Neu_channel_memb.
DR	InterPro; IPR006202; Neur_chan_LBD.
DR	InterPro; IPR006201; Neur_channel.
DR	Pfam; PF02931; Neur_chan_LBD; 1.
DR	Pfam; PF02932; Neur_chan_memb; 1.
DR	PRINTS; PR00252; NRIONCHANNEL.
DR	TIGRams; TIGR00860; LIC; 1.
DR	PROSITE; PS00236; NEUOTR_ION_CHANNEL; 1.
KW	Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
RE	Transmembrane; Signal.
FT	SIGNAL 1 19
FT	CHAIN 20 498
FT	POTENTIAL.
FT	ACETYLCHOLINE RECEPTOR LIKE PROTEIN,
FT	ALPHA-TYPE CHAIN.
FT	EXTRACELLULAR (POTENTIAL).
FT	POTENTIAL.
FT	POTENTIAL.
FT	POTENTIAL.
FT	POTENTIAL.
FT	CYTOPLASMIC (POTENTIAL).
FT	POTENTIAL.
FT	BY SIMILARITY.
FT	ASSOCIATED WITH RECEPTOR ACTIVATION
FT	(BY SIMILARITY).
FT	CARBOHYD 43 43
FT	CARBOHYD 93 93
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).

RA Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
 RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
 RT 2-beta 4 nicotinic acetylcholine receptor subunits and functional
 RT expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
 RT beta 4 subunits";
 RL J. Mol. Neurosci. 7:217-228(1996).
 RN [4]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=97162233; PubMed=9009220;
 RA Groot Kormelink P.J., Luyten W.H.M.L.;
 RT "Cloning and sequence of full-length cDNAs encoding the human neuronal
 RT nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and
 RT expression of seven nAChR subunits in the human neuroblastoma cell
 RT line SH-SY5Y and/or IMR-32";
 RL FEBS Lett. 400:309-314(1997).
 RN [5]
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=99118870; PubMed=9921897;
 RA Rempel N., Heyers S., Engels H., Sleepers E., Steinlein O.K.;
 RT "The structures of the human neuronal nicotinic acetylcholine receptor
 RT beta2- and alpha3-subunit genes (CHRNA2 and CHRNA3)";
 RL Hum. Genet. 103:645-653(1998).
 RN [6]
 RN SEQUENCE FROM N.A., AND VARIANT LEU-21 INS.
 RX MEDLINE=21342809; PubMed=11450844;
 RA Lev-Lehman E., Bercovich D., Xu W., Stockton D.W., Beaudet A.L.;
 RT "Characterization of the human beta4 nAChR gene and polymorphisms in
 RT CHRNA3 and CHRNA4";
 RL J. Hum. Genet. 46:362-366(2001).
 RN [7]
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RP TISSUE=Lung;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussidi T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Richardson S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A.;
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RN SEQUENCE OF 30-503 FROM N.A.
 RP TISSUE=Brain;
 RC Submitted (JUN-1990) to the EMBL/GenBank/DBJ databases.
 RA Anand R., Lindstrom J.;
 RL Submitted (JUN-1990) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RN SEQUENCE OF 6-493 FROM N.A.
 RC TISSUE=Epidermal keratinocytes;
 RA Arrondo J., Grando S.A.;
 RT "Cloning cholinergic receptors in human keratinocytes";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE
 CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;

CC CC Name=1;
 CC CC IsoId=P32297-1; Sequence=Displayed;
 CC CC Name=2;
 CC CC IsoId=P32297-2; Sequence=VSP_000073;
 CC CC Note-No experimental confirmation available;
 CC CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC CC -----
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 CC CC or send an email to license@isb-sib.ch).
 CC CC -----
 CC DR EMBL; M86383; AAC84176.1; -;
 CC DR EMBL; M37981; AAS59942.1; -;
 CC DR EMBL; U62432; AAB40110.1; -;
 CC DR EMBL; Y08418; CAA69695.1; -;
 CC DR EMBL; AJ007783; CAA07682.1; JOINED.
 CC DR EMBL; AJ007784; CAA07682.1; JOINED.
 CC DR EMBL; AJ007785; CAA07682.1; JOINED.
 CC DR EMBL; AJ007786; CAA07682.1; JOINED.
 CC DR EMBL; AJ007787; CAA07682.1; JOINED.
 CC DR EMBL; BC001642; AAH01642.1; -;
 CC DR EMBL; BC002996; AAH02996.1; -;
 CC DR EMBL; BC000513; AAH00513.1; -;
 CC DR EMBL; AF385584; AAK68110.1; -;
 CC DR EMBL; X53559; CAA37625.1; -;
 CC DR PIR; A37040; A37040.
 CC DR PIR; A53956; A53956.
 CC DR Genew; HGNC:1957; CHRNA3.
 CC DR MIM; 118503; -;
 CC DR GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan.; TAS.
 CC DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se.; TAS.
 CC DR GO; GO:0005215; F:transporter activity; TAS.
 CC DR GO; GO:0007165; P:signal transduction; TAS.
 CC DR GO; GO:0006832; P:small molecule transport; TAS.
 CC DR InterPro; IPR006029; Neu_chan_memb.
 CC DR InterPro; IPR006202; Neu_chan_LBD.
 CC DR InterPro; IPR006201; Neu_chan.
 CC DR Pfam; PF02931; Neur_chan_LBD; 1.
 CC DR Pfam; PF02932; Neur_chan_memb; 1.
 CC DR PRINTS; PR00252; NRIONCHANNEL.
 CC DR TIGRFAMS; TIGR00860; LIC; 1.
 CC DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 CC KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family; Alternative splicing; Polymorphism.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 503 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT DOMAIN 30 238 ALPHA-3 CHAIN.
 FT TRANSMEM 239 263 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 271 289 POTENTIAL.
 FT TRANSMEM 305 326 POTENTIAL.
 FT DOMAIN 327 475 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 476 495 POTENTIAL.
 FT DISULFID 157 171 BY SIMILARITY.
 FT DISULFID 221 222 ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 1 5 MALAV -> MGSGL (in isoform 2).
 FT VARSPLIC 1 5 /FTIG-VSP_000073.
 FT VARIANT 21 21 L -> LL.
 FT VARIANT 21 21 /FTIG-VAR_013240.
 FT CONFLICT 5 13 VSLPALSP -> ALAAGAVA (IN REF. 2).
 FT CONFLICT 11 14 LSPP -> CRA (IN REF. 1).
 FT CONFLICT 100 100 D -> G (IN REF. 1).
 FT CONFLICT 132 133 DD -> TT (IN REF. 1).
 FT CONFLICT 235 235 I -> S (IN REF. 1).
 FT CONFLICT 430 430 L -> V (IN REF. 1).
 SQ SEQUENCE 503 AA: 57309 MW; 8A9BEC5D71AEC7D6 CRG64;

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Query Match 36.0%; Score 960; DB 1; Length 503;
Best Local Similarity 41.0%; Pred. No. 7.9e-74;
Matches 203; Conservative 90; Mismatches 172; Indels 30; Gaps 10;

QY 12 APAGILLLLCLLPARGAGCYGHEKRLHLLDHYNVLPVNESDPLQSLFGLTMOII 71
DB 12 SPRLLLLLSLLP-VARASAEHLRFLERFEDNEIRPVANVSDPVIHFVESQVLV 70
QY 72 DVDEKNOLLITNIWLEKNDMLNRLWNTSDFGGVKDLRVPVPHRLKPKDVLVMSADGFD 131
DB 71 KVDEVNQMELTNLKLQWINDYKLKNPDSYGAEEFMRVPAQIKWPDIVLYNNAVGDFQ 130
QY 132 STYPTNVVNRNGSCLYVPPGIFKSTCKIDITWPEDDQRCMKFGSWTYDGYQLDLQLQ 191
DB 131 VDDTKALKKYTGVTWIPPAIFKSKCKIDITYPFQYQNTKMGFSWYDKAKIDVLVI 190
QY 192 DEGGDLSSTFTNGEWELIGVGRNETIYNCCPEPYIDITFAVVIKRTLYFFNLIVP 251
DB 191 G-SMNLDYWESEWELIKAPGYKHDIKYNCCIEYDITISLYIRKPLIFYTINLIIP 249
QY 252 CVLIASMALGFTLPDSGKSLGVTILLSTVFLNVAETPATSDAVPLLGTYFNCI 311
DB 250 CLLISFLTVLVFLPSDGERKVTLCISVLLSLTVFLLVITETIPSTSLVPLICEYLLFT 309
QY 312 MFWVASSVSTILNLNTHRHADTHMSDWIRCVFLVPLWPLWMSRP----GSATPPPP 367
DB 310 MIFVTLISIVTVFLVNLVHYRPTTHMPESWYKTVFLNLLPRVMTPTSTNEGNAQKPRP 369
QY 368 ARVPPPPDLRLERS-SKSLLANVLIDDDFRHPQAQPOC--CRYVRGGEEN-GAGLA- 422
DB 370 LYGAELSNLNCFSRAESKGCEG-----YP-CQDGMCGYCHHRIKISNFSANUTR 419
QY 423 AHSFCGVDYELSL-----ILKEIRVITDQMKDEDEDADISRDWKFAMVVDRLCLI 473
DB 420 SSSSESDAVLSLSALSPEIKAEIQSVKYIAENKAQNEKEIQDDWKFVAMVIDRFLW 479
QY 474 IFTLFTIATLAVLL 488
DB 480 VFTLVCLGTAGLFL 494

RESULT 10
ACH2_HUMAN
ID ACH2_HUMAN STANDARD; PRT; 529 AA.
AC Q15822; Q9HAQ3;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
GN CHRNA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RX MEDLINE=97062879; PubMed=8906617;
RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
RA Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
RT 2-beta 4 nicotinic acetylcholine receptor subunits and functional
RT expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
RT beta 4 subunits."
RL J. Mol. Neurosci. 7:217-228(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Groot Kormelink P.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Blechschmidt K., Rosenthal A.;
```

Db 209 AKIDLE-QMEQVLDKDYWESEMAIVNATGYNSKKYDCCAEIYPDVTFYAFVIRRLPLF 267
QY 244 YFENLIVPCVLIASMALLGFTLPDPSGKLSGLVTLISLTVFLANVAETMATSADAVPL 303
Db 268 YINLIIPCLLSCLTVFLYLPDSCGCKITLISVLLSLTVFLLLIITPSTSLVPL 327
QY 304 LQTYNCIMFVASSVSTILINYHHRHADTHMSDWIRCVFLYWLWVLRMSRPGSAT 363
Db 328 IGEYLLFTMIFVTLISVITVFLNVHRSPTHTMPHVVRGALLGCVPRWLLMRP--- 383
QY 364 TTPPARVPPPLELRSSKSLANVLD-----IDDFR----- 398
Db 384 -PPVELCHP--LRLLSPSYHWLESNDVAEREYVVEEDRWACAGHVAPSVGTLCSHG 440
QY 399 --HPQAOPOCCRYRYRGENGAGLAHSCFGVGYELSLILKEIRVITDQMKDEADADI 456
Db 441 HLHSGASGPKAALQEGE---LLSPH-----MOKALEGVHYIADHLRSEADSSV 489
QY 457 SRDWKFAAMVDRLCLIIFTLTIIATLAVLL 488
Db 490 KEDWKYAMVIDRIELWLFIIVCFGLGTIGLFL 521

RESULT 11

ACH2_CHICK STANDARD; PRT; 528 AA.
AC P09480;
DT 01-WAR-1989 (Rel. 10, Created)
DT 01-WAR-1989 (Rel. 10, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RC MEDLINE=88283624; PubMed=3267226;
RA Nef P., Onysier C., Alliod C., Couturier S., Ballivet M.;
RT "Genes expressed in the brain define three distinct neuronal
nicotinic acetylcholine receptors.";
RL EMBO J. 7:595-601(1988).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
MEMBRANE.
CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (ALSO CALLED BETA). A
FUNCTIONAL RECEPTOR SEEMS TO CONSIST OF TWO ALPHA-CHAINS AND
THREE NON-ALPHA CHAINS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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or send an email to license@isb-sib.ch).
CC
CC EMBL; X07339; CAB59645.1;
DR EMBL; X07340; CAB59645.1; JOINED.
DR EMBL; X07341; CAB59645.1; JOINED.
DR EMBL; X07342; CAB59645.1; JOINED.
DR EMBL; X07343; CAB59645.1; JOINED.
DR EMBL; X07344; CAB59645.1; JOINED.
DR EMBL; AJ250360; CAB59625.1;
DR PIR; S00377; ACCH2N.
DR InterPro; IPR006029; Neu_channel_memb.

DR InterPro; IPR006020; Neur_chan_LBD.
DR InterPro; IPR006201; Neur_channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PRO0232; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 23
FT CHAIN 24 528 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
ALPHA-2 CHAIN.
EXTRACELLULAR.
FT DOMAIN 24 239
FT TRANSMEM 240 264
FT TRANSMEM 272 290
FT TRANSMEM 306 327
FT TRANSMEM 328 501
FT DOMAIN 502 520 CYTOPLASMIC.
FT DOMAIN 394 410
FT DISULFID 158 172
FT DISULFID 222 223
FT CARBOHYD 54 54
FT CARBOHYD 104 104
FT CARBOHYD 528 AA; 60675 MW; E76C6360AF876364 CRC64;
SQ
Query Match 36.0%; Score 959; DB 1; Length 528;
Best Local Similarity 39.2%; Pred No. 1e-73;
Matches 198; Conservative 84; Mismatches 161; Indels 62; Gaps 10;
QY 31 GYHEKRLHLLHDHYNVLRPVVNESDPLQLSFGTLTLMQIIDVDEKNOLLITNWLKLEW 90
Db 31 GFAEDRLFKHLFTGYNRSRVPNTSDVIVKFGLSIAQLIDVDEKNQMTTNVWLKQEM 90
QY 91 NDMNLRWYTSDFGKYDLRVPPLRLWKPDVLMYNSADEGSDFTYPTNVVVRNNGSLVYP 150
Db 91 SDYKLRWNPEDFDNVTISRVPSEMIWIPDIVLYNADGEFAVHTMKAHLFSGKVKKWP 150
QY 151 PGIFKSTCKIDITWFPDQRCMKFGSWTYDGYOLDLQDEGGDISFSFVNGEWELI 210
Db 151 PAIYKSSCSIDVTYFFDQCKMKFGSWTYDKAKIDLE-NMEHVDLKDYESEGEWAIL 209
QY 211 GVPGRKREIYNCCPEYIDITFAVIRKRLTYFFNLIVPCVLIASMALLGFTLPDPSG 270
Db 210 NAIGRYNSKKYDCCTEYIPDITFYVIRRLFLYINLIIPCLLSCLTVFLYLPDSCG 269
QY 271 EKLSGLVTLISLTVFLANVAETMATSADAVPLLTGYNCIMFVASSVSTILINVHH 330
Db 270 EKITLCISVLSLTVFLLLIITPSTSLVITPLIGEYLLTFMIFVTLISITVFLNVHH 329
QY 331 RHADTHMSDWIRCVFLYWLWVLRMSRPGSATTPPARVP-----PPDLELRERS 382
Db 330 RSPSTHTMPHVVRSEFLGFIPLWLFMKR-----PPLLLPAEGTTGYDPPGTRL--ST 380
QY 383 SKSLANVLDIDDDFRHPQAQPPQ-----CCRYRYRGENGAGLAH--SC---- 426
Db 381 SRCWLET--DVDDKWEKEEEEEEEEEEEKAYPSRVPVSGSQ---GTOCHYSCEROA 435
QY 427 -----FGVDYELSL-----ILKEIRVITDQMKDEADADISRDWKEFA 463
Db 436 GKASGGAPQVPLKGEVSGSQGLFLSPSILRALEGVQVIADHLRAEDADFVSKEDWKYV 495
QY 464 AMVVDRLCLIIFTLTIIATLAVLL 488
Db 496 AMVIDRIELWFIIVCLLGTVGLFL 520
RESULT 12
ID ACH1_DROME STANDARD; PRT; 567 AA.
AC P09478; Q9VC74;
DT 01-MAR-1989 (Rel. 10, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)

QY 310 C1MFVWVSSVSTILINLTHHRRADTHEMSDNRVCLVWLPVLRMSRSGSATPPPAR 369
Db 309 FTMLVTLVSVVTVIADVNFSPVTHMAPVQRLFIQILPKLLCIERP--KKEEPED 366
QY 370 VPP-----PPDLE-LRERSKSL-----L 387
Db 367 QPPEVLTVDYHLPDVKVNDKRFSDYDYGIPALPASHRFDLAAGISAHCFAPPL 426
QY 388 ANVLDI---DDDFRHPQAO---QPQCCRYRGGENGAGLAHS-----CFGVYD-ELS 434
Db 427 PSSLPPLGADDDLSFSGLNGDISGCC-----PAAAAAADLSTFEKPYAREME 478
QY 435 LILKEIRVTDQMRKDDDEDADISRWKFAAMVVDRICLIIFLTITLTIATVALLSAPHI 493
Db 479 KTEGSRFTAQHVKNKDFESVEDWKYVAVLDRLMFLWIFAIAACVVGFTALILQAPSL 537
RESULT 13
ACH2_RAT
ID ACH2_RAT STANDARD; PRT; 511 AA.
AC P12389; O08952;
DT 01-OCT-1989 (Rel. 12, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
GN CHRNA2 OR ACRA2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=88178113; PubMed=2832952;
RA Wada K., Ballivet M., Boulter J., Connolly J.G., Wada E.,
RA Deneris E.S., Swanson L.W., Heinemann S.F., Patrick J.;
RT "Functional expression of a new pharmacological subtype of brain
RL nicotinic acetylcholine receptor.";
RL Science 240:330-334(1988).
RN [2]
REVIEWS.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Boulter J.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES
CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-2 SUBUNIT CAN BE
CC COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC
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CC
CC EMBL; L10077; AAB60900.1; -;
DR EMBL; M20297; AAA40664.1; -;
DR EMBL; M20292; AAA40664.1; JOINED.
DR EMBL; M20293; AAA40664.1; JOINED.
DR EMBL; M20294; AAA40664.1; JOINED.
DR EMBL; M20295; AAA40664.1; JOINED.
DR EMBL; M20296; AAA40664.1; JOINED.
DR PIR; A40110; A40110.
DR InterPro; IPR006029; Neu_chan_memb.
DR InterPro; IPR006020; Neur_chan_LBD.
DR InterPro; IPR006201; Neur_channel.

DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PRO0252; NRIONCHANNEL.
DR TIGRfams; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 27
FT CHAIN 28 511
FT DOMAIN 28 241
FT TRANSMEM 242 266
FT TRANSMEM 274 282
FT TRANSMEM 308 329
FT TRANSMEM 330 348
FT TRANSMEM 391 402
FT TRANSMEM 403 425
FT DISULFID 160 174
FT DISULFID 224 225
FT CARBOHYD 56 56
FT CARBOHYD 106 106
FT CARBOHYD 212 212
FT CARBOHYD 494 494
FT CONFLICT 511 AA; 58611 MW; 3824E83BB01D613B CRC64;
SQ SEQUENCE 511 AA; 58611 MW; 3824E83BB01D613B CRC64;
Query Match 35.7%; Score 951; DB 1; Length 511;
Best Local Similarity 39.4%; Pred. No. 4.7e-73;
Matches 198; Conservative 90; Mismatches 167; Indels 48; Gaps 8;
QY 16 LLLLCCLWPRGARGCYHEKRLHLLHDHYNLVRPVNESDPLQSLFGLTLMQIIDVDE 75
Db 19 LLLVPAVLTTQGSHT-HAEDRLFKHFGYGNWRARPVNTSDVIVRFGLSIAQLIDVDE 77
QY 76 KNOLLITNLWLKLEWDMNLKRWNTSDFGCVKDLRYPHPHLPKPDVLYMNSAGDGSTYP 135
Db 78 KNQMTNVNLKQEWNDYKLRWDPAEFGNVTSLRVPSEMIWIPDIVLYNNADGEFAVTHM 137
QY 136 TNVVRNNGSLYVPPGIFKSTCKIDITWFPDDQRCENKFGSWTYDGYQLDQLQDEGG 195
Db 138 TKAHLFTGTGVHWVPPAIVKSSCIDVTFPFDOQCKMKFGSWTYDKAKIDLE-QMERT 196
QY 196 GDISSFVNGEWELIGVPGKREIYNNCCPEYIDITFAVIRRKTYLYFFNLIVPCVLI 255
Db 197 VDLKDYWESEWAIINATGYSKRYDCAEYDPVTVYFVIRRLPFTIILIIICLLI 256
QY 256 ASMALGFTLPDSEKLSLGVITLLSLTVFMVAETMPATSDAVPLGLTYFNCIMRW 315
Db 257 SCLTVLVFVLPSECEKITLCISVLSLTVFLLITEIIPSTSLVPLIGEYLLFTMIFV 316
QY 316 ASSVYSTILILNHHRHADTHEMSDNRVCLVWLPVLRMSRSGSATPPPARVPPPD 375
Db 317 TLSIVITVFLVNVHRSPTSHNPNVVRVALLGRVPRWLMNRP-----LPPMELHGS 371
QY 376 LELRERSKSLANVLDDDDFRHPQAOQCCRYRGGENG-----GAGLAHSCFGVDY- 431
Db 372 LKL--SPSYHWLETNDAGEREEETEEEE-----DENICVCAGL-PDSSMGVLVG 420
QY 432 -----ELSLILKEIRVTDQMRKDDDEDADISRWKFAAM 465
Db 421 HGLHLRAMEPTKTPFSQASEILLSPQIQAKLEGVHYTADRLRSEDADSVKEDMKRYAM 480
QY 466 VVDRCLLIIFTLTITATLAVLL 488
Db 481 VVDRIFLWFLIIVCPLGTIGLFL 503
RESULT 14
ID ACH3_BOVIN STANDARD; PRT; 495 AA.
AC Q07263;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)
 Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
 GN CHNA3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92319195; PubMed=1620271;
 RA Criado M., Alamo L., Navarro A.;
 RT "Primary structure of an agonist binding subunit of the nicotinic
 RT acetylcholine receptor from bovine adrenal chromaffin cells.";
 RL Neurochem. Res. 17:281-287(1992).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
 CC TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X57032; CAA40348.1; -
 DR PIR; S60589; S60589.
 DR InterPro; IPR006029; Neu_channel_memb.
 DR InterPro; IPR006020; Neur_chan_LBD.
 DR InterPro; IPR006201; Neur_channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 DR Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 21
 FT CHAIN 22 495
 FT NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-3 CHAIN.
 FT DOMAIN 22 230
 FT TRANSMEM 231 255
 FT TRANSMEM 263 281
 FT TRANSMEM 296 318
 FT DOMAIN 319 467
 FT TRANSMEM 468 487
 FT DISULFID 149 163
 FT DISULFID 213 214
 FT ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).
 FT CARBOHYD 45 45
 FT CARBOHYD 162 162
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT SEQUENCE 495 AA; 56914 MW; 322825629821EA07 CRC64;
 Query Match 35.1%; Score 936.5; DB 1; Length 495;
 Best Local Similarity 39.5%; Pred. No. 7.7e-72;
 Matches 198; Conservative 89; Mismatches 181; Indels 33; Gaps 9;
 OY 5 ARRSLAAGLLLLLLPRGARGCGVHEKRLHLLHDYNNLVRPVNWDLPQLSFG 64
 DB 2 ARRLRLR-----LILLLLLP-VASTDAERHLERLEFEDYNEIIRPVANVSDPVITQFE 55
 OY 65 LTLQIITDVEKNOLLITNWLKLEWDMNLRWNTSDFGVKDLRPPHRLKWDPLVLM 124
 DB 56 VMSQLVKVDEVNOIMETNLWKQIWDYKLNWPSDYDGAEEFMVPAEKIKWPKDVLVN 115
 OY 125 SADEGFSDTYTNTVVRNNGSLVYPGCIKSTCKIDITWFPDDQRCMKFGSWTYDGY 184

Db 116 NAVGDFQVDDKTKALLKYTGVTWIPPAIFKSSCKIDVTYFPFDYQNTMKFGSWSYDKA 175
 OY 185 QLDLQLODEGGDISFVTNGEWELIGVPGKRNIYYNCCPEPIDITFAVVRKRTLY 244
 Db 176 KIDLVLIG-SSMNLKDYWEGEWAIKAPGKHDIKYNCCIEIYPDITYSLYIRLPLFY 234
 OY 245 FENLIVPCVLIASMALLGFTLPDGSBGLSGVTVLLSLVFLNMVAETMPATSDAVPLL 304
 Db 235 TINLIIPCLLSFLTVLVFLVLPSCGKEKVTLCISVLLSLTVFLVAVITETIPSTSLVPLI 294
 OY 305 GTFNCIMFWVASSVSTILLNLYHHRHADTHEMSDWIRCVFLYWLFWLMSRP-----G 360
 Db 295 GEXLLFTMIETVLSIVITVFLVNHVYRTPHTTPAWVKTFILNLLPRVFMFTRPASNEG 354
 OY 361 SATTPPPARVPPDPDLRRSSKSLANVLIDDDFRHFOAQPOC--CRYYRGGEN- 417
 Db 355 NTQRPFRFYSAELSNLNCFSRIESKVCKEGYPQDGL-----CGYCHHRAKISNF 405
 OY 418 GAGLA-AHSCFGVDYELSL-----ILKEIRVITDQMRKDDDEDADISRDWKAFAAVV 467
 Db 406 SANLTSSSESVDVAVLSALSALSPKIAEQSVKYIAENKKAQNEAKEIODWKYVAMVI 465
 OY 468 DRICLIITFTTIATLAVLL 488
 Db 466 DRIFLWVFIILVILGTAGLFL 486
 RESULT 15
 ACH3_RAT
 ID ACH3_RAT STANDARD; PRT; 499 AA.
 AC P04757;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
 GN CHNA3 OR ACRA3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86118671; PubMed=3753746;
 RA Boulter J., Evans K., Goldman D.J., Martin G., Treco D.,
 RA Heinemann S.F.,
 RA Patrick J.;
 RT "Isolation of a cDNA clone coding for a possible neural nicotinic
 RT acetylcholine receptor alpha-subunit.";
 RL Nature 319:368-374(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88041184; PubMed=2444984;
 RA Boulter J., Connolly J.G., Deneris E.S., Goldman D.J., Heinemann S.F.,
 RA Patrick J.;
 RT "Functional expression of two neuronal nicotinic acetylcholine
 RT receptors from cDNA clones identifies a gene family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7763-7767(1987).
 RN [3]
 RP SEQUENCE OF 1-21 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=94193711; PubMed=8144606;
 RA Yang X., McDonough J., Fyodorov D., Morris M., Wang F.,
 RA Deneris E.S.;
 RT "Characterization of an acetylcholine receptor alpha 3 gene promoter
 RT and its activation by the Pou domain factor SCIP/Tst-1.";
 RL J. Biol. Chem. 269:10252-10264(1994).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES
 CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-3 SUBUNIT CAN BE

CC COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC -----
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CC -----
DR EMBL; X03440; CAA27170.1; -
DR EMBL; L31621; AAA1673.1; -
DR EMBL; U04961; AAA18001.1; -
DR InterPro; IPR006029; Neu_chan_memb.
DR InterPro; IPR006202; Neu_chan_LBD.
DR InterPro; IPR006201; Neu_chan.
DR Pfam; PF02931; Neu_chan_LBD; 1.
DR Pfam; PF02932; Neu_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 25
FT CHAIN 26 499
FT DOMAIN 26 234
FT TRANSMEM 235 259
FT TRANSMEM 267 285
FT TRANSMEM 301 322
FT DOMAIN 323 471
FT TRANSMEM 472 491
FT DISULFID 153 167
FT DISULFID 217 218
FT CARBOHYD 49 49
FT CARBOHYD 166 166
SQ SEQUENCE 499 AA; 56997 MW; D66C491E832B9C34 CRC64;

Query Match 34.9%; Score 930; DB 1; Length 499;
Best Local Similarity 39.0%; Pred. No. 2.8e-71;
Matches 194; Conservative 92; Mismatches 181; Indels 30; Gaps 9;

QY 10 LAAPAGLLLLCILLPRGARGCYHEKRLHLHLLDHVNLVLPVWVESDPLQLSFGLTLMQ 69
DB 6 LPPPLSMLVLMWLLP-AASASEAHRLEFQYLFEDNEIRPVANVSHPVIIQFEVMSQ 64

QY 70 IIDVDEKNOLLITNWLKLEWMDMLRWNTSDFGVKDLRVPVPHRLKPDVLMYNSADEG 129
DB 65 LVKQDEVNQIMETNLWLKQIWNQYKWKPSDYQGVFEFMRVPAEKIWKPFDIVLYNADGD 124

QY 130 FDSYPTVNVVRNKSCLVPGIFKSTCKIDITWFPDDQRCMKFGSWYDGYQLDQ 189
DB 125 FQVDDKTKALLKTYGEVTWIPFAIFKSKCKIDVTYFPDYQNCYKFGSWYDGYQLDQ 184

QY 190 LQDEGGDISFVTCNCEWELIGVPGKRNEIYVCCPEYIDITEAVVIRKTLYYFFNLI 249
DB 185 LIG-SSMNLKDWESGEWAIIRKAPGYKHEIKYNCCEEIYQDITYSLYIRRLPLFTINLI 243

QY 250 VPCVLIASMALLGFTLPDPSGKLSLGVITLISLVFLNMVAETPATS DAVPLLGTYFN 309
DB 244 IFCLLISFTLVFLVPSGCKEVTLCISVLLSLAVFLAVITETIPSTSLVIPLIGEYLL 303

QY 310 CIMEFWASSVSTIILNHHRHADTHEMSDWIRCVFLWLPVLRMSRPSGAT-TPPPA 368
DB 304 FTMIFVTLISIVTVFVNLVHYRTPTHTMTWVKAFLNLLPRVFMFTPTSGEGDTPKT 363

QY 369 RYPPPPDLE- ---LRERSKSLANVLIDDDHFRHQAQPOC- -CRYRGGEEN-GAGL 421
DB 364 RTFYGAELSNLNCFRSADSKCKEG- -----YP-CODGTCGYCHRRVRKISNFSANL 413

QY 422 -----AAHSCFGVDYELSLILKEIRVITDQMRKDDDEDADISRDKKFAAMVVDRLC 471
DB 414 TRSSSSESYNAVLSLSALSPEIKETQSVKYIAENKMAQNVAKEIODDKKYVAMVIDRIF 473
QY 472 LIIFTLFTIATLAVLL 488
DB 474 LWFVILVCILGTAGLFL 490

Search completed: August 13, 2003, 15:26:11
Job time : 11.386 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:21:45 ; Search time 18.5263 Seconds
(without alignments)
2574.698 Million cell updates/sec

Title: US-09-303-232-4
Perfect score: 2665
Sequence: 1 MGRARRSHLAAPAGLLLL.....LFTTIATLAVLLSAPHIMVS 496
Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1267	47.5	502	2 JN0113	nicotinic acetylch
2	1242	46.6	502	2 G02259	alpha 7 neuronal n
3	1241	46.6	502	1 ACHUA7	nicotinic acetylch
4	1241	46.6	502	2 A57175	nicotinic acetylch
5	1232.5	46.2	502	2 T01378	nicotinic receptor
6	1219.5	45.8	511	2 JH0173	alpha-bungarotoxin
7	1201	45.1	498	2 S68588	nicotinic acetylch
8	1141	42.8	461	2 T25671	hypothetical prote
9	1060	39.8	560	2 T19622	hypothetical prote
10	1055.5	39.6	542	2 T19862	hypothetical prote
11	979	36.7	557	2 S12359	nicotinic acetylch
12	962	36.1	503	2 A53956	nicotinic acetylch
13	959	36.0	528	1 ACCH2N	nicotinic acetylch
14	957.5	35.9	567	1 ACFFA1	nicotinic acetylch
15	954	35.8	502	2 A37040	nicotinic acetylch
16	953	35.8	511	2 A40110	nicotinic acetylch
17	936.5	35.1	495	2 S60589	acetylcholine rece
18	932	35.0	499	2 A24572	nicotinic acetylch
19	926	34.7	576	1 ACFFA2	nicotinic acetylch
20	918.5	34.5	456	1 ACCHN	nicotinic acetylch
21	908.5	34.1	491	1 ACCHN	nicotinic acetylch
22	904	33.9	622	1 ACCH4N	nicotinic acetylch
23	903.5	33.9	498	2 G02421	nicotinic acetylch
24	902.5	33.9	502	2 S10505	nicotinic acetylch
25	902	33.8	461	2 I50548	acetylcholine rece
26	901	33.8	503	2 JH0174	nicotinic acetylch
27	900.5	33.8	494	2 T02889	nicotinic acetylch
28	899	33.7	461	1 ACRYA1	nicotinic acetylch
29	898.5	33.7	512	2 B37014	nicotinic acetylch

ALIGNMENTS

RESULT 1

JN0113

nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken
N;Alternate names: alpha-bungarotoxin-binding protein alpha chain
C;Species: Gallus gallus (chicken)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1999
C;Accession: JN0113; JH0172; S28018; B25738; S26566
R;Couturier, S.; Bertrand, D.; Matter, J.M.; Hernandez, M.C.; Bertrand, S.; Millar, N.
Neuron 5, 847-856, 1990
A;Title: A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is development
A;Reference number: JN0113; MUID:91097796; PMID:1702646
A;Accession: JN0113
A;Molecule type: DNA
A;Residues: 1-502 <CD>
A;Cross-references: GB:X69586; NID:g287756; PIDN:CAA48576.1; PID:g287757
A;Experimental source: white leghorn; brain
R;Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
Neuron 5, 35-48, 1990
A;Title: Brain alpha-bungarotoxin binding protein cDNAs and MABS reveal subtypes of t
A;Reference number: JH0172; MUID:90315158; PMID:2369519
A;Accession: JH0172
A;Molecule type: mRNA
A;Residues: 1-502 <SCH>
A;Cross-references: EMBL:X52295; NID:g63077; PIDN:CAA36543.1; PID:g63078
A;Experimental source: brain
R;Matter-Sadinski, L.; Hernandez, M.C.; Rztocil, T.; Ballivet, M.; Matter, J.M.
EMBO J. 11, 4529-4538, 1992
A;Title: Neuronal specificity of the alpha7 nicotinic acetylcholine receptor promoter
A;Reference number: S28018; MUID:93049204; PMID:1425587
A;Accession: S28018
A;Molecule type: DNA
A;Residues: 1-18 <MAS>
A;Cross-references: EMBL:X68246; GB:S49751; NID:g65319; PIDN:CAA48317.1; PID:g65320
A;Experimental source: white leghorn; erythrocyte
R;Conti-Tronconi, B.M.; Dunn, S.M.J.; Barnard, E.A.; Dolly, J.O.; Lai, F.A.; Ray, N.;
Proc. Natl. Acad. Sci. U.S.A. 82, 5208-5212, 1985
A;Title: Brain and muscle nicotinic acetylcholine receptors are different but homolog
A;Reference number: A94055; MUID:85270494; PMID:3860855
A;Accession: B25738
A;Molecule type: protein
A;Residues: 24-25,'ET',28-41,'X',43-45,'X',47 <CON>
C;Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is locali
C;Genetics: 19/1; 65/3; 80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3
C;Superfamily: acetylcholine receptor
C;Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprote
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pr
F;231-254/Domain: transmembrane #status predicted <TR1>
F;262-280/Domain: transmembrane #status predicted <TR2>
F;296-317/Domain: transmembrane #status predicted <TR3>
F;470-488/Domain: transmembrane #status predicted <TR4>

nicotinic acetylch
nicotinic acetylch
nicotinic acetylch
nicotinic acetylch
nicotinic acetylch
nicotinic acetylch
acetylcholine rece
nicotinic acetylch
probable nicotinic
nicotinic acetylch
nicotinic acetylch
hypothetical prote
nicotinic acetylch
nicotinic acetylch
hypothetical prote

F:46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:365,367,413,427,465/Binding site: phosphate (Ser) (covalent) #status predicted
F:415/Binding site: phosphate (Thr) (covalent) #status predicted
F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 47.5%; Score 1267; DB 2; Length 502;
Best Local Similarity 48.6%; Pred. No. 1.9e-102;
Matches 249; Conservative 83; Mismatches 144; Indels 36; Gaps 6;

Qy 1 MGRARRSHLAAPAGLLLLCLLWPRGARGCYHEKRLHLLHDHYNVLERVNVNESPLQ 60
Db 1 MGLRALMLWLLAAGLV-----RESLQGEFORKLYKELLKNYNPLERPVANDSPLT 52

Qy 61 LSGGLTLMQIIDVDEKNOLLITNIWLKLEWMDMLRWNTSDFGVKDLRPVPHRLWKP 120
Db 53 VYFTLSLMQIMDVDEKNOLLITNIWLQWYTDHYLQWNVSEYPGVKVNRFPDGLIWK 112

Qy 121 LMVNSADGFDSTPTNVVNRNNGSCLYVPGIFKSCCKIDITWFPDDQCEMKFGSWT 180
Db 113 LLYNSADRFDATEHTNVLVNSSGHQYLPPIFKSSCYIDRVFPDFVQCNLKFSGWT 172

Qy 181 YDGLQDLQDEGGDISFVTNGEWELIGVPGKRNIEYNCPEPYDITFAVIRRK 240
Db 173 YGWSLDDLMQE---ADISGYSINGEWDLVIGPKRTESFYECCKEYPDITFTVTHRR 229

Qy 241 TLYTFENLIVPCVLIASMALLGFTLPDPSGKLSLGVITLLSLVFLNMVAETMPATSDA 300
Db 230 TLYGLNLLIPCVLISALALLVFLPADSGEKISLIGITVLLSLVFLMVAEIMPATSDS 289

Qy 301 VPLLGTFVNCIMFVASSVSTILLINYYHRRHADTHEMSDWIRCVLYLWPLVLRMSRPG 360
Db 290 VPLIAQFASPMIIVGLSVVTVIVLQYHHHDPDGGKMPKWRVILLNWCAMFLRMKRP 349

Qy 361 SATTPPARVPPDLELRSSKSLANVLD-----IDDDFRHPQAOQ 404
Db 350 E-----DKVRPAQHQRRCSSLSMEMNTVSGQCSNGNMLYIGFRLDGVCHTPTD 403

Qy 405 PQCCRYRGG--ENGAGLAHSCFGVDYELSLILKEIRVITDQMRKDEADISRWKF 462
Db 404 GVICGRMTCSPTEENLHSGHPSEG-DPDLAKILEEVRYIANFRQDEBEACNWK 462

Qy 463 AAMVVDRLCLIFLFTIATLAVLLSAPHIM 494
Db 463 AASVVDRLCLMAFSVFTIICITIGILMSAPNEV 494

RESULT 2
G02259

alpha 7 neuronal nicotinic acetylcholine receptor - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
C:Accession: G02259
R:Leonard, S.
submitted to the EMBL Data Library, November 1995
A:Reference number: H00936
A:Accession: G02259
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-502 <LEO>
A:Cross-references: EMBL:U40583; NID:g1125076; PIDN:AAA83561.1; PID:g1125077
C:Superfamily: acetylcholine receptor

Query Match 46.6%; Score 1242; DB 2; Length 502;
Best Local Similarity 46.0%; Pred. No. 2.8e-100;
Matches 240; Conservative 84; Mismatches 128; Indels 70; Gaps 6;

Qy 12 APAGLLLLCLLWPRGARGCYHEKRLHLLHDHYNVLERVNVNESDPLQISFGLTLMQII 71
Db 4 SPGGWALAAASLLHVSLSQGEFORKLYKELVKNYNPLERPVANDSPLTYVFSNLQIM 63

Qy 72 DVDEKNOLLITNIWLKLEWMDMLRWNTSDFGVKDLRPVPHRLWKPDLVLMNSADEGFD 131
Db 64 DVDEKNOLLITNIWLQWYTDHYLQWNVSEYPGVKVNRFPDGLIYNLSADRF 123

Qy 132 STYPTNVVNRNNGSCLYVPGIFKSCCKIDITWFPDDQCEMKFGSWTYDGYOLDLQ 191
Db 124 ATPHTNLVNPSSGHQYLPPIFKSSCYIDRVWFPDQVHCKLKFSGSYSGWSLDLMQ 183

Qy 192 DEGGDISFVTNGEWELIGVPGKRNIEYNCPEPYDITFAVIRKTYLFFNLI 251
Db 184 E---ADISGYSINGEWDLVIGPKRSERFYECCKEYPDVTFTVTHRRRTIYGLNLLIP 240

Qy 252 CVLIASMALLGFTLPDPSGKLSLGVITLLSLVFLNMVAETMPATSDAVLLGTYFN 311
Db 241 CVLISALALLVFLPADSGEKISLIGITVLLSLVFLMVAEIMPATSDSVPLIAQYFAST 300

Qy 312 MFVASSVSTILLINYYHRRHADTHEMSDWIRCVLYLWPLVLRMSRPG----- 360
Db 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKWRVILLNWCAMFLRMKRPDGVKVPACQHK 360

Qy 361 -----SATTPPAR-----VPPDLELRSSKSLANVLD 392
Db 361 QRRCSLASVEMSAVAPPASNGNMLYIGFRLDGVCHVCTPTDPSGVCGVMACSPH----- 416

Qy 393 IDDDFRHPQAOQPCCRYYRGGEENGAGLAHSCFGVDYELSLILKEIRVITDQMRKDE 452
Db 417 -DEHLH-----GGQPEG-----DPDLAKILEEVRYIANFRQDE 452

Qy 453 DADISRWKFAAMVVDRLCLIFLFTIATLAVLLSAPHIM 494
Db 453 SEAVCSEWKFAACVVDRLCLMAFSVFTIICITIGILMSAPNEV 494

RESULT 3
ACHUA7

nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human
N:Alternate names: cholinergic nicotinate receptor alpha-7 chain
C:Species: Homo sapiens (man)
C:Date: 12-Aug-1996 #sequence_revision 31-Jan-1997 #text_change 22-Jun-1999
C:Accession: I37185; A54194; S60309
R:Peng, X.; Katz, M.; Gerzanich, V.; Anand, R.; Lindstrom, J.
Mol. Pharmacol. 45, 546-554, 1994
A:Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from th
omers expressed in Xenopus oocytes.
A:Reference number: I37185; MUID:94195283; PMID:8145738
A:Accession: I37185
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-502 <PEN>
A:Cross-references: EMBL:X70297; NID:g496606; PIDN:CAA49778.1; PID:g496607
A:Experimental source: brain neuroblastoma cell line SHSY-5Y
R:Chini, B.; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzaretti, M.; Heinemann, S.
Genomics 19, 379-381, 1994
A:Title: Molecular cloning and chromosomal localization of the human alpha-7-nicotini
A:Reference number: A54194; MUID:94245214; PMID:8188270
A:Accession: A54194
A:Molecule type: mRNA
A:Residues: 24-363, 'S', 365-374, 'A', 376-408, 'AWPAP', 414-502 <CHI>
A:Cross-references: GB:Z23141; NID:g457736; PIDN:CAA80672.1; PID:g457737
A:Experimental source: retina
C:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is locali
C:Genetics:
A:Gene: GDB:CHRNA7
A:Cross-references: GDB:I38751; OMIM:118511
A:Map position: 15q14-15q14
A:Note: defects in this gene have been associated with mental retardation and schizop
C:Complex: the functional receptor molecule is a heteropentamer with two alpha chains
C:Superfamily: acetylcholine receptor
C:Keywords: brain; glycoprotein; heteropentamer; ion channel; neurotransmitter recept
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pr
F:231-254/Domain: transmembrane #status predicted <TR1>
F:262-280/Domain: transmembrane #status predicted <TR2>
F:296-317/Domain: transmembrane #status predicted <TR3>
F:470-488/Domain: transmembrane #status predicted <TR4>
F:46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 46.6%; Score 1241; DB 2; Length 502;
Best Local Similarity 47.1%; Pred. No. 3.4e-109;
Matches 243; Conservative 90; Mismatches 139; Indels 44; Gaps 6;

```

QY      1  MCGRRRSHLAAPAGLLLLCLLWPRGARGCYHEKRLHLLDHYNVLPRPVVNESDPLO 60
DB              ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
            1  MCGRRGGIWLALAAALLHV-----SLQGEQRRLYKELVKYNPLRPVANDSQPLT 52

QY      61  LSGFLIMQIIDVEKNQLLTITNIWKLENDNMNLRWNTSDFGGVKDLRVPPHRLWKPDV 120
DB              : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
            53  YFVLSILQIMDVDEKNQVLTITNIWLMQSWTDHYLQWNMSEYPGVKNVRFPDGQIWKPDI 112

QY      121  LMYNADAEGFDSITYPNVVVRNNGSCLYVPPIFKSTCKIDITWFPPDDQRCMKRGSWT 180
DB              : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
            113  LYNSADERFDATFHFNVLNVNASGHCOYLPGPIFKSSCYIDVRFFPDVQCCKLKFGWS 172

QY      181  YDGYQLDLQDQBGGDISSFVTNGEWELIGVPGKRNEIYNCPCPEYIDITFAVVRKK 240
DB              : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
            173  YGWSLDLQOE---ADISSYPNGEWDLMGIPGRKEKFECCKEPYDVIVTYVTMRRR 229

QY      241  TLYYFNLIVPVCVLIASMALLGFTLPDPDSEKLSGLVITLLSYTFVLMNVAETMPATSDA 300
DB              : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
            230  TLYYGLNLTIPCILSALALLVFLLPADSGEKISGITVLLSYTFVMLLVAREIMPATSDS 289

QY      301  VPLLGTIFYNCINFMASSVSTILLNYHHRHADTHEMSDWIRCFVLYWLPWVLRMSRPG 360
DB              : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
            290  VPITAYFASTLIIVGLSVVTVIVLYHHHDGPGGMKPKWTRIIILLNCAWFLRMKFRG 349

QY      361  SATTPPARVPVPPDLELRERSKSLLANVLIDDDFRHPQAQQPOCCRYRGE----- 415
DB              : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
            350  EDKVRPACHKP-----RRCSLASV-ELSAGAGPTTSNGNLLYIGFRGLEGMHCA 398

QY      416  ---ENGAGLAHSFCGV-----DYELSLLIKEIRVTIDQNRKDDEDADISR 458
DB              : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
            399  PTPDSGVVGCRLACSPTHDEHLMHGHTPHSDGDPDLAKILEEVRIANRRCODESEVICS 458

QY      459  DNKFAAMVDRLCLFIIFTTIATLAVILLSAPHIM 494
DB              : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
            459  ENKFAACVVDRCLMAFSVFTICTIGILMASPFV 494

RESULT 5
TO1378
nicotinic receptor alpha 7 chain - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 12-Feb-1999 #sequence_revision 12
C:Accession: TO1378
R:Seguella, P.; Wadiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W.
J. Neurosci. 13, 596-604, 1993
A>Title: Molecular cloning, functional properties, and distribution of rat brain
A:Reference number: Z14310; MUID:93147931; PMID:7678957
A:Accession: TO1378
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-502 <SEG>
A:Cross-references: EMBL:S53987; NID:9264770; PIDN:AAB25224.2; PID:g5705903
A:Experimental source: brain
C:Superfamily: acetylcholine receptor

Query Match 46.2%; Score 1232.5; DB 2; Length 502;
Best Local Similarity 47.2%; Pred. No. 1.9e-99;
Matches 244; Conservative 83; Mismatches 141; Indels 49; Gaps 8;
```

```

QY      2  GGRARRSHLAAPAGLLLLCLLWPRGARGCYHEKRLHLLDHYNVLPRPVVNESDPLO 61
DB              ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
            3  GGR-----GGIWLALAAALLHVSLQGEQRRLYKELVKYNPLRPVANDSQPLTV 53

QY      62  SFGFLIMQIIDVEKNQLLTITNIWKLENDNMNLRWNTSDFGGVKDLRVPPHRLWKPDV 121
DB              : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
            54  YFVLSILQIMDVDEKNQVLTITNIWLMQSWTDHYLQWNMSEYPGVKNVRFPDGQIWKPDI 113

QY      122  MYNSADEGDSVPNPVVVRNNGSCLYVDPPIFKSTCKIDITWFPPDDQRCMKRGSWT 181
```


Db 365 -----NRHESLIRIKDNEHSLSRANSFDACRLNQVIMQTSVNSGLTSLGSPSTM 417
Qy 424 HSCFGVDYELS-----LIL-----KEIRVITDQMRKDEADISRDWKFAAMVVDRLCLII 474
Db 418 ISSNGTTDVSQATLILHLRIYHKLVIYKRMIEGDEQACNNKFAAMVVDRLCLIV 477
Qy 475 FTLTFTIATLAVLSAPHIM 494
Db 478 FTTFIIVSTIGIFWSAPYL 497
RESULT 8
T25671
hypothetical protein D2092.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T25671
R:Gattung, S.; Meggl, L.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid D2092.
A:Reference number: Z20067
A:Accession: T25671
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-461 <GAT>
A:Cross-references: EMBL:U88167; PIDN:AA842223.1; GSPDB:GN00019; CESP:D2092.3
A:Experimental source: strain Bristol N2; clone D2092
C:Genetics:
A:Gene: CESP:D2092.3
A:Map position: 1
A:Introns: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2
C:Superfamily: acetylcholine receptor
Query Match 42.8%; Score 1141; DB 2; Length 461;
Best Local Similarity 46.2%; Pred. No. 1.6e-91;
Matches 218; Conservative 85; Mismatches 121; Indels 48; Gaps 7;
Qy 34 EKRLHLLHDHYNVLRPVVNSDPLQLSFGTLFQIIVDDEKNQLLITNWLKLEWDM 93
Db 26 ETLEFDDLLKGYNPLRPVNSQPLEVKIKLFQIILVDDEKNQIVSNAMLSYWFEDH 85
Qy 94 NLRWNTSDGGVKKDLRVP--PHRLKPDVLMYNSADEGSDSYPTNVVNRNGSLYVPP 151
Db 86 KIQWPKYGGIQQDIIRPGSSDHIIKRPDVLVNSAAEDFDTSKSNLLTYHTGVVWIPP 145
Qy 152 GIFKSTCKIDITWFPDDQRCMKFGSWTDYQYOLDQLQDEGG-----DISFVTNGEW 207
Db 146 GVLFKVCOLDVTFWFPDDQVCEMKFGSWTFHGAYIDLQDDDTNGTQSDMLSTYLVNGEW 205
Qy 208 ELIGVPGKNEIYNNCCPEYIDITFAVIRKRTLYFFNLVPCVLIASMAILGFTLPP 267
Db 206 QVISTNAKRVSYKCCPEYPTVNYLHRRRTLYYGFNLIPSLISMAILGFMFPP 265
Qy 268 DSGEKLGLVITLLSLTVFLNVAETWTPATSDAVPLGLTYFCIMFWASSVSTLIIN 327
Db 266 DAGEKITLEVITLLATVFLSVSEMTPTTSEAVPLIGVFSCMLVWSAVVFTTVL 325
Qy 328 YHRRHADTHEMSDWIRCVFLVPLVLRMSRPGSATTPPPARVPPPPDLELRSSKSL 387
Db 326 LHFRSADSHMNPVLRVLLEFLPMLFMSRPG-----YKFVK 363
Qy 388 ANVLDIDDDFRHPQAQOQCCRYRGGEEAGLAHSCFGVDYELSLIL-----KEIRV 442
Db 364 ANVIDSTDM-KPKKNPLDCNL-----PSNHAG-----YEAQILLHSHVHTELRR 408
Qy 443 ITDQMRKDEADISRDWKFAAMVVDRLCLIIFTLTFTIATLAVLSAPHIM 494
Db 409 VVAFYNKEEHERIOTDWRFAAMVVDRLCLIIFTFTFIVISILAIMMSAPHII 460
RESULT 9
T19622
hypothetical protein C31H5.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T19622
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19622
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-560 <WIL>
A:Cross-references: EMBL:Z93778; PIDN:CAB07843.1; GSPDB:GN00019; CESP:C31H5.3
A:Experimental source: clone C31H5
C:Genetics:
A:Gene: CESP:C31H5.3
A:Map position: 1
A:Introns: 24/1; 70/3; 139/2; 270/1; 299/1; 336/3; 372/2; 456/3
C:Superfamily: acetylcholine receptor
Query Match 39.8%; Score 1060; DB 2; Length 560;
Best Local Similarity 37.6%; Pred. No. 2.5e-84;
Matches 217; Conservative 96; Mismatches 142; Indels 122; Gaps 11;
Qy 16 LLLLLCLLWPRGARC-----GYHEKRLHLLHDHYNVLRPVVNSDPLQLSFGTLQMQ 69
Db 9 VLSVSTILWE--TKSKVIWTGDHERRLYAKLAENYKLRPVNRSEAVVLLGMDYQQ 66
Qy 70 IIDVDEKNOLLITNWLKLEWDMNLRWNTSDFGVYKDLRVPVPHRLKPDVLMYNSADEG 129
Db 67 ILIDIDEKHQIMNSNWLRMSWTDHYLTWDPSEFNGNKEVRLPINNWKPDVLYNSVDQ 126
Qy 130 FDSYPTNVVNRNGSLYVPPGIFKSTCKIDITWFPDDQRCMKFGSWTDYQYOLDQLQ 189
Db 127 FDSWPNVNAVLYTGNVTWIPPAIRSSCAIDAIYFPDTHCTMKFGSWTYSGFETDL- 185
Qy 190 LQDEGGDISSFVT-----NGEWELIGVPGKNEIYNNCCPEYIDITFAVIRKRTLY 243
Db 186 -----INTTISPATYKPNGEWELLGTSQRSIFFECCPEYDYDTFTVSIRRTLY 237
Qy 244 YFNLIVPCVLIASMAILGFTLPPDSGEKLSLGVITLLSLTVFLNVAETWTPATSDAVPL 303
Db 238 YGFLNLLPCMLISSALLSFTLPADCGEKLNLGVTFMSLCVFMIMVAEMPOTSALPL 297
Qy 304 LGTYFCIMFWASSVSTILINYLHRRHADTHE-MSDWIRCVFLVPLVLRMSRPGSA 362
Db 298 IQIFYSCIMFQVGSVATVIALNFHRSPEQYKPNKFLKTLILLGLWLTLLGMRPDV- 356
Qy 363 TTPPPARVPPDLEL-----RERSKSLANV-----L 391
Db 357 -----LELSVHGAHYASDNKKKQOYLIEVERHILTRPNGNGHSAVDKAVHL 403
Qy 392 DIDDDFRHPQAQOQ-----CCRYRGGENG 419
Db 404 DLSTGNPHSDAKSSPKRTSASIMGMTGLPTQMGALDSSINKYCTKTRPLENGS 463
Qy 420 GLAAH-----SCFG-----VYELSLILKEIRVITDQMRKDEADISR 458
Db 464 ATINHKSSQPINNNNIYKCANNOQTQFDRHFHILNELRVISARVRKEAMHALQA 523
Qy 459 DHKFAAMVVDRLCLIIFTLTFTIATLAVLSAPHIMV 495
Db 524 DMFASRVYDVRCVCFASFSAFLFMCTAIISYNAPHLEV 560
RESULT 10
T19862
hypothetical protein C40C9.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T19862
R:Hembry, C.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19188
A:Accession: T19862

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-542 <WIL>
A:Cross-references: EMBL:Z70266; PIDN:CAA94206.1; GSPDB:GN00028; CESP:C40C9.2
A:Experimental source: clone C40C9
C:Genetics:
A:Gene: CESP:C40C9.2
A:Map position: X
A:Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1; 49
C:Superfamily: acetylcholine receptor

Query Match 39.6%; Score 1055.5; DB 2; Length 542;
Best Local Similarity 40.5%; Pred. No. 5.9e-84;
Matches 214; Conservative 94; Mismatches 136; Indels 85; Gaps 12;
QY 34 EKRLHLLHLDHYNLVRPNVNESDPLQSLFGLTLMQIITDDEKKNOLLTNLWLENDM 93
DB 30 EYRLADLRHNDYPERVANASEPLVSVKIIYQQIILDVDEKNOITVLAVIEWEQWTDY 89
QY 94 NLRWNTSDFGGKDLRVP--PHRLWKPDVLMYNSADEGSDTYPTNVVVRNNGSCLYVPP 151
DB 90 KKWDPSEYGGIKDIRPCGNANA IWKPDVLLYNSADENFDSTYPVNYVVSYTGVDVLQVPP 149
QY 152 GIFKSTCKIDITWFPDQDORCEMKFGSWTYGYQLDLQLO-----DEGGDISSFVTN 204
DB 150 GILKLSCKIDITYFPDQDICHKFGSWTYSNGFNIDLRINGPEGKNISDEGIDVQYVQN 209
QY 205 GEWELIGVPGKNEIYYNCCPEPYDITFAVIRKTLTYFENLIVPCVLIASMALLGFT 264
DB 210 GENWLVAPARHETNFD--EQYPSLFYLIQRTLYGLNLIFSLTSLMTVLGFT 267
QY 265 LPPDGEKLSGVITILLSLTVFLNMVAETMPATSDAVPLL-----GTYNCFIMFMASS 318
DB 268 LPPDAGERITLITILLSVCFSLMVADMTPTSEAVPLIGLITFGAFFSCCLMVVAS 327
QY 319 VYSTILLIYHRRHADTHEMSDWIRCVFLYLPWVLRMSRG-----SATTPPPA 368
DB 328 VYFTVLNLHNRKPTHEMSDFPRLLELLIWLPLLMLRRPCKTIFNCTHLKAEAEKA 387
QY 369 RV-----PPPPDLERLRSKSLANV-----LDIDDDF--RH-----PQAOQ 404
DB 388 KOGSKNGVGCKPDSVHPSEGLSLMKNILGRQOTIDFEYFHVQHNLMPVAPSEMT 447
QY 405 PQCC-----RYYRGEENGAGLAHSCFGVDYELSLIKETRVITD 445
DB 448 PRVTSKYMAESYVEDVYMTLNKYMQ-----KACL-----ELKNISSQTRAMRK 492
QY 446 QMRKDEDDADISRWKFAAMVVDRLCLIFTIITLTIATLAVLLSAPHIM 494
DB 493 KHEEDERQAANDWKFAAMVVDRLCLITFSFIVVSTGIMFSPHLI 541

RESULT 11
S12359
nicotinic acetylcholine receptor alpha-L1 chain precursor - desert locust
C:Species: Schistocerca gregaria (desert locust)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C:Accession: S12359
R:Marshall, J.; Buckingham, S.D.; Shingai, R.; Lunt, G.G.; Goosey, M.W.; Darlison, M.G.;
EMBO J. 9, 4391-4398, 1990
A:Title: Sequence and functional expression of a single alpha subunit of an insect nicot
A:Reference number: S12359; MUID:91092263; PMID:1702381
A:Accession: S12359
A:Molecule type: mRNA
A:Residues: 1-557 <MAR>
A:Cross-references: EMBL:X55439; NID:g10133; PIDN:CAA39081.1; PID:g10134
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-557/Product: nicotinic acetylcholine receptor alpha-L1 chain #status predicted <MAT
F:245-266/Domain: transmembrane #status predicted <TM1>
F:274-295/Domain: transmembrane #status predicted <TM2>
F:308-329/Domain: transmembrane #status predicted <TM3>

F:501-523/Domain: transmembrane #status predicted <TM4>
F:47,235/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 36.7%; Score 979; DB 2; Length 557;
Best Local Similarity 40.0%; Pred. No. 2.9e-77;
Matches 217; Conservative 88; Mismatches 160; Indels 78; Gaps 10;
QY 11 AAPAGLLLLCLLMPRGARCYHEKRLHLLHLDHYNLVRPNVNESDPLQSLFGLTLMQI 70
DB 4 ALPMLLLLLLLLLLHHPAAAPDAKRLYDLDLLSNYNRLIRPVSNNTDVLVKGRLSQL 63
QY 71 IDVDEKKNOLLTNLWLENDMNLWNTSDFGGKDLRVPVPHRLWKPDVLMYNSADGFG 130
DB 64 IDLALKDQILATNWLHEHWDHFKFWDPAEYGGVTELYVPSEHILWLDIVLYNNADGEY 123
QY 131 DSTYPTNVVVRNNGSCLVPPGIPKSTCKIDITWFPDQDORCEMKFGSWTYGYQLDL-- 188
DB 124 VTTMTKAVLHHTGKVVWTPPAIFKSSCEIDVRFPPDQDQCFMKFGSWTYGDDQIDLKH 183
QY 189 --QLQDEG---GGDISFVTNGEWELIGVPGKNEIYYNCCPEPYDITFAVIRRRTL 242
DB 184 INQYDDNKVKVGIDIREYYPSEWMDILGVPAERHEKYYPCCAEYPDIFENITLRRKTL 243
QY 243 YFFNLIVPCVLIASMALLGFTLPPDGEKLSGLVITILLSLTVFLNMVAETMPATSDAVP 302
DB 244 FYTNLIIVPCVIGISYLSVLVFLPADSGEKIALCISILLSQTMFEFLISEIIPSTSLAP 303
QY 303 LLGYFNCIMFMASSVSVTILLIYHRRHADTHEMSDWIRCVFLYLPWVLRMSRPGSA 362
DB 304 LLGXYLFTWVLVGLSVVITLWNLVHYRKPSHKMAPWRKVRIRRLPKLLM----- 357
QY 363 TTPPPARVPPPDLELRERSKSL-----ANVLDDDDFRHPQ 401
DB 358 -----RV---PEQLADLASKRLLRHAAHNSLSAAAAAASAAASPDLSLRHHH 408
QY 402 AQQQCCRY-----YRGGEENGAGLAH-----SCFVD----- 430
DB 409 LHQHQHQLHLHLQRPFGCGNLSATNREGGSAGAFGGPLSVVVGSLSDVATRKKY 468
QY 431 -YELSLIKETRVITDQMRKDE--DADISRWKFAAMVVDRLCLIFTIITLTIATLAVLL 488
DB 469 PFELEKAIHNVLFQNHMQRODEFAE--DQDWGFVAVVLDRLFLWFIITIASIVGTFAIL 527
QY 489 SAP 491
DB 528 EAP 530

RESULT 12

A53956
nicotinic acetylcholine receptor alpha-3 chain precursor, neuronal - human
C:Species: Homo sapiens (man)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 20-Aug-1999
C:Accession: A53956; S21338
R:Minovilovic, M.; Roses, A.D.
Exp. Neurol. 111, 175-180, 1991
A:Title: Expression of mRNAs in human thymus coding for the alpha3 subunit of a neuro
A:Reference number: A53956; MUID:91114756; PMID:1989896
A:Accession: A53956
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-503 <MIH>
A:Cross-references: GB:M37981; NID:g189252; PIDN:AAA59942.1; PID:g189253
R:Anand, R.; Lindstrom, J.
submitted to the EMBL Data Library, June 1990.
A:Description: Nucleotide sequence of the mature human nicotinic acetylcholine recept
A:Reference number: S21338
A:Accession: S21338
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 30-503 <ANA>
A:Cross-references: EMBL:X53559; NID:g34985; PIDN:CAA37625.1; PID:g34986
C:Genetics:

Query Match	36.0%;	Score 959;	DB 1;	Length 528;
Best Local Similarity	39.2%;	Pred. No. 1.5e-75;		
Matches 198;	Conservative 84;	Mismatches 161;	Indels 62;	Gaps 10;

QY	31	GYHEKRLHLLHDHYNVLRPPVNVESDPQLSGFLTLMKIIDIYDEKNQLLITNIWLKLEW	90
DB	31	GFAEDRLKHLFGYGNRWRSPVNTSDVITVRKGLSIAQLIIDYDEKNQMTTNIWLKQEW	90
QY	91	NDMNLRWNTSDFGGVXDLRVPPHRLKPKDVLVMSADEGFSDTSPYTNVNVRRNGSLVYP	150
DB	91	SDYKLRNPEDEFNVTISIRVSEMIWPDVILYNNADGEFAVTHMKAHLFSGKGVKWP	150
QY	151	PGIFKSTCKIDITWFFPDQRCBKMFGSTWYDGYLDLQDQDEGGDIISFVTNGEWELI	210
DB	151	PAIYKSSCSIDVTFYFPDQONCKMKFGSWTYDKAKIDLE-NMEHHVDLKDYWESEGMII	209
QY	211	GVPGKREIYNNCCPEPYDITFAVIRKTLVYFNFLVPCVLIASMAALLGFLTPDSCG	270
DB	210	NAIGRVNSKKYDCCTEYDPDITFYVIRRLPEYTNLIIPCLISCLVAVLYLPSDCG	269
QY	271	EKLSLGVTTILSLTVFLNVAETMPATSDAIVPLLTGYTNCIMFWASVSVTILINVHH	330
DB	270	EKITLCSVLLSTVLLLTIELIIPSTSLVPLIGEYLLFTMIFVLTLSIIITVFLNVHH	329
QY	331	RHADTHEMSDWIRCVLYLWLPWWLRMSRGSATTPPPARVP-----PPDLELRERS	382
DB	330	RSPSTHTMPHWRSFFLGFPRWLFMKR-----PPLLLPAEGTTGQVDPGTRL--ST	380
QY	383	SKSLLANVLIDDDFRHPQAQOPQ-----CCRYRGEENGAGLAAH-SC-----	426
DB	381	SRCWLET--DVDDKWEEEEEEEEEEEEEEKAYSRVPSGSGQ---GFQCHYSERQA	435
QY	427	-----FGVDYELSL-----TLKEIRVITDMRKDDDEDADISROWKFA	463
DB	436	GRASGGPAPQVPLKGEVSDQGLTFLSPSILRALEGVQYIADHLRAEDADFVKEDKYY	495
QY	464	AMVVDRLCLIFLTITIIATLAVLL	488
DB	496	AMVIDRIELWMFIIVCLLGTGVGLFL	520

RESULT 14	
ACFFAI	
C:Species: Drosophila melanogaster	
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jun-2002	
C:Accession: S00381; A38801	
R:Bossey, B.; Ballivet, M.; Spierer, P.	
EMBO J. 7, 611-618, 1988	
A:Title: Conservation of neural nicotinic acetylcholine receptors from Drosophila	
A:Reference number: S00381; MUID:88283626; PMID:2840281	
A:Accession: S00381	
A:Molecule type: DNA	
A:Residues: 1-567 <BO>	
A:Cross-references: GB:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576	
A:Accession: A38801	
A:Molecule type: mRNA	
A:Residues: 1-567 <BO2>	
A:Cross-references: EMBL:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576	
A:Note: 538-Tyr was also found	
C:Genetics:	
A:Gene: FlyBase:nACR-alpha-96Aa	
A:Cross-references: FlyBase:FBgn00000036	
A:Map position: 3R 96A	
A:introns: 64/3; 79/3; 116/2; 176/3; 330/2; 401/1; 499/3	
C:Superfamily: acetylcholine receptor	
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic r	
F:1-21/Domain: signal sequence #status; predicted <SIG>	
F:22-567/Product: nicotinic acetylcholine receptor alpha-like chain #status pre	
F:22-240/Domain: extracellular #status predicted <EX>	
F:272-290/Domain: transmembrane #status predicted <TM2>	

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●
●

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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:14:30 ; Search time 43.5088 Seconds
(without alignments)
1809.483 Million cell updates/sec

Title: US-09-303-232-4

Perfect score: 2665

Sequence: 1 MCGRRARRSHLAAPAGLLLL.....LFTTIATLAVLLSAPHIMVS 496

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
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7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2665	100.0	496	21	AA198015
2	1850	69.4	770	21	AA198014
3	1803.5	67.7	501	21	AA198016
4	1417.5	53.2	311	22	ABB63683
5	1267	47.5	502	18	AAW12368
6	1253	47.0	498	22	ABB60432
7	1246	46.8	502	15	AAW44153
8	1246	46.8	502	15	AAW09025
9	1246	46.8	502	21	AAW24088

10	1246	46.8	502	22	AAW82690	Nicotinic acetylch
11	1246	46.8	502	22	AAW50012	Wild-type human al
12	1246	46.8	502	23	ABB82435	Human neuronal NAC
13	1246	46.8	502	23	ABG70492	Human neuronal nic
14	1242	46.6	502	19	AAW69216	V274T variant huma
15	1240	46.5	502	22	AAW50015	Mutant human alpha
16	1236	46.4	502	22	AAW50016	Mutant human alpha
17	1230	46.2	502	22	AAW50017	Mutant human alpha
18	1219.5	45.8	511	18	AAW12369	Neuronal alpha-bun
19	1053.5	39.5	554	22	AAE12824	Caenorhabditis ele
20	1053.5	39.5	554	24	ABP96318	Caenorhabditis ele
21	989	37.1	470	22	AAW50014	Chimeric alpha7/5-
22	984	36.9	448	22	AAW50018	Mature cell surfac
23	965	36.2	193	22	ABB60716	Drosophila melanog
24	964.5	36.2	631	23	AAO17243	Modified acetylcho
25	960	36.0	504	18	AAW09022	Neuronal nicotinic
26	960	36.0	529	15	AAW44155	Human neuronal nic
27	960	36.0	529	16	AAW73966	Alpha 2 subunit of
28	960	36.0	529	18	AAW09021	Neuronal nicotinic
29	960	36.0	529	23	ABB82430	Human neuronal NAC
30	960	36.0	529	23	ABG31800	Human neuronal nic
31	960	36.0	529	23	ABG61850	Prostate cancer-as
32	954	35.8	622	23	AAO17245	Modified acetylcho
33	954	35.8	622	23	ABB08885	Modified acetylcho
34	926	34.7	576	22	ABB61954	Modified hen ACR s
35	918	34.4	494	18	AAW09018	Drosophila melanog
36	918	34.4	494	18	AAW09018	Neuronal nicotinic
37	918	34.4	494	23	ABG70491	Human neuronal NAC
38	914	34.3	580	22	ABB62727	Human neuronal nic
39	910	34.1	504	15	AAW44156	Human neuronal NAC
40	910	34.1	504	23	ABB82431	Human neuronal nic
41	910	34.1	504	23	ABG70488	Human neuronal nic
42	906.5	34.0	502	23	AAE15160	Human mutant neuro
43	906.5	34.0	631	23	AAO17244	Modified acetylcho
44	906.5	34.0	631	23	ABB08884	Modified hen ACR s
45	903.5	33.9	498	18	AAW09027	Neuronal nicotinic

ALIGNMENTS

RESULT 1
AA198015
ID AA198015 standard; Protein; 496 AA.
XX
AC
AA198015;
XX
DT 17-FEB-2000 (first entry)
XX
DE H. virescens acetyl-choline receptor protein from clone Hva7-1.
XX
DE H. virescens acetyl-choline receptor protein from clone Hva7-1.
XX
KW Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
KW neurotransmission; plant protection agent; conductance; AChR.
XX
OS Heliothis virescens.
XX
PN DE19819829-Al.
XX
PD 11-NOV-1999.
XX
PF 04-MAY-1998; 98DE-1019829.
XX
PR 04-MAY-1998; 98DE-1019829.
XX
XX (FARB) BAYER AG.
XX
PI Adamczewski M, Oellers N, Schulte T;
XX
DR WPI; 2000-014207/02.
XX
DR N-PSDB; AA224476.
XX
PT New nucleic acid encoding a nicotinic acetylcholine receptor from
PT insects, used to identify potential insecticides -

Matches 265; Conservative 14; Mismatches 16; Indels 9; Gaps 2

Qy 2 GGRARRSHLAAPAGLILLCLLWPRGARGCYHEKRLHLLDHYNVLPRPVVNESDPLQ 61
 Db 16 GGRM-----LVYGLGLIMI-----PACAAGPHEKRLHLLDHYNVLPRPVVNESDPLQ 66
 Qy 62 SFGTLMOIIDDVEKNOLLITNIWLKLEWMDNMLRWNTSDFGGVKDLRVPPHRLWKPDVL 121
 Db 67 SFGTLMOIIDDVEKNOLLITNIWLKLEWMDNMLRWNTSDFGGVKDLRVPPHRLWKPDVL 126
 Qy 122 MNSADEGFDSTYPTNVVNRNGSCLYVPPGIFKSTCKIDITWFPDDQRCMEKFGSWTY 181
 Db 127 MNSADEGFDSTYPTNVVNRNGSCLYVPPGIFKSTCKIDITWFPDDQRCMEKFGSWTY 186
 Qy 182 DGYQLDLQDEGGDISSTFTNGEWELIGVPGKRNIEIYNCCPEYIDITFAVIRRK 241
 Db 187 DGYQLDLQDEGGDISSTFTNGEWELIGVPGKRNIEIYNCCPEYIDITFAVIRRK 246
 Qy 242 LYFFNLIVPCVLTIASALLGFTLPDPSGKLSLGVTLISLTVFLNVAETMPATSDAV 301
 Db 247 LYFFNLIVPCVLTIASALLGFTLPDPSGKLSLGVTLISLTVFLNVAETMPATSDAV 306
 Qy 302 PLLG 305
 Db 307 PLLG 310

RESULT 5

AAW12368
 ID AAW12368 standard; Protein; 502 AA.

AC AAW12368;

DT 17-JUN-1997 (first entry)

Neuronal alpha-bungarotoxin binding protein alpha 1; cholinergic.

Neuronal alpha-bungarotoxin binding protein alpha 1; cholinergic;
 ligand binding; ion channel.

Gallus sp.

Key Location/Qualifiers
 FT Peptide 1..22
 FT Protein /label= Sig_peptide
 FT 23..502
 FT /label= Mat_protein

US5599709-A.

PD 04-FEB-1997.

PF 28-SEP-1989; 89US-0413947.

PR 28-SEP-1989; 89US-0413947.

PA (SALK) SALK INST BIOLOGICAL STUDIES.

PI Lindstrom JM, Schoeffer RD;

DR WPI; 1997-118297/11.

DR N-PSDB; AAT59196.

PT New isolated neuronal alpha-bungarotoxin-binding protein DNA - used
 PT to screen cholinergic agents and other drugs which may affect ligand
 PT binding, ion channel or other activities of the protein.

PS Example; Fig 2A-B; 18pp; English.

XX The alpha subunit (AAW12368) and alpha2 subunit (AAW12369) amino acid
 CC sequences of chick neuronal alpha-bungarotoxin binding protein
 CC (ABBP) were deduced from newly isolated DNA molecules (AAT59196-97)
 CC obtd. from an 18-day chick embryo cDNA library. ABBP subunits can
 CC be produced in recombinant host cells, pref. a bacterium, and used

CC in the screening of cholinergic agents and other drugs that may
 CC affect the ligand binding, ion channel or other activity of intact
 CC ABBP subtypes. The ABBP alpha and alpha2 subunits can also be
 CC used to produce subunit peptides for use as immunogens for
 CC preparing antibodies to permit affinity purification of subtypes
 CC and their histological location.

XX Sequence 502 AA;

Query Match 47.5%; Score 1267; DB 18; Length 502;
 Best Local Similarity 48.6%; Pred. No. 5.6e-118;
 Matches 249; Conservative 83; Mismatches 144; Indels 36; Gaps 6;

Qy 1 MGRARRSHLAAPAGLILLCLLWPRGARGCYHEKRLHLLDHYNVLPRPVVNESDPLQ 60
 Db 1 MGLRALMLWLLAAGLV-----RESLQGEFORKLYKELLYNPLERPVANDSPLT 52
 Qy 61 LSFGTLMOIIDDVEKNOLLITNIWLKLEWMDNMLRWNTSDFGGVKDLRVPPHRLWKPDV 120
 Db 53 VYFTLSLMOIIMDVDEKNQVLTNIWLQMYTWDHYLQMNWSEYPGVKNVRFDPGLIWKPDV 112
 Qy 121 LMNSADEGFDSTYPTNVVNRNGSCLYVPPGIFKSTCKIDITWFPDDQRCMEKFGSWT 180
 Db 113 LLYNSADERDATTFTNVLVNNSGHCQYLPPIKSSCYIDVRWFPDVQCNLKFSGWT 172
 Qy 181 YDGYQLDLQDEGGDISSTFTNGEWELIGVPGKRNIEIYNCCPEYIDITFAVIRRK 240
 Db 173 YGWSLDLQMOE---ADISGYISNGEWDLVGPGRKTESFYECCKEPEYDITFTVTRRR 229
 Qy 241 TLYFFNLIVPCVLTIASALLGFTLPDPSGKLSLGVTLISLTVFLNVAETMPATSDA 300
 Db 230 TLYTGLNLLIPCVLTIASALLGFTLPDPSGKLSLGVTLISLTVFLNVAETMPATSDS 289
 Qy 301 VPLLGTYNFCIMFVAVSVVSTILITLYNHHHADTHEMSDWIRCVLYFLWPLVLRMSRPG 360
 Db 290 VPLIAQYFASTMIIVGLSVVTVIVLYVHHHDPDGGKMPKTRVILLNWCFAWFLRMKRP 349
 Qy 361 SATPPPARVPPPPDLELRSSKSLANVLID-----IDDDFRHPQAOQ 404
 Db 350 E-----DKVRPACQHKQRCCLSSMEMNTVSGQCSNGNMLYIGFRGLDGVHCTPTTDS 403
 Qy 405 PQCCRYRGG--EENGAGLAHSCFVDYELSLILKEIRVITDQMRKDEDAISRDKWF 462
 Db 404 GVIGRMTCSPTEENLLHSGHPSEG-DPDLAKLILEEVRYIANFRDQDEEAICNEKWF 462
 Qy 463 AAMVVDRLCLIIFTTIIATLAVLLSAPHIM 494
 Db 463 AASVVDRLCLMAFSVETIICITILMSAPNEV 494

RESULT 6

ABB60432
 ID ABB60432 standard; Protein; 498 AA.

AC ABB60432;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 8088.

Drosophila melanogaster polypeptide; cell signalling; insecticide;
 pharmaceutical.

Drosophila melanogaster.

WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US092931.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PN WO200053755-A2.
 XX 14-SEP-2000.
 XX 06-JAN-2000; 2000WO-US00376.
 XX 08-MAR-1999; 99WO-US05028.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.
 PR 26-JUL-1999; 99US-0145698.
 PR 30-NOV-1999; 99WO-US28313.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
 PI Watanabe CK, Wood WI;
 XX WPI; 2000-572270/53.
 DR N-PSDB; AAC58395.
 XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
 PT treatment, diagnosis and prevention of cancer -
 XX Claim 61; Fig 58; 286pp; English.
 XX The present invention describes an isolated antibody that binds to
 CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
 CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
 CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
 CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,
 CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
 CC growth. The PRO polypeptides and nucleotides are useful in the
 CC treatment, diagnosis and prevention of cancer. The antibodies and other
 CC anti-tumour compounds may be used to treat various conditions, including
 CC those characterised by overexpression and/or activation of the amplified
 CC PRO genes. Exemplary conditions or disorders to be treated with such
 CC antibodies and other compounds include benign or malignant tumours
 CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
 CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic
 CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
 CC leukemias and lymphoid malignancies, other disorders such as neuronal,
 CC glial, astrocytic, hypothalamic and other glandular, macrophagal,
 CC epithelial, stromal and blastocoeleic disorders, and inflammatory,
 CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
 CC primers and hybridisation probes used in the isolation of the human PRO
 CC PRO polynucleotide and AAC58396 and AAB24057 to AAB24089 represent human
 CC the present invention.
 XX Sequence 502 AA;
 SQ

Query Match 46.8%; Score 1246; DB 21; Length 502;
 Best Local Similarity 46.0%; Pred. No. 7.2e-116;
 Matches 240; Conservative 86; Mismatches 126; Indels 70; Gaps 6;
 12 APAGLLLLCLLPARGCYHEKRLHLLHLLHYNVLPVNVESDPLQLSGLTLMQII 71
 4 SPGVWLAALAAALLHVSLOGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQIM 63
 72 DVDEKNQLITNIWLKLENDNMLRWNTSDFGVGKDLRVPPHRLWKPVDVLMYNSADEGFD 131
 64 DVDEKNQVLTNIWLQMSWDHYLQWNVSEYFGVKTVPFDGQIWKPDILLVNSADERED 123
 132 SYTPTNVVRRNGSCLYVPPGIFKSCCKIDITWFFPDQCEMKFGSYDGYQLDLQ 191
 124 ATFTNVLVNSSGHCQYLPPIGFKSSCYIDVRWFPDQVCKLKFSGWSYGWGLDLQMQ 183
 192 DEGGDISFVINGEWELGVGPKRNEYNCPEPIDITAVVIRRTLYFFNLIYP 251
 184 E---ADISGIYPNGEWDLVGIPKRSEREFYECCKEPPDVTFTVTRRTLYGLLLIP 240

QY 252 CVLIASMAILGFTLPDPSGKLSLGVYILLSLTVFLNMVAETMPATSDAVPLGLTYFNCI 311
 DB 241 CVLISALALLVLLPADSGEKISLGITVLLSLTVFLMLVAEIMPATSDVPLIAQYFAST 300
 QY 312 MFWVASSVSTILILNHYHRHADTHMSDWIRCVFLYWLPLWILMRSPG----- 360
 DB 301 MIIIVGLSVVTVIVLQYHHHPDGGKMPKWTTRVILLNWCFAWFLMRKRPGEKVRPACQHK 360
 QY 361 -----SATTTPPPAR-----VPPPDLELRERSSKSLLANVLD 392
 DB 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVVCGRMACSPTH---- 416
 QY 393 IDDFRHPQAQPPQCCRYRGGEGAGLAHSCFGVDYELSILILKEIRVITDOMRKDDE 452
 DB 417 -DEHLLH-----GGOPPEG-----DPDLAKILEEVRIANRRFCQDE 452
 QY 453 DADISRDWKFAMVVDRLCLLIIFTTIIATLAVLLSAPHIM 494
 DB 453 SEAVCSEMKFAACVVVDRLCLMAFSVFTIITIGILMSAPNFV 494
 RESULT 10
 AAB82690
 ID AAB82690 standard; Protein; 502 AA.
 XX
 AC AAB82690;
 XX
 DT 15-OCT-2001 (first entry)
 XX Nicotinic acetylcholine receptor alpha7.
 DE
 XX Nicotinic acetylcholine receptor; nAChR; human;
 KW acetylcholine binding protein; AChBP; mollusc;
 KW ligand-binding protein; ligand-gated ion channel; crystal;
 KW drug design; protein co-ordinate data; schizophrénia;
 KW Alzheimer's disease; nicotine addiction; Tourette's syndrome;
 KW therapy; nootropic; neuroprotective.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 108..115
 FT /note= "conserved ligand-binding region, residues
 FT Tripl08 and Tyr115 are essential"
 FT Region 171..173
 FT /note= "conserved ligand-binding region, residues
 FT Tripl71 and Tyr173 are essential"
 FT Region 210..217
 FT /note= "conserved ligand-binding region, residues
 FT Tyr210, Cys212, Cys213 and Tyr217 are
 FT essential"
 XX
 PN WO200158951-A2.
 XX
 XX 16-AUG-2001.
 PD
 XX
 XX 09-FEB-2001; 2001WO-EP01457.
 PF
 XX
 PR 10-FEB-2000; 2000EP-0200443.
 PR 31-OCT-2000; 2000EP-0203810.
 XX
 XX (TEWE-) STICHTING TECH WETENSCHAPPEN.
 PA
 PI Smit AB, Sixma TK;
 XX WPI; 2001-497071/54.
 DR
 XX Water-soluble ligand-binding proteins derived from molluscs and analogues
 PT of ligand-gated ion channels, useful in drug screening assay, where the
 PT drugs identified can be used in the treatment of Alzheimer's disease or
 PT schizophrénia -
 XX

RESULT 11

— — — — —

RESULT 11

QY 361 -----SATTTPPPAR-----VPPPPDLELRSSKSLLANVLD 392
 Db 361 QRRCSLASVEMSAVAPPASGNLLYIGFRLDGVHCVPDPDSGVVCGRMACSPH---- 416
 QY 393 IDDDFRHPOAQOCCRYRGGENGAGLAHSCFGVDYELSLILKEIRVITDQMRKDE 452
 Db 417 -DEHLHL-----GGQPPEG-----DPDLAKILEEVRIANRRCODE 452
 QY 453 DADISDMKFAAMVVDRLCLIIFTLTITATLAVLSAPHIM 494
 Db 453 SEAVCSEWKAACVVDRLCLMAFSVFTICTIGILMSAPNFV 494

RESULT 12
 ID ABB82435 standard; Protein; 502 AA.
 XX ABB82435;
 AC ABB82435;
 XX 22-JAN-2003 (first entry)
 DT Human neuronal NACHr alpha7 subunit.
 DE Human; neuronal; nicotinic acetylcholine receptor; NACHr; drug screening;
 KW Immunohistochemistry; NACHr alpha7 subunit; receptor.
 XX Homo sapiens.
 OS WO200259266-A2.
 PN 01-AUG-2002.
 XX 29-OCT-2001; 2001WO-US50985.
 PR 01-NOV-2000; 2000US-0703951.
 XX (MERI) MERCK & CO INC.
 PA Gillespie A, Claeps BO, Chavez-Noriega LE, Siegel R, Elliott KJ;
 PI WPI; 2002-698532/75.
 DR N-PSDB; ABV73248.
 XX Cell comprising nucleic acids encoding human alpha and beta subunits of
 PT neuronal nicotinic acetylcholine receptors, useful for in vitro
 PT screening of a drug substance in a test system specific for humans
 XX Examples; Page 130-131; 143pp; English.

CC The invention relates to a suitable host cell transfected with an
 CC isolated nucleic acid molecule comprising a sequence of nucleotides or
 CC ribonucleotides that encodes at least one alpha or beta subunit of a
 CC human neuronal nicotinic acetylcholine receptor (NACHr). The compositions
 CC and methods of the present invention, which provide a means to prepare
 CC synthetic or recombinant receptors and receptor subunits that are
 CC substantially free of contamination from many other receptor proteins,
 CC are useful for observing the effect of a drug substance on a particular
 CC subtype to perform in vitro screening of the drug substance in a test
 CC system that is specific for humans. The antibodies can be used in
 CC immunochemistry and for diagnostic and therapeutic applications. The
 CC present sequence represents a human neuronal NACHr alpha7 subunit.
 XX Sequence 502 AA;

Query Match 46.8%; Score 1246; DB 23; Length 502;
 Best Local Similarity 46.0%; Pred. No. 7.2e-116;
 Matches 240; Conservative 86; Mismatches 126; Indels 70; Gaps 6;

QY 12 APAGLLLLCLLPRGARGCYHEKRLHLLHDHYNVLERPVVNESDPLQLSFGLTMOII 71
 Db 4 SPGGWLAALASLLHVSLOGEFQRLKYLKVNPNLERPVANDSQPLTVYFSLQLQIM 63

QY 72 DVDEKNQLITNWLKLEWMDNLRNTSDFGGVKDLRVPPHRLKPKDVLMYNSADEGFD 131
 Db 64 DVDEKNQLITNWLKLEWMDNLRNTSDFGGVKDLRVPPHRLKPKDVLMYNSADEGFD 123
 QY 132 STYPTNVVRNNGSCLYVPPGIFKSTCKIDITWFFPDODORCEMKFGSWTYDGYLDLQLO 191
 Db 124 ATFTNVLNVNNGHCOYLPPIGIFKSSCYIDVRWFDFVQHCKLKFSGWSYDGYLDLQLO 183
 QY 192 DEGGDGSFVTNGEWELIGVPGKNEIYNGCCPEYIDITFAVIRRRKTLTYFFNLIVP 251
 Db 184 E---ADISGYIPNGENDLVGIFGKSEREFYECCKEYPDVTFTVTRRTLYYGLNLLIP 240
 QY 252 CVLIASMAALLFTLPDPSGKLSLGTITLLSTVFLNMVAETMPATSDAVPLLGTYFNCI 311
 Db 241 CVLISALALLVFLPADSGEKISLGTITLLSTVFLNMVAETMPATSDAVPLIAQVFAST 300
 QY 312 MEMVASSVSTILILNYHHRHADTHEMSDWIRCVLYLWLPWLKMSRPG----- 360
 Db 301 MIIVGLSVVTVIVIOYHHDDPDGKMPKWRVILLNMCAMFLMRKRPGEKVRPACQHK 360
 QY 361 -----SATTTPPPAR-----VPPPPDLELRSSKSLLANVLD 392
 Db 361 QRRCSLASVEMSAVAPPASGNLLYIGFRLDGVHCVPDPDSGVVCGRMACSPH---- 416
 QY 393 IDDDFRHPOAQOCCRYRGGENGAGLAHSCFGVDYELSLILKEIRVITDQMRKDE 452
 Db 417 -DEHLHL-----GGQPPEG-----DPDLAKILEEVRIANRRCODE 452
 QY 453 DADISDMKFAAMVVDRLCLIIFTLTITATLAVLSAPHIM 494
 Db 453 SEAVCSEWKAACVVDRLCLMAFSVFTICTIGILMSAPNFV 494

RESULT 13
 ID ABB70492 standard; Protein; 502 AA.
 XX ABB70492;
 AC ABB70492;
 XX 06-DEC-2002 (first entry)
 DT Human neuronal nicotinic acetylcholine receptor alpha 7 subunit.
 DE Human; neuronal nicotinic acetylcholine receptor; nNACHr; receptor;
 KW ion flux; alpha 7 subunit.
 XX Homo sapiens.
 OS US6440681-B1.
 PN 27-AUG-2002.
 PD 07-JUN-1995; 95US-0487596.
 XX 03-APR-1990; 90US-0504455.
 PR 30-NOV-1992; 92US-0938154.
 PR 08-MAR-1993; 93US-0028031.
 PR 08-NOV-1993; 93US-0149503.
 XX (MERI) MERCK & CO INC.
 PA Elliott KJ, Ellis SB, Harpold MM;
 PI WPI; 2002-711528/77.
 DR N-PSDB; ABS54875.
 XX Identifying antagonists or agonists of human neuronal nicotinic
 PT acetylcholine receptors, by contacting recombinant cells with test
 PT compound, and measuring ion flux of cells or binding of compound to
 XX nNACHr
 PS Claim 101; Column 59-64; 56pp; English.
 XX

CC The invention relates to a method for identifying compounds that are
 CC antagonists or agonists of human neuronal nicotinic acetylcholine
 CC receptors (nAChRs), by contacting recombinant cells with a test
 CC compound and measuring ion flux, the electrophysiological response of the
 CC cells or binding of the test compound to the nAChR. The recombinant
 CC cells are produced by transfection with a nucleic acid encoding at least
 CC one human nAChR (alpha or beta) subunit, such that the cells express an
 CC nAChR comprising one human subunit encoded by the transfected nucleic
 CC acid. This sequence represents the alpha 7 subunit of the human nAChR
 CC polypeptide.

XX SQ Sequence 502 AA;

Query Match 46.0%; Score 1246; DB 23; Length 502;
 Best Local Similarity 46.0%; Pred. No. 7.2e-116;
 Matches 240; Conservative 86; Mismatches 126; Indels 70; Gaps 6;

Qy 12 APAGLLLLCLLWPRGARGCYHEKRLHLLHDHYNVLERPVVNESDPLQLSFGTLQII 71
 Db 4 SPGGVWLAALASLLHVSLOGEFORKLYKELVKNYPLERPVANDSQPLTVFSLSLQIM 63
 Qy 72 DVDEKNOLLITNIWKLWMDMLRWNTSDFGVKDLRVPVPHRLWKPDLVLMYNSADEGFD 131
 Db 64 DVDEKNQVLTNTIWLQSWTDHYLQWNVSEYPGVKTVPFDPGQIWKPDILLYNSADERFD 123
 Qy 132 STYPTNVVNRNNSCLVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGYLDLQIQ 191
 Db 124 ATHTNTVLNVSSGHCQYLPPIKFSKCYIDVRWPFDPVQHCCLKFGSWSGYSLDQMQ 183
 Qy 192 DEGGDLSFVTCGEWELIGVPGKRNIEIYNCCEPYDITFAVIRKTKLYFFNLIVP 251
 Db 184 E---ADISGIPNGEWDLVGIPGRSERFECCKEYPDVTFTVMRRRTLYGLNLLIP 240
 Qy 252 CVLIASALLGFTLPDPSGKLSGLVTLLSLVFLNMVAETPATSDAVPLLTGYFNCI 311
 Db 241 CVLISALLVFLPADSGEKISGITVLLSLVFLNMVAETPATSDSVPLIAQYFAS 300
 Qy 312 MFVASSVSTILINLHHRHADTHEMSDWIRCVLYLWLPVLMYNSADEGFD 360
 Db 301 MIIVGLSVVTVIVLYQHHDPDGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
 Qy 361 -----SATTPPPAR-----VPPPPDLELRSSKSLANVLD 392
 Db 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPH 416
 Qy 393 IDDFRHPQAQPOCCRYRGEENGAGLAHSCFGVDYELSLILKEIRVITDQMRKDE 452
 Db 417 -DEHLH-----GGQPEG-----DPLAKTLEEVRIANFRQDE 452
 Qy 453 DADISRDWKAAMVVDRLCLIFTLTIATLAVLLSAPHIM 494
 Db 453 SEAVCSEWKAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494

RESULT 14

AAW69216
 ID AAW69216 standard; Protein; 502 AA.

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

PD 02-JUL-1998.

XX 22-DEC-1997; 97MO-US23405.

XX 20-DEC-1996; 96US-0771737.

XX (ABBO) ABBOTT LAB.

XX Briggs CA, Gopalakrishnan M, McKenna DG, Monteggia LM;

XX PI Roch J, Sullivan JP, Touma E;

XX WPI; 1998-377593/32.

XX N-PSDB; AAV44687.

XX Nucleic acid encoding variant of human alpha7 nicotinic

XX acetylcholine receptor sub-unit - used to identify modulators of

XX the receptor, potentially useful for treating neuro-degeneration,

XX cancer, affective disorders etc.

XX Claim 15; Fig 2; 44pp; English.

XX This sequence is the V247T variant of human alpha7 nicotinic

XX acetylcholine receptor (nAChR) subunit of the invention. Cells containing

XX the DNA are used to express the protein and to identify modulators of

XX alpha7 nAChR activity or cytoprotective agents, e.g. antisense

XX compounds or antagonists that are potentially useful for treating

XX neurodegeneration, enzyme dysfunction, affective disorders and immune

XX dysfunction, such as cancer, post-herpetic neuralgia, diabetic

XX neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,

XX psychosis and schizophrenia. Probes based on the DNA are used to detect

XX the DNA in usual hybridization or amplification tests, while monoclonal

XX antibodies are used to detect the protein for diagnosis (in vitro or by

XX in situ immuno-fluorescent assay). Compared with wild-type alpha7 nAChR,

XX the protein has about 100-fold greater sensitivity to cholinergic

XX receptor agonists (nicotine or acetylcholine) and response to these

XX agonists decays more slowly, but the wild-type inward rectification is

XX retained.

XX SQ Sequence 502 AA;

Query Match 46.6%; Score 1242; DB 19; Length 502;

Best Local Similarity 45.8%; Pred. No. 1.8e-115;

Matches 239; Conservative 86; Mismatches 127; Indels 70; Gaps 6;

Qy 12 APAGLLLLCLLWPRGARGCYHEKRLHLLHDHYNVLERPVVNESDPLQLSFGTLQII 71

Db 4 SPGGVWLAALASLLHVSLOGEFORKLYKELVKNYPLERPVANDSQPLTVFSLSLQIM 63

Qy 72 DVDEKNOLLITNIWKLWMDMLRWNTSDFGVKDLRVPVPHRLWKPDLVLMYNSADEGFD 131

Db 64 DVDEKNQVLTNTIWLQSWTDHYLQWNVSEYPGVKTVPFDPGQIWKPDILLYNSADERFD 123

Qy 132 STYPTNVVNRNNSCLVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGYLDLQIQ 191

Db 124 ATHTNTVLNVSSGHCQYLPPIKFSKCYIDVRWPFDPVQHCCLKFGSWSGYSLDQMQ 183

Qy 192 DEGGDLSFVTCGEWELIGVPGKRNIEIYNCCEPYDITFAVIRKTKLYFFNLIVP 251

Db 184 E---ADISGIPNGEWDLVGIPGRSERFECCKEYPDVTFTVMRRRTLYGLNLLIP 240

Qy 252 CVLIASALLGFTLPDPSGKLSGLVTLLSLVFLNMVAETPATSDAVPLLTGYFNCI 311

Db 241 CVLISALLVFLPADSGEKISGITVLLSLVFLNMVAETPATSDSVPLIAQYFAS 300

Qy 312 MFVASSVSTILINLHHRHADTHEMSDWIRCVLYLWLPVLMYNSADEGFD 360

Db 301 MIIVGLSVVTVIVLYQHHDPDGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360

Qy 361 -----SATTPPPAR-----VPPPPDLELRSSKSLANVLD 392

Db 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPH 416

Qy 393 IDDFRHPQAQPOCCRYRGEENGAGLAHSCFGVDYELSLILKEIRVITDQMRKDE 452

Db 417 -DEHLLH-----GGOPPEG-----DPLAKILEEVRYIANRFRQDE 452

QY 453 DADISRDWKFAAMVVDRLCLIIIFTLFTIATLAVLSAPHIM 494

Db 453 SEAVCSEWKFAACVVDRLCLMAFSVFTICTIGILMSAPNFV 494

RESULT 15

AAB50015

ID AAB50015 standard; Protein; 502 AA.

XX

AC AAB50015;

XX

DT 14-MAR-2001 (first entry)

XX

DE Mutant human alpha7 ligand gated ion channel #1.

XX

KW Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;

XX 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein.

OS Homo sapiens.

OS Synthetic.

XX

Key Location/Qualifiers

FT Misc-difference 230

FT /note= "Wild-type Thr substituted by Pro"

XX

PN W0200073431-A2.

XX

PD 07-DEC-2000.

XX

XX 25-MAY-2000; 2000WO-US11862.

XX

XX 27-MAY-1999; 99US-0136174.

XX

XX (PHAA) PHARMACIA & UPJOHN CO.

XX

XX Groppi VE, Wolfe ML, Berkenpas MB;

XX

XX WPI; 2001-061524/07.

XX

XX N-PSDB; AAC90385.

XX

XX Special cell culture medium for treating cells and for inducing

XX mammalian cell lines to conduct calcium ions, comprising specified

XX concentrations of ions of sodium, calcium and potassium at specified pH

XX

PS Claim 100; Pages 70-72; 77pp; English.

XX

CC The present sequence is a mutant human alpha7 nicotinic acetylcholine

CC gated ion channel. The human alpha7 ion channel was used in the

CC construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand

CC gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric

CC ion channel can be expressed by recombinant cells in the present

CC invention, resulting in preferential calcium ion conductance by the

XX cells.

XX

XX Sequence 502 AA;

Query Match 46.5%; Score 1240; DB 22; Length 502;

Best Local Similarity 45.8%; Pred. No. 2.9e-115;

Matches 239; Conservative 86; Mismatches 127; Indels 70; Gaps 6;

QY 12 APAGLLLLLCLLPARGCYHEKRLHLHLDHYNLRLPVVNVESDPLQLSFGLTLMQII 71

Db 4 SPCGVWLAAASLLHVSLOGEFQKLYKELVKNYNPLRPVANDSQPLTVFSLSLQIM 63

QY 72 DVDEKNQLITLNLWLNMDNLRWNTSDFGVKDLRVPPHRLKWKPDVLMYNASDEGFD 131

Db 64 DVDEKNQVLTNLWLQMSWDHVLQWNSEYPCVKTVPFDGQIWKPDILLNYSADERFD 123

QY 132 STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPDQRCENKMGSGWTYDGYQLDLQLO 191

Db 124 ATFTNTVLNSSGHCQYLPPIGFKSCYIDVRNPFDFVQHCKLFGWSYSGWSLQMQ 183

QY 192 DEGGGDISSFTVNGEWELIGVPGKRNFIYNNCCPEPYIDITFAVWLRRTKLYFFENLIVP 251

Db 184 E---ADISGYIPNGEWDLVGIPGKRSERFYECCKEPIPDVFTVTWRRRLYIYGLNLLIP 240

QY 252 CVLIASMAILGFTLPDPSGEKLSLGVITILSLTVFLNMVAETMPATSDAVPLLGTGFNCI 311

Db 241 CVLISALALLVFLLPADSGEKISLGITVLLSLTVFVLLVAEIMPATSDSVPLIAQYFAST 300

QY 312 MFVASSVSTILILNYHRRHDTHEMSDWIRVCVFLYWLPLWLRMRPG----- 360

Db 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKWTIRVILLNWCWAFLRMKRPGEDKYRPACQHK 360

QY 361 -----SATTTPPAR-----VPPPDLELRERSKSLANVLD 392

Db 361 QRCRSIASVEMSAVAPPASNGNLLYIGFGLDGVHCVPPTPDGCVVCGRMACSPTH---- 416

QY 393 IDDFRHPQAQQPCCCRYRGGEENGAGLAHSCFGVDYELSLILKEIRVITDQMRKDD 452

Db 417 -DEHLLH-----GGOPPEG-----DPLAKILEEVRYIANRFRQDE 452

QY 453 DADISRDWKFAAMVVDRLCLIIIFTLFTIATLAVLSAPHIM 494

Db 453 SEAVCSEWKFAACVVDRLCLMAFSVFTICTIGILMSAPNFV 494

Search completed: August 13, 2003, 15:25:26

Job time : 44.5088 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2003, 03:48:31 ; Search time 3249.96 Seconds
(without alignments)
11127.831 Million cell updates/sec

Title: US-09-303-232-3_COPY_335_1822

Perfect score: 1488

Sequence: 1 atggcgggcgggcgccg.....cgccacacatcatgtgtcg 1488

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	476.2	32.0	885	10	BG632919
2	320.6	21.5	1201	9	AL530299
3	281.6	18.9	1864	11	AK053497
4	281.6	18.9	2916	11	AK051730

5	281.6	18.9	3126	11	AK080415	Mus muscu
6	280.4	18.8	4290	11	AK029177	Mus muscu
7	269.4	18.1	607	9	AI292581	GH15518.5
8	263.4	17.7	2010	11	AK080475	Mus muscu
9	258	17.3	4037	11	AK049722	Mus muscu
10	258	17.3	4046	11	AK051742	Mus muscu
11	253.8	17.1	2940	11	AK034228	Mus muscu
12	253.8	17.1	3230	11	AK083157	Mus muscu
13	245.2	16.5	908	13	BUI149265	AGENCOURT
14	244.4	16.4	3483	11	AK081254	Mus muscu
15	241.4	16.2	615	14	CB149460	K-EST0205
16	236.8	15.9	1034	13	EX403124	EX403124
17	232.8	15.6	922	13	BU915857	AGENCOURT
18	226.2	15.2	411	12	BI516733	BI516733
19	226.2	15.1	410	12	BI516843	BB160023A
20	214.6	14.4	833	14	CB245337	UT-M-FY0-
21	213.8	14.4	640	14	CB244439	UT-M-FY0-
22	213.8	14.4	1101	29	CNS0001F	AL038211
23	212.8	14.3	1007	29	CNS000HJU	Drosophila
24	208	14.0	1036	13	EX437801	EX437801
25	203.8	13.7	978	29	CNS006F9	AL064281
26	202	13.6	720	14	CA373069	Drosophila
27	199.6	13.4	2513	11	AK033068	647093 NC
28	198	13.3	755	10	AW914206	Mus muscu
29	191.6	12.9	864	9	AUI20692	AW914206
30	189.6	12.7	658	12	BM711715	EST345510
31	187.4	12.6	755	13	BU702422	UT-E-CL1-
32	187.2	12.6	818	13	BU161024	UT-M-FIO-
33	184.4	12.4	1201	13	EX421718	AGENCOURT
34	183.4	12.3	2074	11	AK087554	EX421718
35	182.2	12.2	939	13	BO720344	Mus muscu
36	181.8	12.2	763	14	CA374163	AGENCOURT
37	178.2	12.0	586	13	EX299163	CA374163
38	177.8	11.9	3827	11	AK041217	EX299163
39	175.8	11.8	797	14	CA326954	Mus muscu
40	172.6	11.6	882	12	BUI195149	CA326954
41	172	11.6	754	29	CNS02R2B	UT-M-FIO-
42	168.8	11.3	4589	11	AK030464	BUI195149
43	168	11.3	1835	11	AK010496	AL210044
44	167.2	11.2	554	10	BE664308	Tetraodon
45	166	11.2	932	29	CNS02DCP	BE664308

ALIGNMENTS

RESULT 1
BG632919/c
LOCUS
DEFINITION
BG632919 885 bp mRNA linear EST 23-APR-2001
GH16126.3prime GH Drosophila melanogaster head pOT2 Drosophila
melanogaster cDNA clone GH16126 3 similar to CG4128; FBan0004128
'ion channel' located on: 2L 30D1-30E1;: 04/10/2001, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BG632919 GI:13758409
Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 885)

Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,

Lewis, S., and Rubin, G.M.

BDGP/HMMI Drosophila EST Project

Unpublished

Other_ESTs: GH16126.Sprime

Contact: Stapleton, M.

BDGP

Lawrence Berkeley National Lab

One Cyclotron Rd, Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu

Based upon the presence of a XhoI site followed by a run of 14 or

FEATURES	Location/
source	1. .885

Qy	193	CTCAGCTCATG	CAGATCATCG	AGTGGACG	AGAGAAC	CAGCTTTAA	TAAACAAC	AATC	252	
Db	885	CTAACCTCAT	GCGAGATTAT	CGATGTCG	CAAGAGAA	TCAACTGCT	TATAAACGA	AATATT	826	
Qy	253	TGGCTAAAC	CTAGAGTGG	AACTGATAT	GAACCTTG	AGGTGGA	CACTTCAG	ATTTCCGCGGG	312	
Db	825	TGGCTCAAT	TTGGAATG	GAACGATAT	GAATCTTC	GATGGAAT	TCGAGTG	AGTTCGGTGGT	766	
Qy	313	GTCAAGACT	TTAAGAGTG	CCACCAG	ACTATG	GAAACAG	ACGTCCCTT	TATGTACAAC	372	
Db	765	GTGCGGAT	CTCGCAAT	TCGCCAC	ATCGCCTAT	TGAAACCG	GATGACT	GATGTACAAC	706	
Qy	373	AGCCGAC	GAAGGTTT	CCGACAG	CACCTAT	TCCAACG	ACGTGGT	TCGGGAACAACGGC	432	
Db	705	AGTCCG	ACGAGGCT	TCGATG	GAACGTAC	CCCAACA	ATGTGTG	TGGTTCGCNATANTGGG	646	
Qy	433	TCGTGCT	GTA	CTGCGCC	CGCGCAT	CTTCAAG	AGCACCTG	CAAGATCGACATCACCTGG	492	
Db	645	AGCTGTCT	GTA	CTGACGT	ACCGCAGG	TATATTT	AAGTCA	ACGTGTAAGATCGACATTAACGTGG	586	
Qy	493	TTCCCC	TTGCAG	CACCAAG	ATCGG	AGATGA	AGTTTGC	AGCTTGACCTATGATGGTTAT	552	
Db	585	TTTCCAT	TCGACG	ATCAG	AGATG	GAATGA	ATTTG	TCGTGGACCTACGATGGGTTT	526	
Qy	553	CAGTTGG	ATCTACA	CAACTAC	AGGATGA	AGGGCGG	AGATATA	TAAGCAGTTTGTACCAAT	612	
Db	525	CAGTTGG	ACCTTGC	AGTTGC	AGGACGA	AGCTG	GTGGCACA	TTTCTAGCTTTTATAACCAAT	466	
Qy	613	GCCAA	TTGGGATTA	ATAGG	AGTCCC	CGGCAAG	CGCAAGAGAT	CTACTACAAC	672	
Db	465	GGCAAT	TTGGGACT	TTGTAG	GTGTCC	CGGTAA	ACGAAATCT	ACTATAATTTGTGTC	406	
Qy	673	CCGGAG	GCATAC	ATCGAC	TCACTT	TCGGTGTG	ATCCGG	AGGAAAACGCTCTACTAC	732	
Db	405	CCAGAC	CTTATTTG	ACATTA	CAATTC	GCCATTTT	GATAAG	CGCAAAACGTTGACTAT	346	
Qy	733	TTCTTCA	ATCTGAT	CTGGCC	CTCGTCT	CAATCG	CTCCAT	TGGCTCTATTTGGGGTTCAAC	792	
Db	345	TTTTTCA	ATCTGAT	TGTG	CCGTGCT	ACTGAT	TCGCTCC	ATCGGCACTGCTAGGGTTTACA	286	
Qy	793	TTGGCT	CTCAG	ACTCCG	GAGAAA	AGTTGTCT	TTAGTGTG	ACGATTA	CTCTCGTTGACG	852
Db	285	CTGCC	ACGAGAT	CTCGTGA	AAAACG	TTTCGCT	TTGGAG	TTACAAATCTATTA	CTCGTTACA	226
Qy	853	GTGTTCT	CAACAT	TTGGTGG	CGGACG	ATGCC	AGCGAG	CTCGGACG	CGCGTGCCTTGCTC	912
Db	225	GTCTTCT	CTCAAT	TTGGTGG	CGAACA	ATCGCG	CGACCTCC	GATGGG	ATACCGCTGCTC	166

[illegible]

QY	249	CATCTGGCTAAACATAGAGTGGAAATGATATGAATCTGAGGTGGAAACACTTTCAGATTTCGG	308
Db	348	CATTGTGCTCAAAATGCTTTGGAGAGATCATCTATTACAGTGGAGTGTGTCAGAAATATCC	407
QY	309	CGGGTCAAGAGATTAAAGATGTCGCCACCCACACAGTATGGAACACAGACGCTCTTATGTA	368
Db	408	AGGGGTGAAGACACTGTTGGTTTCCAGATGTCGCCAGATTGGAACACACAGACTTCTCTCTA	467
QY	369	CAACAGCGCGGACGAAGGGTTGCACAGCAGTATCCAAACCAACGTTGGTGGCGGAACAA	428
Db	468	TACAGTGCATGATGAGCGCTTTGACGCCACATCCACACATGATGTTGGTGAATCTTTC	527
QY	429	CGGTCGTGCTGTACGTGCGCCCGGCGCATCTTCAAGAGCACCTGCAAGATGACATCAC	488
Db	528	TGGSCATTGCGCAGTWCCTGCTCCAGGCATATTCAAGAGTTCCTGCTACATCATGATGACG	587
QY	489	CTGGTTCCTCTTGCAGCCAAACGATGCGAGATGAAGTTTGGCAGCTGGACTTATGATGG	548
Db	588	CTGGTTCCTCTTGCAGCTGCGAGCATGCAAACTGAAGTTTGGTCTGCTTACCGGAGG	647
QY	549	TTATCAGTTGGATCTCAACATACAGGATGAAGGGCGGAGATATAAGCAGTCTTGTGTCAC	608
Db	648	CTGGTCTCTGATCTGAGATGTCAGATGACGAGGC-----AGATATCATGTCGCTATATCCC	698
QY	609	GAATGGCGAATGGAGTTAATAGAGTCCCGGCAAGCGCAACGAGATCTTACTACAAGT	668
Db	699	CAATGGAGATGGACCTAGTGGATCCCGGCAAGAGAGTGAAGGTTCTATGATGATK	758
QY	669	TTGTCGGGAGCCATACATCATCAGTTCAGTTTGGGTTGGTATCGGAGGAAACGCTCTA	728
Db	759	CTGCAAGAGCCCTACCCCGATGTCACCTTACAGTGCACATGCGCGCGAGGAGCTCTA	818
QY	729	CTACTTCTCAATCTGATCGTCCCTGCTGCTCATCGCTCATGCTCTATTGGGGTT	788
Db	819	CTATGGCTCAACCTGCTGATCCCTGTGTGCTCATCTCCGCTCGCCCTGCTGCTGTT	878
QY	789	CACCTTCCCTCGAGCTCGGAG--AAAGTTGCTTTAGTGTGAGCATATTACTGTGCG	846
Db	879	CCTGCTTCTCGCATCTCCGGGGGAGAGATTTCCCTKGGGATACAGTGTACTCTCT	938
QY	847	TTGACGGTGTCTCAACATGTTGGCGGAGACCATGCCAGCGTGGCGGCGCGTCC	906
Db	939	CTTACCGCTCTTCATGCTGCTGCTGCTGAGATGCCCGCAACATCCGATTCGGTACCA	998
QY	907	TTGCTCGGACCTACTTCAACTGCATCATCTTCTATGTTGG	946
Db	999	TTGAWGCCAGTCTTCGCCAGCACCATCATCATCTGCG	1038
RESULT 3			
AK053497			
LOCUS			
DEFINITION	1864 bp mRNA linear HTC 05-DEC-2002		
	Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched		
	library, clone:E130103E14 product:NEURONAL NICOTINIC ACETYLCHOLINE		
	RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.		
ACCESSION	AK053497		
VERSION	AK053497.1 GI:26343494		
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	95279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to		

JOURNAL	prepare full-length cDNA libraries for rapid discovery of new genes		
MEDLINE	Genome Res. 10 (10), 1617-1630 (2000)		
PUBMED	20499374		
REFERENCE	11042159		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		
AUTHORS	Arakawa, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Kawai, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kotsuki, S. and Hayashizaki, Y.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409 (6821), 685-690 (2001)		
MEDLINE	21085660		
PUBMED	11217851		
REFERENCE	5		
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
JOURNAL	Nature 420, 563-573 (2002)		
REFERENCE	6 (bases 1 to 1864)		
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)		
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.		

URL: <http://genome.gsc.riken.go.jp/>
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Location/Qualifiers
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polyA site

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DEFINITION	Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:DI30069A06 product:NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.	mrna	
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VERSION	GI:26342155		
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ORGANISM	Mus musculus		
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REFERENCE	1		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20493374		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,		

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nicotinic, beta polypeptide 2 (neuronal), full insert sequence.
AK049722
VERSION
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SOURCE
Mus musculus (house mouse)
ORGANISM

REFERENCE
1 Carninci, P., and Hayashizaki, Y.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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TITLE
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED
10349636
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
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11042159
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
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Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
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Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
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Genome Res. 10 (11), 1757-1771 (2000)
20530913
PUBMED
11076861
AUTHORS
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
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Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
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Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
and Hayashizaki, Y.

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TITLE
JOURNAL
MEDLINE
PUBMED
11217851
AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4037)
JOURNAL
REFERENCE
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, tel:81-45-503-9222,
Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
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RESULT 12

AK083157

LOCUS

DEFINITION Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:C630019M18 product:cholinergic receptor, nicotinic, alpha polypeptide 4, full insert sequence.

ACCESSION

AK083157

VERSION

AK083157.1

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE

1

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

JOURNAL

92729253

MEDLINE

10349636

PUBMED

REFERENCE

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, H., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL

20499374

MEDLINE

11042159

PUBMED

REFERENCE

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL

20530913

MEDLINE

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PUBMED

REFERENCE

4

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,

Sato, K., Schonbach, C., Seva, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka-K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 585-590 (2001)

21085660

11217851

REFERENCE

AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 3230)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, I., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.go.jp/>

URL: <http://fantom.gsc.riken.go.jp/>

FEATURES

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ORIGIN

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AUTHORS			


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LOCUS

DEFINITION K-EST0205995 L15CKK1 Homo sapiens cDNA clone L15CKK1-50-D08 5', linear EST 29-JAN-2003

CB149460

CB149460.1

GI:28132277

EST.

Homo sapiens

Homo sapiens (human)

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and

Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished

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Email: yongsung@mail.kribb.re.kr

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Location/Qualifiers

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intact mRNA was ligated with DNA-RNA linker including

EcoRI site by treatment of T4 RNA ligase and the first

strand cDNA was synthesized from oligo dt-selected mRNA by

priming with dt-tailed vector. The dt-tailed vector was

adjusted to have about 60nt. The cDNA vector was

circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transformation of

competent cells E. coli Top10F' by electroporation method.

The cDNA libraries constructed by this method are

full-length enriched cDNA library."

BASE COUNT 125 a 176 c 155 g 159 t

ORIGIN

Query Match

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Matches 393; Conservative 0; Mismatches 221; Indels 9; Gaps 1;

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

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SUMMARIES

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2	575	38.6	3109	21	AAZ24477
3	512.8	34.5	2886	21	AAZ24475
4	470	31.6	936	23	ABL13733
5	458.2	30.8	1540	23	ABL07231
6	405.6	27.3	1509	22	AAZ90380
7	405.6	27.3	1876	18	AAZ48239
8	405.2	27.2	1876	15	AAV12197

9	405.2	27.2	1876	24	ABV73248	Human neuronal NAC
10	405.2	27.2	1876	24	ABS54875	Human neuronal nic
11	404	27.2	1509	21	AAZ58395	Human PRO2145 nucl
12	404	27.2	1509	22	AAZ90385	Mutant human alpha
13	404	27.2	1509	22	AAZ90386	Mutant human alpha
14	402.4	27.0	1509	22	AAZ90387	Mutant human alpha
15	394	26.5	1590	19	AAV44687	V274T variant huma
16	386.8	26.0	1964	24	ABZ11298	Human polynucleoti
17	327.4	22.0	2769	18	AAZ59196	Neuronal alpha-bun
18	312.2	21.0	2101	18	AAZ59197	Neuronal alpha-bun
19	309.2	20.8	2277	15	AAV12199	Human neuronal nic
20	309.2	20.8	2277	16	AAZ90387	Alpha 2 subunit of
21	309.2	20.8	2277	24	ABV73243	Human neuronal NAC
22	309.2	20.8	2277	24	ABS54870	Human neuronal nic
23	309.2	20.8	2664	18	AAZ48235	Neuronal nicotinic
24	309.2	20.8	2664	24	ABK92165	Prostate cancer-as
25	302.4	20.3	803	23	ABL07799	Drosophila melanog
26	292	19.6	1908	18	AAZ48236	Neuronal nicotinic
27	290	19.5	1416	22	AAZ90382	Chimeric alpha7/5-
28	286.6	19.3	1771	24	AAZ26345	Human mutant neuro
29	286.2	19.2	1809	23	AAZ591552	DNA encoding novel
30	286.2	19.2	2082	18	AAZ59527	Alpha4 subunit of
31	285.2	19.2	1654	24	ABV73244	Human neuronal NAC
32	285.2	19.2	1654	24	ABS54871	Human neuronal nic
33	285.2	19.2	1757	15	AAV12200	Human neuronal nic
34	285	19.2	2448	15	AAZ15343	Human CHRN2 codin
35	285	19.2	2448	15	AAV12201	Human neuronal nic
36	285	19.2	2448	18	AAZ48240	Neuronal nicotinic
37	285	19.2	2448	24	ABV73249	Human neuronal NAC
38	285	19.2	2448	24	ABS54876	Human neuronal nic
39	284.6	19.1	2082	18	AAZ59528	Alpha4 subunit of
40	284.6	19.1	3496	18	AAZ48237	Neuronal nicotinic
41	281.8	18.9	1521	12	AAZ14288	Human neuronal nic
42	280	18.8	3649	6	AAZ50416	Calf acetyl cholin
43	275.2	18.5	1667	21	AAZ38821	Human acetylcholin
44	272.8	18.3	1869	24	AAZ45873	Modified acetylcho
45	272.8	18.3	1869	24	ABL54794	Modified hen ACR s

ALIGNMENTS

RESULT 1

AAZ24476

ID AAZ24476 standard; cDNA to mRNA; 3700 BP.

XX AC AAZ24476;

XX DT 17-FEB-2000 (first entry)

XX DE H. virescens acetyl-choline receptor DNA from clone Hva7-1.

XX DE Acetyl-choline receptor; nicotinic; insect; insecticide; screening;

XX KW neurotransmission; plant protection agent; conductance; ACHR; ds.

XX OS Heliothis virescens.

XX FH Key Location/Qualifiers

XX FT CDS 335..1825

XX FT /*tag= a

XX FT /product= "acetyl-choline receptor"

XX PN DE19819829-A1.

XX PD 11-NOV-1999.

XX PF 04-MAY-1998; 98DE-1019829.

XX PR 04-MAY-1998; 98DE-1019829.

XX XX (FARB) BAYER AG.

XX PA Adamczewski M, Oellers N, Schulte T;

XX PI

XX WPI: 2000-014207/02.
 DR P-PSDB; AAY50815.
 XX
 PT New nucleic acid encoding a nicotinic acetylcholine receptor from
 insects, used to identify potential insecticides
 XX
 PS Claim 1a; Page 14-17; 26pp; German.
 XX
 CC This invention describes a novel nucleic acid (NA) encoding a nicotinic
 CC acetyl-choline receptor (I) from insects which can be used as an
 CC insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
 CC (also vectors containing it, its regulatory regions, and antibodies
 CC directed against (I)-encoded proteins) are used to screen for: (a) plant
 CC protection agents that alter conductance of AChR, potentially useful as
 CC insecticides, or (b) genes which encode polypeptides that are involved in
 CC formation of functionally related AChR in insects. (I) are also used to
 CC isolate and characterize the specified regulatory regions and for
 CC recombinant production of (II). This sequence encodes an acetyl-choline
 CC receptor isolated from *Heliothis virescens*.
 XX
 XX Sequence 3700 BP; 893 A; 953 C; 944 G; 910 T; 0 other;
 Query Match 100.08; Score 1488; DB 21; Length 3700;
 Best Local Similarity 100.08; Pred. No. 0;
 Matches 1488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGCGGGCGGGCGCGCTCGACATTGGCGGCGCGCGGCGCTGCTGCTGCTG 60
 DB 335 ATGGCGGGCGGGCGCGCTCGACATTGGCGGCGCGCGGCGCTGCTGCTGCTG 394
 QY 61 TGCTGCTGCTGCGGAGGGGGCGAGCTGCGGCTACACGAGAGCGGCTACTGACAC 120
 DB 395 TGCTGCTGCTGCGGAGGGGGCGAGCTGCGGCTACACGAGAGCGGCTACTGACAC 454
 QY 121 CTATTGGACCTACACGCTACTGGAGAGCGGCTGCTGACGAGAGCGGCGCTGCGAG 180
 DB 455 CTATTGGACCTACACGCTACTGGAGAGCGGCTGCTGCTGACGAGAGCGGCGCTGCGAG 514
 QY 181 CTCTCTTGGCGCTCACGCTCATGCGATCATGCGAGTGGGAGAGCAAGCAAGCTTTTA 240
 DB 515 CTCCTCTTGGCGCTCACGCTCATGCGATCATGCGAGTGGGAGAGCAAGCAAGCTTTTA 574
 QY 241 ATACAAACATCTGGCTAAACTAGAGTGAATGATATGAACTTGAAGTGAACACTTCA 300
 DB 575 ATACAAACATCTGGCTAAACTAGAGTGAATGATATGAACTTGAAGTGAACACTTCA 634
 QY 301 GATTTGCGGGGTCAAAGATTTAAGAGTGCACCCACAGACTATGGAACACGACGTC 360
 DB 635 GATTTGCGGGGTCAAAGATTTAAGAGTGCACCCACAGACTATGGAACACGACGTC 694
 QY 361 CTTATGTACAAACAGCGGAGGAGGTTTCAGACAGCAGTATCCAAAGCAAGCTGGTG 420
 DB 695 CTTATGTACAAACAGCGGAGGAGGTTTCAGACAGCAGTATCCAAAGCAAGCTGGTG 754
 QY 421 CGAACAACAGGCTGCTGTGCTAGCTGCGCGCGCGCATCTTCAAGAGCACTGCAAGATC 480
 DB 755 CGAACAACAGGCTGCTGTGCTAGCTGCGCGCGCGCATCTTCAAGAGCACTGCAAGATC 814
 QY 481 GACATCACCTGTTCCCTCTCGACCAACAGATGCGAGATGAAGTTTGGCAGCTGGACT 540
 DB 815 GACATCACCTGTTCCCTCTCGACCAACAGATGCGAGATGAAGTTTGGCAGCTGGACT 874
 QY 541 TATGATGTTATCAGTTGGATCTACAACTACAGGATGAAGGGCGGAGATATAGCAGT 600
 DB 875 TATGATGTTATCAGTTGGATCTACAACTACAGGATGAAGGGCGGAGATATAGCAGT 934
 QY 601 TTTGTCAGAAATGGGAATGGAGTTAATAGAGTCCCGGCAAGCGCAAGCATCTAC 660
 DB 935 TTTGTCAGAAATGGGAATGGAGTTAATAGAGTCCCGGCAAGCGCAAGCATCTAC 994
 QY 661 TACAACCTGTGTCGGAGCCATACATCGACATCAGCTTTGCGGTGCTATCCGGAGAAA 720

DB 995 TACAACCTGTGTCGGAGCCATACATCGACATCAGCTTTGCGGTGATCCGGAGAAA 1054
 QY 721 ACGCTACTACTACTTCTTCAATCTGATCGTGCCTCGCTGCTCATCGCTCCATGCTCTA 780
 DB 1055 ACGCTACTACTACTTCTTCAATCTGATCGTGCCTCGCTGCTCATCGCTCCATGCTCTA 1114
 QY 781 TTGGGGTTCACCTTTCCTCCAGACTCCGGAGAAAAGTTGCTTTAGGTGTGACGATATA 840
 DB 1115 TTGGGGTTCACCTTTCCTCCAGACTCCGGAGAAAAGTTGCTTTAGGTGTGACGATATA 1174
 QY 841 CTGTCGTGAGGGTTCCTCAACATGTTGGCGGAGAGATGCCAGCAGCTCCGACGCC 900
 DB 1175 CTGTCGTGAGGGTTCCTCAACATGTTGGCGGAGAGATGCCAGCAGCTCCGACGCC 1234
 QY 901 GTGCCCTTGTCTGCGCACCTACTTCAACTGCAATGTTCACTGTGGTGTCTCTCGTCTGC 960
 DB 1235 GTGCCCTTGTCTGCGCACCTACTTCAACTGCAATGTTCACTGTGGTGTCTCTCGTCTGC 1294
 QY 961 TCCACCATAGTATCTCAACTACACACCGGAGCAGACACTCAGCAATAGTAT 1020
 DB 1295 TCCACCATAGTATCTCAACTACACACCGGAGCAGACACTCAGCAATAGTAT 1354
 QY 1021 TGGATTGCTGCTGCTTCTTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 DB 1355 TGGATTGCTGCTGCTTCTTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1414
 QY 1081 TCGGCGAGCAGCGCGCGCGCGCTACTCTCCGCGCGGAGCTGGAGCTGCGCGAG 1140
 DB 1415 TCGGCGAGCAGCGCGCGCGCGCTACTCTCCGCGCGGAGCTGGAGCTGCGCGAG 1474
 QY 1141 CGCTCTCAAGTCTGCTTCTAGCGAACTGCTCGACATCGATGAGGACTTCCGCGACCGG 1200
 DB 1475 CGCTCTCAAGTCTGCTTCTAGCGAACTGCTCGACATCGATGAGGACTTCCGCGACCGG 1534
 QY 1201 CAAGCGAGCAGCGCGCGCGCGCTACTCTACAGGGGGGTGAGGAGAAATGGCGCGGG 1260
 DB 1535 CAAGCGAGCAGCGCGCGCGCGCTACTCTACAGGGGGGTGAGGAGAAATGGCGCGGG 1594
 QY 1261 TTGGCGGCGCAGTTGCTTCCGTTGCTGACTACGAGCTCTCCCTCATTTCTGAAGGAGAT 1320
 DB 1595 TTGGCGGCGCAGTTGCTTCCGTTGCTGACTACGAGCTCTCCCTCATTTCTGAAGGAGAT 1654
 QY 1321 AGAGTCATCAGATCAGATCGGCAAGGACGACGAGATCGGACATTTCCGCGGACTGG 1380
 DB 1655 AGAGTCATCAGATCAGATCGGCAAGGACGACGAGATCGGACATTTCCGCGGACTGG 1714
 QY 1381 AAGTTCCGCGCCATGGTCTGCGAGAGCTGTGCTTATTTATCTTTACCTGTTCACAATC 1440
 DB 1715 AAGTTCCGCGCCATGGTCTGCGAGAGCTGTGCTTATTTATCTTTACCTGTTCACAATC 1774
 QY 1441 ATCGCCAGCTAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1488
 DB 1775 ATCGCCAGCTAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1822

RESULT 2
 AAZ24477
 ID AAZ24477 standard; cDNA to mRNA; 3109 BP.
 XX
 AC AAZ24477;
 XX
 DT 17-FEB-2000 (first entry)
 XX
 DE H. virescens acetyl-choline receptor DNA from clone hva7-2.
 XX
 KW Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
 XX neurotransmission; plant protection agent; conductance; AChR; ds.
 OS *Heliothis virescens*.
 XX
 PN DE19819829-A1.
 XX
 PD 11-NOV-1999.

XX 04-MAY-1998; 98DE-1019829.
 XX 04-MAY-1998; 98DE-1019829.
 XX (FARB) BAYER AG.
 XX Adamczewski M, Oellers N, Schulte T;
 PI WPI; 2000-014207/02.
 DR P-PSDB; AAY50816.
 XX
 PT New nucleic acid encoding a nicotinic acetylcholine receptor from
 PT insects, used to identify potential insecticides -
 XX Claim 1a; Page 19-22; 26pp; German.
 XX This invention describes a novel nucleic acid (NA) encoding a nicotinic
 CC acetyl-choline receptor (I) from insects which can be used as an
 CC insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
 CC (also vectors containing it, its regulatory regions, and antibodies
 CC directed against (I)-encoded proteins) are used to screen for: (a) plant
 CC protection agents that alter conductance of AChR, potentially useful as
 CC insecticides, or (b) genes which encode polypeptides that are involved in
 CC formation of functionally related AChR in insects. (I) are also used to
 CC isolate and characterize the specified regulatory regions and for
 CC recombinant production of (II). This sequence encodes an acetyl-choline
 CC receptor isolated from *Heliothus virescens*.
 XX
 SQ Sequence 3109 BP; 923 A; 610 C; 742 G; 834 T; 0 other;
 Query Match 38.6%; Score 575; DB 21; Length 3109;
 Best Local Similarity 54.6%; Pred. No. 3.7e-130;
 Matches 929; Conservative 0; Mismatches 460; Indels 48; Gaps 3;
 97 CACGAGAGCGCTACTGCACCACTATTTGGACCCTACAGCTACTGAGAGGCGCGTC 156
 158 CACGAGAGAGACTCTGAACCGTGTGGCGGAACATACACACCCTGGAGCGCGGTG 217
 157 GTCACAGAGAGCGCGCTGCGCTCTCTTGGCGCTCACGCTCATGCGATCATCGAC 216
 218 GCCAAGAGAGCGACCGCTAGAGTCAAGTTCGGCTTGACCTTGACGCAATCATGAC 277
 217 GTGGAGAGAGAACCGAGCTTTTAAACAACATCTGGCTAAAAGTAGAGTGGAAATGAT 276
 278 GTGGAGAGAGAACCACTACTTATACCAATATATATGCTGCTGGTGGAGTGAATGAC 337
 277 ATGAAGTTCAGTGGAACTTCAGATTTCCGCGGGTCAAGATTTAAGATGCCACCC 336
 338 TACAACCTGAGTGGAAACGACAGCGAGTATGCGGGGTCAAGGACCTCAGGATCAGCGCC 397
 337 CACAGACTATGGAACACGACCTCTTATGTACAACAGCGCGGAGCGGTTTCGACAGC 396
 398 ACAAGTGTGGAAGCGGACCTCTTATGTATATATAGTCTGACGAGGTTTTCACGGG 457
 397 AGCTATCCAAACGAGTGTGTGGCGGAACAGCGCTGTGTCTACGTGCGCGCGCGCGC 456
 458 ACCTACCAACGAGCGTGTGTGGCGGAACAGCGCGGCTGTGTCTACGTGCGCGCGCGC 517
 457 ATCTTCAAGAGACCTGCAAGATCGACATCACCCTGGTCCCTTCGACGACCAAGATGC 516
 518 ATATTCAAGAGACATGCAAGATGACATCGCGTGTGTTCCTTCGACGACCAACACTGT 577
 517 GAGATGAAGTGTGGCAGCTGGACTTATGATGTTTATCAGTTGATCTACAACTACAGGAT 576
 578 GATATGAAGTGTGGAGTGGACATATACGCGCAATCAGTTGGATCTGGTGTAAAGAT 637
 577 GAAGGGGGCGGAGATATAAGCAGTTTGTACGAATGGCGAATGGGAGTTAATAGAGTC 636
 638 GAGGAGGCGGCGGATCTATCGGACTTCAACAATATGGGAGTGTGTATCTAATAGGATG 697
 637 CCCGCGAAGCGAAGCACTACTACAACTGTTCGCGGAGCCCATACATCGACATCAGC 696

Db 698 CCAGGCAAAAGAACACAAATAACATACGCGTGTGCCCCGAGCCCTACGTGACGTACCC 757
 QY 697 TTTGGCGGTGGTATCGGAGAGAAACGCTCTACTTCTTCAATCTATCTGTCGCCCTGC 756
 Db 758 TTTCCACATCATATGAAGAGACGACCTTGTACTACTTCTTCACTGATCGCGTGC 817
 QY 757 GTGCTCATGCGCTCATGCTCTATTTGGGGTTTCACTTTCGCCCTCCAGACTCCCGGAGAAAG 816
 Db 818 GTGCTCATCTCATGCTCATGCTCTCGGCTTTCACACTGCCACGAGACTCCCGAGAGAAA 877
 QY 817 TTGCTTTAGTGTGACGATATTTACTGTCTGTGAGCGGTCTTCTCAACATGTTGGCGGAG 876
 Db 878 CTCACACTTGGAGTCACTATTCTTATCGCTGAGCGGTGTCTCAACCTGGTAGCCGAG 937
 QY 877 ACGATGCCAGCGACGTCGGAGCGCGCTTTCCTTCGCGCACCTACTTCAACTGCATCATG 936
 Db 938 ACCCTGCCACAGGTCTCCGACGCTATCCCCCTGTAGGACGCTACTTCAATTGCATCATG 997
 QY 937 TTTATGGTGGCTTCTCTCGCTCTCCACCATCTATGATCTCTCAACTACACACCGGAC 996
 Db 998 TTTATGGTGGCTTCTCTCGCTCTCCACCATCTATGATCTCTCAACTACACACCGGAC 1057
 QY 997 GCAGACACTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1056
 Db 1058 GCTGATATACATGAATGCCACAGTGAATAAATCAGTATCTCTACAAATGGTGGCTGAT 1117
 QY 1057 GTGCTGCGCATGTCACGCGCGCTCGGCG---AGACGCGCGCGCGCGCGGTACCT 1113
 Db 1118 ATACTGCGNATGTCGAGCGCCAGGAGAGATCACCAGAAAGACTATATGATGAACAG 1177
 QY 1114 CCGCGCGCGGACCTGGAGTGGCGGAGCGCTCTCTCAAGTCTGCTCTTAGCGAACGTGCTC 1173
 Db 1178 AGGATGAGGAGCTGGAACCTGAAGGAGAGGTGCTGGAAGTCTTGTGCGGAATGTCTA 1237
 QY 1174 GACATCGATGACGACTTCCGCCACCGCGCAAGCGCAGC-----AGCCGCAATGCTGCG 1226
 Db 1238 GATATTGATGATGACTTTCAGACACGCGCCCTCCGCTCTTAACAGTACTGCTCGACCGGG 1297
 QY 1227 ATACTACAGGGGGGTGAGGAGAAATGGCGGGGTGGCGGCGCACAGTTGCTTCG---- 1282
 Db 1298 AATTTGGGACCTGGTGTCTCAATATTCGCGAGGATTTCCGTCGGTCTGCTCGCTCGC 1357
 QY 1283 -----GTGTCGACTAGAGCTTCCCTCATTT 1308
 Db 1358 TCCACGATGGAAGAGCTGGGCGCGGCTGGGTAGCCACCATCGGAGTGCACCTCAT 1417
 QY 1309 CTGAAGGAGATAGAGTCAATCAGATCGCAGGAGCGAGGAGAGATCGGACATT 1368
 Db 1418 CTGAGAGAGCTCCAGTTTCATCAGCGCGAGGATGAAGAGGCTGATGAGGAAGCCGAGCTG 1477
 QY 1369 TCGCGCGACTGGAAGTTCCGCCCATGTTGCTGGGACAGACTGTGCTTATTTATCTTTAC 1428
 Db 1478 ATCAGGAGTGAAGTTCGTCGATGTTGTTGATAGTGTGCTGCTGCTGCTGCTGCTGCT 1537
 QY 1429 CTGTTTCAATCATCGCACGCTAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1485
 Db 1538 CTTTTCACAAATCATCGGACAGTAGTGTCTGTTATCGGCAAGCCGATATCATCTG 1594
 RESULT 3
 AAZ24475
 ID AAZ24475 standard; cDNA to mRNA; 2886 BP.
 XX
 AC AAZ24475;
 XX
 DT 17-FEB-2000 (first entry)
 DE
 DE D. melanogaster acetyl-choline receptor DNA from clone Da7.
 XX
 KW Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
 KW neurotransmission; plant protection agent; conductance; AChR; ds.
 XX
 OS Drosophila melanogaster.

XX FH Key Location/Qualifiers
XX CDS 372..2684
XX FT /*taq= a
XX FT /product= "acetyl choline receptor."
XX XX
XX DE19819829-A1.
XX PD 11-NOV-1999.
XX PF 04-MAY-1998; 98DE-1019829.
XX PR 04-MAY-1998; 98DE-1019829.
XX PA (FARB) BAYER AG.
XX PI Adamczewski M, Oellers N, Schulte T;
XX WPI; 2000-014207/02.
XX P-PSDB; AAY50814.
XX New nucleic acid encoding a nicotinic acetylcholine receptor from
XX insects, used to identify potential insecticides
XX Claim 1a; Page 8-12; 26pp; German.
XX
XX This invention describes a novel nucleic acid (NA) encoding a nicotinic
XX acetyl-choline receptor (I) from insects which can be used as an
XX insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
XX (also vectors containing it, its regulatory regions, and antibodies
XX directed against (I)-encoded proteins) are used to screen for: (a) plant
XX protection agents that alter conductance of AChR, potentially useful as
XX insecticides, or (b) genes which encode polypeptides that are involved in
XX formation of functionally related AChR in insects. (I) are also used to
XX isolate and characterize the specified regulatory regions and for
XX recombinant production of (II). This sequence encodes an acetyl-choline
XX receptor isolated from *Drosophila melanogaster*.
XX
XX Sequence 2886 BP; 942 A; 687 C; 640 G; 617 T; 0 other;
XX
XX Query Match 34.5%; Score 512.8; DB 21; Length 2886;
XX Best Local Similarity 62.5%; Pred. No. 5.4e-115;
XX Matches 878; Conservative 0; Mismatches 502; Indels 24; Gaps 4;
XX
QY 91 GGGTACACGAGAGCGGCTACTGACACACCTATTGGACCACTACAACGTACTGGAGG 150
DB 1296 GGATATCATGAAAGAGAGACTGTTACACGATCTTTTGGATCCTTATATACACTAGAAGT 1355
QY 151 CCCGTCGCAACGAGAGCGCCGCTGCGAGCTCTCTCGGCTCACGCTCATCGAGATC 210
DB 1356 CCCGTTCTCAATGAATCGGACCCGTTACAAATTAAGCTTTGGTTTAACTTTAATGCAAAAT 1415
QY 211 ATCGACGTGGACGAGAACACGAGCTTTTAAACAAACATCTGGCTAAACACTAGAGTGG 270
DB 1416 ATCGATGGGACGAGAAAATCAATGCTAGTCACTAATGTTGGTTAAACTGGAGTGG 1475
QY 271 AATGATATGAATCTAGTGGAACTTCAATGATTTCCGCGGGGTCAAAGATTTAAGAGTG 330
DB 1476 AACGACATGAATCTCCGCTGGAAACACCTCCGACTATGCGGAGTTAAGGATCTCGAATA 1535
QY 331 CCACCCACACACTATGAACACGAGCTCTTATGTACACACGCGCGGAGAGGGTTC 390
DB 1536 CCGCGGCATCGATCTGGAACCGGACGCTGTGTATGATGATACACAGTGGGATGAGGATTT 1595
QY 391 GACAGCAGTATCCAAACGAGCTGGTGGTGGGAAACACGCTGCTGTCTGTAGTGGCG 450
DB 1596 GACGCACTACACACGACGAGTGGTGGTGGGAAACACGCTGCTGTCTATACGTTCCG 1655
QY 451 CCGGCGATCTTCAGAGACGCTGCAAGATCGACATFACCTGGTTCCTTCGACGACCA 510
DB 1656 CCGGGGATCTTCAAGTCGACGCTGCAAGATCGACATFACCTGGTTCCTTCGATGACCA 1715
QY 511 CGATCCGAGATGAAGTTTGGCAGCTGGACTTATGATGTTATCAGTTGGATCACA 570

Db 1716 CGGTCCGAGATGAAGTTCCGGCAGTTGGACCTACGACGAGTTCACAGTTCAGTTCGATTA 1775
QY 571 CAGGATGAAGGGGGCGGAGATATAAGCAGATTTTGTACAGAAATGCGGAATGCGAGTAAATA 630
Db 1776 CAAGATGAAGTGGGGGTGATACAGCAGTTACGTGCTCAACGGGAGTGGGAACTACTG 1835
QY 631 GGAGTCCCGGCAAGCGCAACGAGATCTACTACAACTTTGTCCGGAGCCATACATGAC 690
Db 1836 GGTGTCCCGGCAAAACGTAACGAGATCTATTACAACTGCTGCCGGAACCTATATAGAC 1895
QY 691 ATCAGCTTGGGTGGTGGATCCGGAGAAACGCTCTACTACTTCTTCAATCTGATCGTG 750
Db 1896 ATCACCCTTCGCATCATCCGCGGACGACACTGTACTATTCTTCAACCTGATCAT 1955
QY 751 CCCTGCGTCTCATCGCTCCATGGCTCTATTGGGGTTACCTTGCCTCCAGACTCCCGGA 810
Db 1956 CTTTGTGATGATGCTCCATGGCTTGTCCGATTCACCTGCCGAGATTCGGGT 2015
QY 811 GAAAAGTTGCTTTAGTGTGACGATATCTACTGCTTGGAGGGTGTCTTCTCAACATGTTG 870
Db 2016 GAAAAATTTACGCTGGGTGTTTACCATCTTGTCTGCTGACCGCTGTTTCTGAATATGTT 2075
QY 871 GCGGAGACGATCCGACGACGCTCGGACGCGCTGCTGCTCGGACACCTACTTCAACATGC 930
Db 2076 GCCGAGACAATGCCGCGTACTTCCGATCGGTGCCATTG-----TGGATACGC 2123
QY 931 ATCATGTTTCATGGTGGCTTCTCGTCTCTCCACCATATCATCTCAACTACACAC 990
Db 2124 ATCGTGTGTTTG--TGCTGGCTGCCATGATATTGCGAATGAGTGCCTCCGACGACCGC 2181
QY 991 CGGACGACGACACTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1050
Db 2182 TGATCTAGAGTTTCCGACGACGCTGCTGCGACACAT---CCTCGAGCGGAGACG 2237
QY 1051 CCGTGGTGTGCTGCGATGTCACGCGCGCTCGGACGACGCGCGCGCGCGCGCGCTA 1110
Db 2238 CAGATACTCTCGGAGCTGAAAGAGCGCTGCTGAAATCGCTGCTGCCAACGTA 2297
QY 1111 CCTCCGCGCGGACCTGGAGCTGCGGAGCGCTCTCCAAAGTGCCTCTTAGCGAACGTTG 1170
Db 2298 CTAGACATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2357
QY 1171 CTCACATCGATGACGAGCTTCCGCGCACCGCAAGCGGACGACGCGCGCGCGCTATC 1230
Db 2358 CCACACACCGCGGCTTCTATCGCAGCGGTTTATGGACAAAGGCGAGATGGCAGCATGGG 2417
QY 1231 TACAGGGGGGTGAGGAGATGGCGGGGTTGGCGGCGCACAGTTGCTTC-----GGT 1284
Db 2418 CCAATTGCGACGCCGGAATGCCGATGCGGTCAACCATCATACGTGCTCAATCATCA 2477
QY 1285 GTCGACTACGAGCTCTCCCTCATTTCTGAAGAGATTTAGAGTATCATCAGATCAGATGCGC 1344
Db 2478 ACTGAATATGAATAGGTTTAACTCTTAAAGGAAATTCGCTTTTAACTGATCAGTACGT 2537
QY 1345 AAGACGACGAGATGCGGACATTTCCGCGCACTGGAAGTTTCGCGCGCATGGTCTGTCGAC 1404
Db 2538 AAAGATGACGAGTGCATGACATTTGCCAATGATTTGGAATTTGACGATGATGCTGTTG 2597
QY 1405 AGACTGTCCTTATTATCTTTTACCTGTTCAAAATCATCGCACGCTAGCGCTGCTGCTG 1464
Db 2598 AGACTGTCCTTATTATCTTTTACCTGTTCAAAATCATCGCACGCTAGCGCTGCTGCTG 1464
QY 1465 TCCGCGCACACATCATGGTGTGC 1488
Db 2658 TCGCACACACATATTATTGTCTCG 2681

RESULT 4
ABLI13733
ID ABLI13733 standard; cDNA; 936 BP.
XX
AC ABLI13733;

Db	431	GCATATTACAGAGTTCTGCTACATCATGATGACGCTGGTTCCCTTTGATGTGCAGCACT	490
Qy	515	GCAGAGTGAAGTTTGGCAGCTTGGACTTTATGATGGTTATCAGTTGGATCTACAACCTACAGG	574
Db	491	GCAAACTGAAGTTTGGGTCTGGTCTTACGGAGGCTGGTCTTGGATCTGCAGATGCAGG	550
Qy	575	ATGAAGGGGGGAGATATAAGCAGTTTGTACGAATGGCAATGGAGTTAATAGGAG	634
Db	551	A-----GGCAGATATCAGTGGCTATATCCCAATGGAGAATGGACCTAGTGGGAA	601
Qy	635	TCCCGGCAAGCGCAACGAGATCTACTACAACGTGTGTCTCGGAGGCCATACATCGACATCA	694
Db	602	TCCCGGCAAGAGAGTGAAGGTTCTATGAGTGTCTCAAAAGAGCCCTACCCCGATGTCA	661
Qy	695	CGTTTGGGTGGTGTATCCGGAGGAAAACGCTCTACTACTTCTCAATCTCATCGTGCCT	754
Db	662	CTTTCAGTGAACATGCGCGCAGGACGCTACTATATGGCCTCAACCTGCTGATCCCT	721
Qy	755	CGGTGCTCATCGCTCCATGGCTCTATTGGGTTACCTTGGCTCCAGACTCCGGAGAAA	814
Db	722	GTGTGCTCATCTCCGCCCTCGCCTGTGGTGTCTCTTCTTCCGTGCAGATTCGGGGAGA	781
Qy	815	AGTTGTCTTTAGGTGTACCATATTACTGTCTGTGACGGTGTTCCTCAACATGGTGGCGG	874
Db	782	AGATTTCCCTTGGGGATAACAGTCTTACTCTCTTACCGCTTTCATGCTGCTGCTGGCTG	841
Qy	875	AGACGATGCCAGGACGCTCGGAGCGCGTCCCTTGTCTGGCACCTACTTCAACTGTGCATCA	934
Db	842	AGATCATGCCCGCAACATCCGATTCGGTACCATGATGAGCCAGTACTTGCACGACCA	901
Qy	935	TGTTTCATGTGGTTCCTCCGTGCTTCCACCATACTGATGATCTCAACTACCAACACCGGC	994
Db	902	TGATTCATCGTGGGCTCTCGGTGGTGTGACGGTGTGCTGTGACGTACCAACCAACG	961
Qy	995	ACGCAGACACTCAGAAATGAGTATGAGTATGTTGCTGCTGTTCCCTTATTGCTGCCGT	1054
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Qy	1055	GGTGTCTGCATGTCTACGGCCGGCTCGGCGACGACGCCCGCGCGCGCGGTACCTC	1114
Db	1022	GGTTCTCTCGAATGAGAGGCCCGGGAGGACAAGGTGCGCCCGCTGCCAGCANAAG	1081
Qy	1115	CGCG-----CGGACCTGGAGCTGCGCGAGCGCTCCTCAAGTGCCTCTAGCGA	1165
Db	1082	AGCGGGCGCTGCAGCCTGGCGAGTGTGGAGATGAGCGCGTGGGCGCGCGCGCCGACGA	1141
Qy	1166	ACGTGCTCGACATCGATGACGACTTCGCGCACCGCAAGCGAGCAGCGCAATGCTGCC	1225
Db	1142	ACGGAACTGCTGTATCATCGGTTCCGGCGCTTGGAGCGGTGACGGCGTGCATGTGTCCGACCC	1201
Qy	1226	GATACACAGGGGGGTGAGGAGATGGCGGGGTTGGCGGGCGACAGTT-----	1276
Db	1202	CCGACTCTGGGTAGTGTGTGGCGCATGSCCTCTCCCCACGACGATGACCACTCC	1261
Qy	1277	-----GCTTCGGTGTGATACGATGCTCCCTCTATCTTACCTGTTCCACAACTCA	1321
Db	1262	TGCACGTTGGGCAACCCCGAGGGGACCCGACCTTGGCAAGATCTCTGGAGGAGTCC	1321
Qy	1322	GAGTCAATCAGATCGCAGAAGGACCAAGATGGGACATTTCCGCGCACTGGA	1381
Db	1322	GCTACATTGCCAACCGTTCCGCTGCCAGACGAAGGAGGGGTCTGCAGCGAGTGGGA	1381
Qy	1382	AGTTCCGCGCATGCTGGAGACAGACTGTGCGCTTATTATCTTACCTGTTCCACAACTCA	1441
Db	1382	AGTTCCGCGCTGTGTGGTGSACCGCTGTGCGCTCATGGCTTCTCGGTCTTCCACATCA	1441
Qy	1442	TCGCGAGCTAGCGGTGCTGCTGTCCGCGCCACACATCATGTTGTC	1487
Db	1442	TCGTGCATCTCGCATCTCATCTCGCTCCCAACTTCGTTGGAGG	1487

AAC0039E

AAC90385
ID AAC90385 standard: cpDNA: 1509 BP.

AAC 90385:

XX
DT 14-MAR-2001 (first entry)

DE Mutant human alpha7 ligand gated ion channel coding sequence #1.

KW Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;

XX
XXXX
XX

XX

XX

XX

XX

XX
XXXX
XX

DR P-PSDB; AAB50015.

PT Special cell cult

PT concentrations of ions of sodium, calcium and potassium at specified pH

PS
Claim 50; Page 69; /pp; English.
xx

the present sequence is the coding sequence for a mutant human α 1A nicotinic acetylcholine gated ion channel. The human α 7A ion channel was used in the construction of an α 7A/5-hydroxytryptamine (5-HT₃) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The α 7A/5-HT₃ chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells. The protein encoded by this sequence has the wild-type threonine residue at position 230 substituted by a proline residue.

SQ Sequence 1509 BP; 296 A; 452 C; 429 G; 332 T; 0 other;

Query Match 27.2%; Score 404; DB 22; Length 1509;
Best Local Similarity 56.5%; Pred No 1 5e-88.

Matches 839; Conservative 0; Mismatches 605; Indels 42

[illegible]

DB 11 CGCCGGGAGGCGTCTGGGCTGGCCGCTCGCTCCCTGCACGTGTCCTGC AAGCG 70

95 ACCACGAGAGCGGCTAC¹GGACCACCTATTGGACCACCTACAACGTA²CTGGAGAGGCCCG 134

DB /1 AGTTCAGAGGAAGCTTTACAAGGAGCTGGTCAAGAACTACAACTCCCTTTGGAGAGGCCCG 130

Qy TCGTCAACGAGAGCGACCCGGCTGCAGCTCTCCTTCGGGCTCACGCTCATGCAGATCATCG 214

Db 131 TGGCCAATGACTCGCAACCACTCACCGTCTACTTCTCCCTGAGCCTCCTGCAGATCATGG 190

QY 215 ACGTGGACGAGAGAAGAACCCAGCTTTTAATAACAAACATCTGGCTAAAACTAGAGTGGGAATG 274

Db 191 ACGTGGATGAGAAGCAAGTTTAAACCACCAACATTTGGCTGCCAAATGCTCTTGGACAG 250

QY 275 ATATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGTCAAAGATTTAAGAGTGCCAC 334

Db 251 ATCACTATTACAGTGAATGTGTCAGAATATCCAGGGGTGAAGACTGTTCTCCAG 310

Qy 335 CCCACAGACTATGGAAACCAAGACGTCTTATGTACAACAGCGGACGAAGGTTCCGACA 394

[illegible]

D	b	1262	TGCACGGCGGAAACCCCGGAGGGGACCGCGGACTTGGCCAAAGATCCTGGAGGAGGTCC	1321
Q	y	1322	GAGTCATCACAGATCAGATGCGCAAGGACGACGAAGATGCGGACATTTTCGCGGCACTGGA	1381
D	b	1322	GCTACATGCCAATCGCTTCGCTGCCAGACGAAAGCGGAGCGGCTGCAGCGAGTGA	1381
Q	y	1382	AGTTGCGCGCCATGGTCGTGGACAGAGATGTGCGCTTATTATCTTTACCTGTTCCACAATCA	1441
D	b	1382	AGTTGCGCGCGCTGTGTGTGGACCGCCTGTGCCTCATGGCTTCTCGTCTTCACCATCA	1441
Q	y	1442	TCGCCACGCTAGCGTGTCTGTGTCGGCGCACACATCATGGTGTC	1487
D	b	1442	TCTGCACCATCGCATCCTGATGTCGGCTCCCAACTTCGTGGAGC	1487
RESULT 14				
AAC90387.				
ID	AAC90387 standard; cDNA; 1509 BP.			
XX				
AC	AAC90387;			
XX				
DT	14-MAR-2001 (first entry)			
XX				
DE	Mutant human alpha7 ligand gated ion channel coding sequence #3.			
XX				
KW	Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;			
KW	5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.			
XX				
OS	Homo sapiens.			
XX				
PN	WO200073431-A2.			
XX				
PD	07-DEC-2000.			
XX				
PF	25-MAY-2000; 2000WO-US11862.			
XX				
PR	27-MAY-1999; 99US-013617A.			
XX				
PA	(PHAA) PHARMACIA & UPJOHN CO.			
XX				
PI	Groppi VE, Wolfe ML, Berkenpas MB;			
XX				
DR	WPI; 2001-061524/07.			
DR	P-PSDB; AAB50017.			
XX				
PT	Special cell culture medium for treating cells and for inducing			
PT	mammalian cell lines to conduct calcium ions, comprising specified			
PT	concentrations of ions of sodium, calcium and potassium at specified pH			
PT				
XX				
PS	Claim 64; Page 75; 77pp; English.			
XX				
CC	The present sequence is the coding sequence for a mutant human alpha7			
CC	nicotinic acetylcholine gated ion channel. The human alpha7 ion channel			
CC	was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3)			
CC	chimeric ligand gated ion channel (see AAC90382 and AAB50014). The			
CC	alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells			
CC	in the present invention, resulting in preferential calcium ion			
CC	conductance by the cells. The protein encoded by this sequence has the			
CC	wild-type threonine residue at position 230 substituted by a proline			
CC	residue and the wild-type cysteine residue at position 241 substituted			
CC	by a serine residue.			
XX				
SO	Sequence 1509 BP; 297 A; 452 C; 429 G; 331 T; 0 other;			

	Query Match	27.0%	Score 402.4;	DB 22;	Length 1509;
	Best Local Similarity	56.4%;	Pred. No. 3.7e-48;		
	Matches 838; Conservative	0;	Mismatches 606;	Indels 42;	Gaps 3;
Qy	35	CGCCGCGGGGCCTGCTGCTGTGTGCTGTCTGTGCGAGGGGGACGCTGCCGGT	94		
Db	11	CGCCGGGAGGGTCGTGCTGGCTGCGTGCACGCTGCTGTCACGCTGTCCTGCAAGGGC	70		

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TITLE Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than to other insect nicotinic acetylcholine receptor alpha subunits

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3629)
AUTHORS Schulte, T., Oellers, N. and Adamczewski, M.
TITLE Direct Submission
JOURNAL Submitted (19-APR-1999) ZF-BTB, Bayer AG, Bldg. Q 18., Leverkusen 51368, Germany

FEATURES
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BASE COUNT 880 a 931 c 922 g 895 t 1 others
ORIGIN

Query Match 100.0%; Score 1488; DB 3; Length 3629;
Best Local Similarity 100.0%; Pred. No. 6.4e-231;
Matches 1488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB |
QY 61 TGCCTGCTGCTGCGGAGGGGGCGCGCTGCGGGTACCAGAGAGCGGCTACTGCACAC 120
DB |
QY 395 TGCCTGCTGCTGCGGAGGGGGCGCGCTGCGGGTACCAGAGAGCGGCTACTGCACAC 454
DB |
QY 121 CTATTGGACCACTACACGCTACTGAGAGGGCGGCTGCTCAAGGAGAGCGCGCTGCAG 180
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QY 181 CTCTCTTTCGGGCTCACGCTCATGCGATCATCGACGTGGAGGAGAGCAAGCACTTTTA 240
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QY 515 CTCTCTTTCGGGCTCACGCTCATGCGATCATCGACGTGGAGGAGAGCAAGCACTTTTA 574
DB |
QY 241 ATAACAACATCTGCTAACTAGCTAGGATGATGATGATGATGATGATGATGATGATGAT 300
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QY 575 ATAACAACATCTGCTAACTAGCTAGGATGATGATGATGATGATGATGATGATGATGAT 634
DB |
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DB |
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QY 361 CTATTGTAACAGCGGAGGAGGGTTTCGACAGCAGTATCCAAAGCAAGCGTGGTGGT 420
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QY 541 TATGATGTTTATCAGTTGGATCTTACAACTACAGGATGAAGGGCGGAGATATAAGCAGT 600
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QY 601 TTTGTACGAATGGGAATGGAGTTAATAGAGTCCCGGAGCGCAACAGAGATCTAC 660
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QY 1381 AAGTTCCGCGCATGCTGCTGAGACAGCTGTGCCTTATTATCTTTTACCTGTTCAACATC 1440
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QY 1715 AAGTTCCGCGCATGCTGCTGAGACAGCTGTGCCTTATTATCTTTTACCTGTTCAACATC 1774
DB |
QY 1441 ATCGCCAGCTAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1488
DB |
QY 1775 ATCGCCAGCTAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1822
DB |

RESULT 2
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LOCUS AX009612 3700 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 3 from Patent EP0962528.
ACCESSION AX009612
VERSION AX009612.1 GI:9996844
KEYWORDS

REFERENCE	Ephydroidea; Drosophilidae; Drosophila.	BASE COUNT	547 a	508 c	503 g	465 t
AUTHORS	1 (bases 1 to 2023)	ORIGIN				
TITLE	Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B. Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing	Query Match	41.3%;	Score 615;	DB 3:	Length 2023;
JOURNAL	Genetics 160 (4), 1519-1533 (2002)	Best Local Similarity	64.6%;	Pred. No. 3.4e-114;		
MEDLINE	21969411	Matches	950;	Conservative	0;	Mismatches 515;
PUBMED	11973307				Indels	6;
REFERENCE	2 (bases 1 to 2023)				Gaps	2;
AUTHORS	Grauso, M. and Sattelle, D.B.					
TITLE	Direct Submission					
JOURNAL	Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford OX1 3QX, UK					
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Db	807	GTACGTGCCCTGGTATCTTCAAGAGCATGCAAGATGGATCAGTGGTTCOCAT	866
Qy	501	CGAGACCAACGATCGAGATGAAGTTTGGCAGCTGGACTTATGATGGTTATCAGTTGGA	560
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Qy	561	TCTACAACTACAGATGAAGGGCGGAGATATAAGCAGTTTTGTACGAAATGGCGAATG	620
Db	927	TTTGGTTTTGAATTCGGAAGATGAGGGGATCTTTCCGATTTCAATACAAATGGCAGTG	986
Qy	621	GGACTTAATAGGAGTCCCGCAAGCGCAAGAGATCTACTACAACGTGTTCCGGAGCC	680
Db	987	GTACTTGGCTTGGCATGCGGGAAGAAGATACGATAGTACGCCCTGCTGCCAGAAC	1046
Qy	681	ATACATCGACATCGTTTGGGTGGTGATCCGGAGGAAAACGCTCTACTACTTCTTCAA	740
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Qy	741	TCTGATCGTCCCGCTGCTCATFCGCTCCATGGCTCATATGGGTTACCTTTGCTC	800
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Qy	801	AGACTCCGGAGAAAGTTGCTTTAGCTGTGACGATATTACTGCTGTGACGGTTCCT	860
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Qy	861	CAACATGGTGGCGAGCAGTGCAGCGAGCTCGAGCGCGTGCCTTGCTCGGCACCTA	920
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Qy	1335	TCAGATCGGAAGACACGAGATGCGGACATTTCCGGCAGCTGGAAGTTCCGCGCAT	1394
Db	1707	CGCGATCGGAAGCTCACGACGAAAGCGAATTAATCGCGGATTTGGAAGTTCCGCGCA	1766
Qy	1395	GGTGGTGGACAGCTGTGCCTTATTATCTTTACCTCTTACAAATCATGCCAGCTAGC	1454
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Qy	1455	CGTGCTGCTGTCGCGCCACACATCATGGTG	1485

Db	1827	GGTCTGCTCCGCTCCGCACATAATCGTG	1857
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LOCUS			
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ORGANISM			
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JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
AUTHORS			
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JOURNAL			
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source			
gene			
CDS			
variation			
variation			
variation			

RNA-Mediated A-to-I Pre-mRNA Editing Genetics 160 (4), 1519-1533 (2002) 21969411 11973307 2 (bases 1 to 2907) Grauso, M. and Sattelle, D.B. Direct Submission Submitted (27-MAY-2000) Human Anatomy and Genetics, MRC-FGU, University of Oxford, South Park Road, Oxford OX1 3QX, UK Location/Qualifiers 1..2907 /organism="Drosophila melanogaster" /mol_type="mRNA" /db_xref="taxon:7227" /chromosome="2" /map="2L: 34E4-5" /dev_stage="embryo" 1..2907 /gene="nAcRalpha-34E" /allele="A" 289..2712 /gene="nAcRalpha-34E" /note="ion channel; neurotransmitter transmembrane receptor" /codon_start=1 /product="nicotinic acetylcholine receptor Dalpha5 subunit" /protein_id="AAM13390.1" /db_xref="GI:20152840" /translation="MKNAQLKLEVDDELWLAVRLAHCSNFSSTSTRTSSNQRH NQUTTPQSLSTKHSNIASEQHNSQOQEPASQKDEVDVNHGRSDQOQTHLOQLDSS NMSPKTAATAAGDEATTQOPTNIRLCARQRRLRRRRKRPATNETDIKQOOL SMPEFKRTSDTYSTPAATSCPTATYMOCRASDNFESIPISRHDVSTATFAWVH VOLLVLSQOQWOLHVQORSVLLFERRIAASTIAFISYLGSAFALQNSSSSSSNSS NNSQTQLNGKHSWFLFLLIYNLSAKVCLAGVHEKRLDLDLPYNTLERPVLES DPLQSLGLIMQLIDVDERKOLLVTNWLKLEWDMNLRWNTSDYGVKDLRPPHR IWKPDVLYNSADDFGDTQYTNVVRNNSCLVPPGIFKSTCKIDITWFFPDQRC EMKFSYTGFDQLQDQETGGDISYVNLNGEWELGVPGRNELYNCPEPEYID ITFAIIIRRTLYFFNLIIPCVLIASMAILGFTLPDPSGKLSLGYTILLSLTVFLN MVAETPATSADVPILGTYFNCIMFWASSVSVTILILNYHHRNADPHEMSEIRIVF LCWLPWILRSRGRPLLEPTPCSDTSERKHOILSDVELKERSKSLANVLDI DDDFRHCNRPMTGPPLPHNPAFYRTYVGDDGSGIPGSTRMPDVAVTHHTCKSST EYELGLILKEIRFTIDOLRKDECDNDIANDWKFAAMVVDRLCLLIIFTMFAILATIAVL LSAPHIIVS" 373 /gene="nAcRalpha-34E" /note="compared to B allele" /replace="a" 375 /gene="nAcRalpha-34E" /note="results in phenylalanine to isoleucine substitution; compared to B allele" /replace="c" 827 /gene="nAcRalpha-34E" /note="results in threonine to isoleucine substitution; compared to B allele" /replace="t" 1079..11080 /gene="nAcRalpha-34E" /note="results in lysine to arginine substitution; compared to B allele" /replace="g" 1081..1086 /gene="nAcRalpha-34E" /note="results in deletion of asparagine and serine; compared to B allele" /replace="" 1119~1120 /gene="nAcRalpha-34E" /note="results in serine, glycine, and asparagine insertion; compared to B allele" /replace="accqcaac"		variation 1121 /gene="nAcRalpha-34E" /note="results in asparagine to serine substitution; compared to B allele" /replace="g" 935 a 696 c 642 g 634 t BASE COUNT ORIGIN Query Match 39.2%; Score 583.8; DB 3; Length 2907; Best Local Similarity 65.2%; Pred. No. 7.1e-108; Matches 976; Conservative 0; Mismatches 422; Indels 99; Gaps 4; QY 91 GGGTACCACGAGAGAGCGGTACTGCACCACTATTGGACCACTACAAGTACTGGAGAGG 150 DB 1213 GGATATCATGAAAAGAGAGACTGTTACACGATCTTTTGGATCTTTATAACATAGAACGT 1272 QY 151 CCCGTCGTCAACGAGAGAGCGCCCGCTGCAGCTCTCTTCGGCTCAGCTCATCAGATC 210 DB 1273 CCCGTTCTCAATGAATCGGACCCCGTTACAATTAAGCTTTGGTTTAACCTTTAATGCAAAAT 1332 QY 211 ATCGACGTGGAGAGAGAACCAACGAGCTTTTATAACAACATCTGCCTTAAACACTAGAGTGG 270 DB 1333 ATCGATGTGGAGAGAGAAATCAATTGCTACTCACTAATGTGTGGTTTAAACACTGAGTGG 1392 QY 271 AATGATATGAATTTGAGTGGACACTTCAGATTTTCGGCGGGGTCAAGATTTAAGAGTG 330 DB 1393 AACGACATGAATCTCCGCTGGACACCTCCGACTATGGCGAGTTAAGGATCTCGGAATA 1452 QY 331 CCACCCACAGACTATGAAACACAGAGCTCTTTATGTACACACGCGGAGAGGGTTC 390 DB 1453 CCGCGGATCGCATCTGGAAGCGGAGTGTGTATGTACACAGTGGGATGAGGGAATTT 1512 QY 391 GACAGCAGTATCCAACCAACGCTGGTGGTGGGAAACAACGCTGCTGTCTGTACGTCCG 450 DB 1513 GACGCGACCTACCAGACAGAGCTGGTGGTGGGGAACAACGCTGCTGTCTATACGTTCG 1572 QY 451 CCGCGCATCTTCAAGAGACCTCAAGATCGACATCACTGTTTCCCTTCGACGACCAA 510 DB 1573 CCGGGGATCTTCAAGTCAAGTCAAGATCGACATCACTGTTTCCCTTCGATGACCGAG 1632 QY 511 CGATCCGAGATGAATTTGGCAGCTGGACITATCATGTTATCATGTTTGGATCTACACATA 570 DB 1633 CGGTCCGAGATGAAGTTTCGGCAGTTGGACCTACGACGGATTTCCAGCTGGATTTACAATA 1692 QY 571 CAGGATGAAGGGCGGAGATATAAGCAGATTTTCTGACGAGTGGCAATGGGAGTTAATA 630 DB 1693 CAAGATGAACACTGGCGGTGATATCAGCAGTTACGCTGCTCAACGGCGAGTGGAACTACTG 1752 QY 631 GGAGTCCCGCGCAAGCGCAACGAGATCTACTACAACCTGTTGTCGGAGCCATACATCGAC 690 DB 1753 GGTGTGCCCGCAAAACGTAACGAGATCTATTACAACCTGCTCCCGGGAACCTATATAGAC 1812 QY 691 ATCAGCTTTGGGTGGTGTATCCGGAGGAAACGCTCTACTACTTCTTCAATCTGATCGTG 750 DB 1813 ATCAGCTTTGGCCATCATCATCCGCGGACGACACTGTACTATTTCTTCAACCTGATCATA 1872 QY 751 CCCTCGGTGCTCATCGCTCCATCGCTCTATTGGGGTTCACTTCCCTCCAGACTCCGGA 810 DB 1873 CTTGTGTACTGATTTGCCCTCCATGCTTGTGCGGATTCACCTTCCCGCCAGATTCGGGT 1932 QY 811 GAAAAAGTTGCTTTAGTGTGACGATATTTACTGTCTGTGACGGTGTTCCTCAACATGGTG 870 DB 1933 GAAAAAATTCGCTGGGTGTTTACCATCTTGTCTCGCTGACCGGTGTTCTTGAATATGTT 1992 QY 871 GCGGAGACGATGCCAGCAGCTGCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 930 DB 1993 GCCGAGACAATGCCGGCTACTTCCGATGCGGTGCGCATTTGCTGGGTATACATTTTCAATTCG 2052 QY 931 ATCATGTTTCATGGTGGCTTCCCTCGCTGCTGCCACTACTGATGCTCCAACTACACCCAC 990 DB 2053 ATAAATGTTTATGGTAGCTTCATCCGTTGTGTCAACAGATTTTAAATATTAATATCATCAT 2112 QY 991 CGGCACGACGACACTCAGCAAAATGAGTATGATTCGGTTCGCTGCTGCTGCTGCTGCTGCTG 1050
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DEFINITION 7-2 subunit mRNA, complete cds.
ACCESSION AF143847
VERSION AF143847.1 GI:4895006
KEYWORDS Heliothis virescens (tobacco budworm)
SOURCE Heliothis virescens
ORGANISM Heliothis virescens
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Noctuoidea; Noctuidae; Heliothinae; Heliothis.
1 (bases 1 to 3029)
REFERENCE Schulte,T., Oellers,N. and Adamczewski,M.
AUTHORS Putative alpha subunits of insect nicotinic acetylcholine receptors
TITLE more similar to vertebrate alpha 7 subunits and C. elegans Ce21
than to other insect nicotinic acetylcholine receptor alpha
subunits
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3029)
AUTHORS Schulte,T., Oellers,N. and Adamczewski,M.
TITLE Direct Submission
JOURNAL Submitted (19-APR-1999) 2F-BTB, Bayer AG, Bldg. Q 18,, Leverkusen
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Best Local Similarity 64.6%; Pred. No. 4.3e-106;
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RESULT 10
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AUTHORS
TITLE
JOURNAL
FEATURES
source
CDS

AX009614
Sequence 5 from Patent EP0962528.
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AX009614.1 GI:9996846
Heliothis virescens (tobacco budworm)
Heliothis virescens
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Adamczewski, M.D., Schulte, T.D. and Oellers, N.D.
Nucleic acids encoding acetylcholin-receptor subunits from insects
Patent: EP 0962528-A 5 08-DEC-1999;
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Best Local Similarity 64.6%; Pred. No. 4.3e-106;
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VERSION	AJ554210.1		
KEYWORDS	nAcralpha-18C gene; nicotinic acetylcholine receptor subunit Dalpha7		
SOURCE	Drosophila melanogaster (fruit fly)		
ORGANISM	Drosophila melanogaster		
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REFERENCE	1. (bases 1 to 1683)		
AUTHORS	Millar, N.S.		
TITLE	Direct Submission		
JOURNAL	Submitted (31-MAR-2003) Millar N.S., Department of Pharmacology, University College London, Gower Street, London, WC1E 6BT, UNITED KINGDOM		

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Db	1151	TCTTCTCGAGTTCTCCGCTCGCGGAGAGCAACAGATCCAAACGTTGAGCTC <td>1210</td>	1210
QY	1135	CGGAGCGCTCTCCAGTCTCTACGAAAGTGTCTGACATCGATGACGATTCGCC <td>1194</td>	1194
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QY	1195	CAC-----CCGCAAGCGCAGCAGCGCAATGCTCCGATAC <td>1230</td>	1230
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QY	1231	TACAGGGGGGTGAGGAGAAATGGCGGGGTGGCGCGCACAGTGTCTCGGTGTGCGAC <td>1290</td>	1290
Db	1331	TACAGCAGGGGATGACGCGAGCGTGGGACCCGTGGACACGCTGTCCAGTTGTGGAC <td>1390</td>	1390
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Db	1391	GGCGGTTTGCAGGAGGCCATTCCACACCTGTCTGACATCCTCTCGCGGAGTACGAAC <td>1450</td>	1450
QY	1300	TCCCTCATCTCAAGGAGATTAGATCATACATCATGATGCCAGGACGAGCAAGAT <td>1359</td>	1359
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QY	1420	ATCTTTACCTGTTCCAAATCATGCCACGCTAGCCGTGCTGCTGCCGCGCACATC <td>1479</td>	1479
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LOCUS	2068 bp	mRNA	linear
DEFINITION	Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6 subunit variant type IV (nAcRalpha-30D) mRNA, complete cds, alternatively spliced.		
ACCESSION	AF321448		
VERSION	AF321448.1	GI:20152850	
KEYWORDS			
SOURCE	Drosophila melanogaster (fruit fly)		
ORGANISM	Drosophila melanogaster		
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
AUTHORS	1 (bases 1 to 2068)		
TITLE	Grauso.M., Reenan,R.A., Culetto.E. and Sattelle,D.B. Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing		
JOURNAL	Genetics 160 (4), 1519-1533 (2002)		
MEDLINE	21969411		
PUBMED	11973307		
AUTHORS	2 (bases 1 to 2068)		
TITLE	Grauso.M. and Sattelle,D.B. Human Anatomy and Genetics-Functional		
JOURNAL	Submitted (15-NOV-2000)		

Db	1887	GCCTTCACGATTATTCGAAGGTTACGGTGCCTCTCCGCTCCGACATAATCGTG	1944
RESULT 15			
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LOCUS	AX009610	2886 bp	DNA linear PAT 06-SEP-2000
DEFINITION	Sequence 1 from Patent EP0962528.		
ACCESSION	AX009610		
VERSION	AX009610.1	GI:9996842	
KEYWORDS			
SOURCE	Drosophila melanogaster (fruit fly)		
ORGANISM	Drosophila melanogaster		
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
	Ephydroidea; Drosophilidae; Drosophila.		
REFERENCE			
AUTHORS	Adamczewski,M.D., Schulte,T.D. and Oellers,N.D.		
TITLE	Nucleic acids encoding acetylcholin-receptor subunits from insects		
JOURNAL	Patent: EP 0962528-A 1 08-DEC-1999;		
FEATURES	BAYER AG (DE)		
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CDS	372..2684		
	/note="unnamed protein product"		
	/codon_start=1		
	/protein_id="CAC07499.1"		
	/db_xref="GI:9996843"		
	/translation="MKNAQLKLTEDVDELWLAVRLAHCSNFSFSSSTRSTSSNORH		
	NOQLTLPRLSLTKHNSNIASQHQEPASKDEVDVANHGRSNDQOHTLQQLDSS		
	NMLSPKTAATAAGDEATQOENTRLCARQRRLRRRRKRPAPNETDIKKOOL		
	SMPEFKRSTDYSPATTSCTPATMOCRADNEFSPISRHRDVRSTATFAWLH		
	VLOVLLSQWLQVRSVLLFRRIAISTAFISYLSFAQLNNSSSSSSSSNS		
	NNSTQLNLGNKHSWIFLLIYNLSAKVCLAGYHEKRLHLDDLPTNLERPVLES		
	DLQSLFSLMGIIDVDEKQLLVNWLKLEMDNLRWNTSDYGVKDLRIPPHR		
	IKWFDVLYNSAGDEKYQTVNVVRNNGSLYVPFGIFKSTCKIDITWFPDDORC		
	IKFNGSYTFDQLQDQETGDDISSYVLNGEWELVPGKRNELIYNCCPEYD		
	ITFAIIRRTLYFFNLIIPCVLIASMLLFTLPDSEKILSLGVITLLSLTVFLN		
	MVAETPKSDAPLRIIVELCWHLRMLRSRGRPLIIEFTPTPCSDPSRKHQI		
	LSVDELKERSKLLANVLIDDDFRHNCRPPTGGTLPHNPAFYRIYVGGDDSGIG		
	PIGSTRMPDVAHTHTCTSTSEYELGLILKEIRFITDQLRRKDECDNIANDWKFPAWV		
	VDRCLFIIFMFAITAVILLASPHIIVS"		
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ORIGIN			
Query Match	34.58; Score 512.8; DB 6; Length 2886;		
Best Local Similarity	62.5%; Pred. No. 1.7e-93;		
Matches	878; Conservative 0; Mismatches 502; Indels 24; Gaps 4;		
Qy	91	GGGTACCAGAGAAGCGGTACTGCACACCTATTGGACCACTACAACGTAAGTGGAGG	150
Db	1296	GGATATCATGAAGACACTGTTACACGATCTTTGGATCCTTATATACACTAGACGT	1355
Qy	151	CCCGTCGTCAACGAGAGCCCGCTCGAGCTCTCTTCGCGCTCAACGTCATCGACATC	210
Db	1356	CCCGTCTCAATGAATCGGACCCGTTACAATTAAGCTTTGGTTAACTTTAATGCAAAAT	1415
Qy	211	ATCGAGCTGGAGAGAAGAACAGCTTTTAAATACAAACATCTGGCTAAACATAGAGTG	270
Db	1416	ATCGATGACGAGAGAAAATCAATTCGTAGTCACTAATGTGTGGTTAAACATGGAGTG	1475
Qy	271	AATGATATGAATCTGAGTGGAACTTTCAGATTTCCGCGGGGTCAAGATTTAAGAGTG	330
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Qy	331	CCACCCACAGACTATGGAACACAGCTCTTATGTACACAGCGCGGAGGAGGTTTC	390
Db	1536	CCGCGCGATCGCATCTGGAACCGCGAGCTGCTGATGTACACAGTGGCGGATGAGGATTT	1595
Qy	391	GACAGCAGTATCCAACGACGTTGGTGGTGGGAAACACGCTCGTCTGTAGTCCGCG	450

Db 2658 TCGGCACCACATATTATTGCTCG 2681

Search completed: August 21, 2003, 09:54:17
Job time : 5551.39 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1191.5	29.5	502	1	US-08-278-635B-7	Sequence 7, Appli
2	1191.5	29.5	502	3	US-08-464-235B-7	Sequence 7, Appli
3	1191.5	29.5	502	3	US-08-471-961-7	Sequence 7, Appli
4	1168	28.9	511	1	US-08-278-635B-8	Sequence 8, Appli
5	1168	28.9	511	3	US-08-464-258B-8	Sequence 8, Appli
6	1168	28.9	511	3	US-08-471-961-8	Sequence 8, Appli
7	1159.5	28.7	502	2	US-08-466-589-8	Sequence 8, Appli
8	1159.5	28.7	502	2	US-08-700-636-8	Sequence 8, Appli
9	1159.5	28.7	502	3	US-08-467-574-8	Sequence 8, Appli
10	1159.5	28.7	502	4	US-09-217-345-8	Sequence 8, Appli
11	1159.5	28.7	502	4	US-08-487-596-12	Sequence 12, Appli
12	1155.5	28.6	502	4	US-08-771-737-2	Sequence 2, Appli
13	848.5	21.0	529	1	US-08-496-855A-2	Sequence 2, Appli
14	848.5	21.0	529	4	US-08-487-596-2	Sequence 2, Appli
15	848.5	21.0	529	4	US-08-660-451A-2	Sequence 2, Appli
16	845	20.9	504	4	US-08-660-451A-4	Sequence 2, Appli
17	835	20.7	528	2	US-08-466-589-2	Sequence 2, Appli
18	835	20.7	528	3	US-08-700-636-2	Sequence 2, Appli
19	835	20.7	528	3	US-08-467-574-2	Sequence 2, Appli
20	835	20.7	528	4	US-09-217-345-2	Sequence 2, Appli
21	832.5	20.6	510	1	US-08-278-635B-4	Sequence 4, Appli
22	832.5	20.6	510	3	US-08-471-961-4	Sequence 4, Appli
23	827	20.5	511	3	US-08-464-258B-4	Sequence 4, Appli
24	823.5	20.4	497	1	US-08-278-635B-5	Sequence 5, Appli
25	823.5	20.4	497	3	US-08-464-258B-5	Sequence 5, Appli
26	823.5	20.4	497	3	US-08-471-961-5	Sequence 5, Appli
27	810	20.0	504	2	US-08-466-589-4	Sequence 4, Appli

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RESULT 3
US-08-471-961-7
; Sequence 7, Application US/08471961
; Patent No. 6100046
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; APPLICANT: GRAY CARY WARE & FREIDENRICH
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/471,961
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-961-7

Query Match 29.5%; Score 1191.5; DB 3; Length 502;
Best Local Similarity 46.0%; Pred. No. 4.3e-107;
Matches 240; Conservative 80; Mismatches 117; Indels 85; Gaps 10;
QY 297 IYLNLSA---KVCAGYHEKRLHLDLPYNTLERPVNLSDPQLQSLFGLTLMQIIDVDE 353
DB 8 IWLALAAALLHVSLOGEFORRLKELVKNYNPLERPVPANDSQPLTVFSLSLQINDVDE 67
QY 354 KNQLLVNWLKLEWDMNLRWNTSDYGGVKDLRIHPHRIKWPDVLMYNSADGFGTGYQ 413
DB 68 KNQLVTNIWLQSWTDHYLQNMNSEYPGVKYRFPDQGIWKPDILLYNSADRFDAFTH 127
QY 414 TNVVRNNGSLVPPGIFKSTCKIDITWPFDDQRCMKFGSWTVDGFDLOLODETG 473
DB 128 TNVLVNASGHQVLPFGIFKSSCYIDVRWPFDDVQCKLKFGSWSGHSLDQMOE--- 184
QY 474 GDTSYVNGEWELLGVPGKRNEIYNCCEPYDITFAIIRRTLYYFNNLIIPCVLI 533
DB 185 ADISSYIPNGEWDLGIPGKRNEKYECCKEYPDVTYVTMRRTLYYGLNLLIPCVLI 244
QY 534 ASWALLGFTLPPSGEKLISGLVTLLSLTVFLNVAETMPATSDAVPL----- 581
DB 245 SALALLVFLLPADSGEKISGLITVLLSLTVFLLVAEIMPATSDSVPLIAQYFASTMIIV 304
QY 582 -----WIRIVFLCWLPIRLMSRPG-----RPLILEPTTP 612
DB 305 GLSVVTVIVLYHHDDPGGKMPKWTIRIILLNCAWFLRMKRPGEKVKRPACQHP-RP 363
QY 613 CSOTSSERKHQILSDVELKERSKSLANVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTV 672
DB 364 CS-----LASVELSAG-----PPTSGNLLY--IGFRGL 392
QY 673 YGQ-----GDGSI-PIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRITQLKRDDE 726
DB 393 EGMHCAPTDSGVYCGRLACSPHDEHLMHGAHPSDGDPLAKILEEVRYIANFRRCQDE 452
QY 727 CNDIANDKFAAMVDRCLIIIFTMEAILATIAVLLSAPHII 768
DB 453 SEVICSEWKPACVDRCLMAFVSFTICTIGILMSAPNFV 494

RESULT 4
US-08-278-635B-8
Sequence 8, Application US/08278635B
Patent No. 5683912
GENERAL INFORMATION:
APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,635B
FILING DATE: 21-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 511 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-278-635B-8

Query Match 28.9%; Score 1168; DB 1; Length 511;
Best Local Similarity 44.2%; Pred. No. 8.5e-105;
Matches 238; Conservative 83; Mismatches 117; Indels 100; Gaps 12;
QY 285 NGUNKHSWIFLLIYLNLSAKVCLAGYHEKRLHLDLPYNTLERPVNLSDPQLQSLFGLT 344
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DB 67 LMOIIDDEKNOLLVTNWLKLEWDMNLRWNTSDYGGVKDLRIHPHRIKWPDVLMYNSA 126
QY 405 DEGFDTGYTNVVRNNGSLVPPGIFKSTCKIDITWPFDDQRCMKFGSWTVDGFDLO 464
DB 127 DEREDATEHTNVLVNYSGSCQYIPPGILKSTCYIDVRWPFDDVQCKLKFGSWTHSGWLI 186
QY 465 DLQLODETDGDISYVNGEWELLGVPGKRNEIYNCCEPYDITFAIIRRTLYYFNNLI 524
DB 187 DLQMLE---ADISNYISNGEWDLGVPGKRNEIYECCKEYPDVTYVTMRRTLYYGL 243
QY 525 NLIIPCVLIASMAALLGFTLPPSGEKLISGLVTLLSLTVFLNVAETMPATSDAVPL--- 581
DB 244 NLIIPCVLIASMAALLGFTLPPSGEKLISGLVTLLSLTVFLNVAETMPATSDAVPLIAQ 303
QY 582 -----WIRIVFLCWLPIRLMSRPG-----RPL 604
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DB 364 SCKY-----SYPKHPSLKNTEM-----NVL-----PG-----H 387
QY 665 NPAFYRTVYG-----QGDD--GSGIPGSTRMPDAVTHHTCIKS--STEYELGLI 710
DB 388 QPSGNNMIYSYHTMENPCCPNNDLGSKSKITCPLSED--NEHVOKKALMDTIPVVKI 445
QY 711 LKEIRFITDQLRKDDCNDIANDKFAAMVDRCLIIIFTMEAILATIAVLLSAPHII 768
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; Sequence 8, Application US/08464258B
; Patent No. 6013766
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACTYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: GRAY CARY WARE & FREIDENRICH LLP
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,258B
; FILING DATE: 06/05/95
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/278,635
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9989
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 511 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-464-258B-8

Query Match 28.9%; Score 1168; DB 3; Length 511;
Best Local Similarity 44.2%; Pred. No. 8.5e-105;
Matches 238; Conservative 83; Mismatches 117; Indels 100; Gaps 12;

QY 285 NGLNKHSHWIFLLIYLNLSAKVCLAGYHEKRLHLDLPYNTLERPVNLSDPLQLSFGIT 344
DB 12 SGLCLWASFLSFF-----KVSQGESQRRYDLLRNRLRPMVNDSPQIVVELQLS 66
QY 345 LMQIIDVDKKNOLLVTNNVWLKLEWDMNLRWNTSDYGVKDLRIPIPHRIWKPDVLYNSA 404
DB 67 LLIQIIDVDKKNOLLVTNNVWLKLEWDMNLRWNTSDYGVKDLRIPIPHRIWKPDVLYNSA 126
QY 405 DEGFDTGTQTNVVRNNGSLVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGFOL 464
DB 127 DERFATFTNVLNVVSGSCQYIPGILKSTCYIDVRWPPFDVQKCDLKFGSWTHSGWLI 186
QY 465 DLQLODETDGDISSVLNGEWELLGVPGRNRIYVNCPEPYIDITFAIIRRRRLTYXFF 524
DB 187 DLQMLE---ADISNYSNGEWDLVGVPGRNELYECKPEYPDVYTTITMRRRLTYXGL 243
QY 525 NLIIPCVLIASMALLGFTLPPDSGKLSGLVTLLSLVFLNVAETMPATSDAVPL--- 581
DB 244 NLLIPCVLISGALLVFLLPADSGEKISGLITVLLSVFLMLVAEIMPATSDSVPLIAQ 303
QY 582 -----WIRIVFLCWLPLWRMSRPG---RPL 604
DB 304 YFASIMVIVGLSVVTVLVLPQHHDPQAGKMPRVVRVILLNWCWFLRMKKGGENIKPL 363

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DB 364 SCKY-----SYPKHHPSLKNTM-----NVL-----PG-----H 387
QY 665 NPAFYRTVYG-----QGDD--GSIGPIGSTMPDPAVTHHTCIKS--STEYELGLI 710
DB 388 QPSNGNMIYSYHTMENPCQPQNNDLGSKSGKITCPLSED--NEHVQKKALMDTIPVIVKI 445
QY 711 LKEIRFITDOLRKDDDECNDIANDMKFAAMVWVDRCLLIIFTMFAILATIAVLLSAPHII 768
DB 446 LEEVOFTIAMRFRKDEGEIECSEKFAAAVDRICLVAFVTFLEICTTILMSAPNFI 503

RESULT 6
US-08-471-961-8
; Sequence 8, Application US/08471961
; Patent No. 6100046
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACTYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: GRAY CARY WARE & FREIDENRICH
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,961
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,635
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 511 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-961-8

Query Match 28.9%; Score 1168; DB 3; Length 511;
Best Local Similarity 44.2%; Pred. No. 8.5e-105;
Matches 238; Conservative 83; Mismatches 117; Indels 100; Gaps 12;

QY 285 NGLNKHSHWIFLLIYLNLSAKVCLAGYHEKRLHLDLPYNTLERPVNLSDPLQLSFGIT 344
DB 12 SGLCLWASFLSFF-----KVSQGESQRRYDLLRNRLRPMVNDSPQIVVELQLS 66
QY 345 LMQIIDVDKKNOLLVTNNVWLKLEWDMNLRWNTSDYGVKDLRIPIPHRIWKPDVLYNSA 404
DB 67 LLIQIIDVDKKNOLLVTNNVWLKLEWDMNLRWNTSDYGVKDLRIPIPHRIWKPDVLYNSA 126
QY 405 DEGFDTGTQTNVVRNNGSLVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGFOL 464
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Db 127 DERFDATEHTNVLVNYSGSCQVIPPGLKSTCYIDVRWPEPVDQCDLKFSGWTHSGWLI 186
QY 465 DLQLODETGGDSSVYNGEWELLVGPGKRNIEYVNCCEPYDITFAIIIRRTLYYFF 524
Db 187 DLOMLE---ADISNYSNGEWDLVGPGKRNIEYVNCCEPYDITFAIIIRRTLYYGL 243
QY 525 NLIIPCVLIASMLLGFLLPPDGSGLKSLGVTLLSLTVFLNNAETMPATSDAVPL--- 581
Db 244 NLLIPCVLISGLALLVFLPADSGEKISIGITVLLSLTVFLLVAEIMPATSDSVPLIAQ 303
QY 582 -----WIRIVFLCWLPPWILRMSRPG---RPL 604
Db 304 YFASIMVIVGLSVVTVLVQLFHHDPQAGKPRVVRVILLNWCWFLRMKKGPIKPL 363
QY 605 ILEFPTPCSDTSSEKHOILSDVELKERSKSLANVLDDIDDFRHNCRPMTPGTGLPH 664
Db 364 SKCY-----SYPKHPSLAKTEM-----NVL-----PG-----H 387
QY 665 NPAFYRTVYG-----QGDD--GSIGPIGSTRMPDAVTHHTCIKS--STEYELGLI 710
Db 388 QPSNGNMIYHTMENPCQPQNDLGSKSGKITCPLSED--NEHVQKKALMDTIPVIVKI 445
QY 711 LKEIRITDQKRDDCEANDKFAAMVVDRLCLIIPTMFAIATIAVLSAPHII 768
Db 446 LEEVOFIAMRFRKQDEGEICSEWFAAAVIDRLCLVAFLEFAIITFTILMSAPNFI 503

RESULT 7
US-08-466-589-8
; Sequence 8, Application US/08466589
; Patent No. 5837489
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClaim
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,589
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: March 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9950
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein

US-08-466-589-8
Query Match 28.7%; Score 1159.5; DB 2; Length 502;
Best Local Similarity 45.1%; Pred. No. 5.6e-104;
Matches 237; Conservative 82; Mismatches 115; Indels 91; Gaps 12;
QY 297 IYLNLSAK---YCLAGYHEKRLHLLDLPYNTLERPVNLNESDPLQSLFGLTLMQIDVDE 353
Db 8 VMLAASLLHVSLOGEFQKLYKLVKNYNPLERPVANDSQPLTVYFSLSLQIMDVDE 67
QY 354 KNQLLTVNWLKLEWDMNLRWNTSDYCGVKDLRPPHRIWKPDVLMYNSADEGDTYQ 413
Db 68 KNOVLTITNWLQMSMDHYLOWNVSEYPGKVTREPDGQIWKPDILLYNSADEREDATPH 127
QY 414 TNVYVNRNNGSCLYVPPGIFKSTCKIDITWFPDDQRCENKFGSWTYDGFQDLQLODETG 473
Db 128 TNVLYNSSGHCOYLPPIKSSCYIDVRWFDPVQHQKLFKFGSWYGGWSLQLOMOE--- 184
QY 474 GDISSYVLNGEWELLVGPGKRNIEYVNCCEPYDITFAIIIRRTLYYFFNLIIPCVLI 533
Db 185 ADISGYPNGEWDLVGIPGKRSERFECCKEYPDVTFTVTRRRRTLYYGLNLLIPCVLI 244
QY 534 ASKALLGFTLPDGSGLKSLGVTLLSLTVFLNNAETMPATSDAVPL----- 581
Db 245 SALALLVFLPADSGEKISIGITVLLSLTVFLLVAEIMPATSDSVPLIAQFASTMIIV 304
QY 582 -----WIRIVFLCWLPPWILRMSRPG---RPLIEFPTTP 612
Db 305 GLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCWFLRMKKGDEKVP-ACQHKORR 363
QY 613 CSDTSSEKHOILSDVELKERSKSLANVLDDIDDFRH-----NCRPMTPGTGLPHNPAF 668
Db 364 CSLASVE-----MSAVAPPPASGNLLY-----IGFRLDGVHCV-TP----- 401
QY 669 YRTVYVGGDGSIGPIGSTRMPDAVTH-----HTCIKSSTEYELGLILKEIRITDQKR 723
Db 402 -----DSGVV-----CGMACSPHDEHLHGPGPEPDGLAKILEEVRIANRFR 449
QY 724 DDECNDIANDKFAAMVVDRLCLIIPTMFAIATIAVLSAPHII 768
Db 450 QDESEAVCSEKFAACVVDRLCLMAFSVTIITIGILMSAPNFV 494

RESULT 8
US-08-700-636-8
; Sequence 8, Application US/08700636
; Patent No. 5910582
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,636
; FILING DATE: 16-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993

TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-487-596-12

Query Match 28.7%; Score 1159.5; DB 4; Length 502;
Best Local Similarity 45.1%; Pred. No. 5.6e-104;

Matches 237; Conservative 82; Mismatches 115; Indels 91; Gaps 12;

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QY 297 IYLNLSAK---VCLAGYHEKRLHLLDPYNTLPRVNLNESDPLQLSGLTLMQIDYDE 353
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      8 VWLALASLLHVSLOGEQFKLYKELVKNYNPLRPVANDSOPLTVEYVLSLQIMDYDE 67
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 354 KQLLVNTVWVKLEWDMNLRWNTSDYGVKDLRIPPHRIWKPVDVLMYNSADEGPDGYQ 413
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      68 KQVLTTNWLQMSWTDHYLQWNVSEYGVKTVRFPDQGIWKPDLILLYNSADERDATFH 127
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 414 TNVVRNNGSLYVPPGIFKSTCKIDITWFFDDQRCCKMKGSTWYDGFOLDLQLODETG 473
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      128 TNVLNSSGHCOYLPPIGFKSSCYIDVRWFFDVQHKCKFGSWSYGSWLDLQMQE--- 184
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 474 GDISSYVLNGWELLGVPGKREIYNGCPPEYIDITFAIIRRTLYFFNLIIPCVLI 533
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      185 ADISYIPNGEWDLVGIPGKRSERYECKEPEYDVTFTVMRRRTLYYGLNLLIPCVLI 244
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 534 ASMLLGTFLPPDSGEKLSGLVTILLSLTVFLNVAETMPATSDAVPL----- 581
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      245 SALALLVFLPADSGEKISLGITVLLSLTVFLNVAETMPATSDSVPLIAQYFASMTIIV 304
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 582 -----WIRIVFLCWLPLWILRMSRPG-----RPLILEFTTP 612
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      305 GLSVVTVTVILOYHHDDPGGKMPKWTRVILLNWCANFLMKRPGEDKVRP-ACQHKORR 363
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      613 CSDTSSERKHQILSDVELKRSKSLANVLNIDDDFRH-----NCRPMTPGTGLPHNPAF 668
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      364 CSLASVE-----MSAVAPPASNGNLLY-----IGFRLDGVHCV-TP----- 401
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      669 YRTVYGGDDGSIGPIGSTRMPDAVTH-----HTCIKSTVEYELGLILKEIRFTDQLRK 723
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      402 -----DSGVV-----CGRMACSPTHDEHLLHGQPPGDPDLAKILEEVRYIANRRC 449
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      724 DDECNDIANDKFAAMVVDRLCLIIFTMFAILATIALLSAPHII 768
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      450 QDESEAVCSEWKFACVVDRLCLMAFSVTIICTIGILMSAPNFV 494
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 12

US-08-771-737-2

; Sequence 2, Application US/08771737

; Patent No. 6323000

; GENERAL INFORMATION:

; APPLICANT: Briggs, Clark A.

; APPLICANT: Gopalakrishnan, Murali

; APPLICANT: McKenna, David G.

; APPLICANT: Monteggia, Lisa M.

; APPLICANT: Roch, Jean-Marc

; APPLICANT: Sullivan, James P.

; APPLICANT: Touma, Edward

; APPLICANT: Abbott Laboratories

; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE

; FILE REFERENCE: 6017 US 01

; CURRENT FILING DATE: 1996-12-20

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FASTSEQ for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 502

; TYPE: PRT

; ORGANISM: homo sapien

US-08-771-737-2

Query Match

Best Local Similarity 28.6%; Score 1155.5; DB 4; Length 502;

; Pred. No. 1.4e-103;

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Matches 236; Conservative 82; Mismatches 116; Indels 91; Gaps 12;
QY 297 IYLNLSAK---VCLAGYHEKRLHLLDPYNTLPRVNLNESDPLQLSGLTLMQIDYDE 353
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      8 VWLALASLLHVSLOGEQFKLYKELVKNYNPLRPVANDSOPLTVEYVLSLQIMDYDE 67
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 354 KQLLVNTVWVKLEWDMNLRWNTSDYGVKDLRIPPHRIWKPVDVLMYNSADEGPDGYQ 413
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      68 KQVLTTNWLQMSWTDHYLQWNVSEYGVKTVRFPDQGIWKPDLILLYNSADERDATFH 127
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 414 TNVVRNNGSLYVPPGIFKSTCKIDITWFFDDQRCCKMKGSTWYDGFOLDLQLODETG 473
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      128 TNVLNSSGHCOYLPPIGFKSSCYIDVRWFFDVQHKCKFGSWSYGSWLDLQMQE--- 184
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 474 GDISSYVLNGWELLGVPGKREIYNGCPPEYIDITFAIIRRTLYFFNLIIPCVLI 533
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      185 ADISYIPNGEWDLVGIPGKRSERYECKEPEYDVTFTVMRRRTLYYGLNLLIPCVLI 244
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 534 ASMLLGTFLPPDSGEKLSGLVTILLSLTVFLNVAETMPATSDAVPL----- 581
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      245 SALALLVFLPADSGEKISLGITVLLSLTVFLNVAETMPATSDSVPLIAQYFASMTIIV 304
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 582 -----WIRIVFLCWLPLWILRMSRPG-----RPLILEFTTP 612
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      305 GLSVVTVTVILOYHHDDPGGKMPKWTRVILLNWCANFLMKRPGEDKVRP-ACQHKORR 363
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      613 CSDTSSERKHQILSDVELKRSKSLANVLNIDDDFRH-----NCRPMTPGTGLPHNPAF 668
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      364 CSLASVE-----MSAVAPPASNGNLLY-----IGFRLDGVHCV-TP----- 401
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      669 YRTVYGGDDGSIGPIGSTRMPDAVTH-----HTCIKSTVEYELGLILKEIRFTDQLRK 723
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      402 -----DSGVV-----CGRMACSPTHDEHLLHGQPPGDPDLAKILEEVRYIANRRC 449
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      724 DDECNDIANDKFAAMVVDRLCLIIFTMFAILATIALLSAPHII 768
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      450 QDESEAVCSEWKFACVVDRLCLMAFSVTIICTIGILMSAPNFV 494
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 13

US-08-496-855A-2

; Sequence 2, Application US/08496855A

; Patent No. 5801232

; GENERAL INFORMATION:

; APPLICANT: Elliot, Kathryn J.

; APPLICANT: Ellis, Steven B.

; APPLICANT: Harpold, Michael M.

; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE

; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: CA

; COUNTRY: U.S.A.

; Zip: 92101-2926

; COMPUTER-READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/496,855A

; FILING DATE: 20-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/149,503

; FILING DATE: 08-NOV-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/028,031

; FILING DATE: 08-MAR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Seidman, Stephanie

REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9369B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 529 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-496-855A-2

Query Match 21.0%; Score 848.5; DB 1; Length 529;

Best Local Similarity 36.7%; Pred. No. 1.1e-73;

Matches 183; Conservative 87; Mismatches 154; Indels 75; Gaps 10;

QY 309 GYH---EKRLHLLDLPYNTLERPVNLNESDPLQSLFGLTLMLQIIDVDEKNQLLVNWLK 365
Db 53 GSHTETEDRLFKHLFRGYNRWARPVPTSDVIVRFGLSAQIIDVDEKNQMTTNWLK 112
QY 366 LEWMDNLRWNTSDYGVKDLRIPPHRIKPKDVLNMSADEGFDGTQYQTNVVRNNGSCL 425
Db 113 QEWSDYKLRNPNADFGNITSLRVPSEMIWIPDIVLYNNADGEFAVTHMTKAHLFSTGTVH 172
QY 426 YVPPGIFKSTCKIDITWFFDDQRCCKMFGSWTYDGFQDLQDQDETGGDISSYVLNGEW 485
Db 173 WVPPIYKSCSIDVTFFPDQCNCKMFGSWTYDRAKIDLEQEQT-VDLKDYWESGEW 231
QY 486 ELGVPCKRNEIYNNCCPEYIDITPAIIRRTLYFFNLIIPCVLIASMLLGTLP 545
Db 232 AIVNATGTYNSKKYDCAEYIPDVTYAFVIRRLPFTYINLIIPCLLSCLTVLVFLPS 291
QY 546 DSCEKLSLGTILLSTLVFLNMVAETMPATSDAVPL----- 581
Db 292 DCGEKITCLISVLLSTVFLNLIIPSTSLVPLIGEYLLFTMFVLSIVITVFLN 351
QY 582 -----WIRIVLCWLPWILRMSRPGRLILEFTTPCSDTSERKHQILSDV 628
Db 352 VHRSPSTHTMPHWRGALLGCVPRWLLMNRPPPPVEL---CHPLRLKLSPSYHWLESNV 408
QY 629 ELKERSKSLANVLIDDDFRHNCR-PMTGP-GTLPHPAFYRTVYGGDDSGISGIGS 686
Db 409 DAEERE-----VVVEEDRWACAGHAPSVGTL-----CSHGLHSGASGPKAE 452
QY 687 TRMPDA---VTHHTCIKSSTEYELGLILKEIRITDQLRKDDCNDIANDKFAAMVDR 743
Db 453 ALLQEGELLSPH-----MOKALEGVHIAHLRSEDADSSVKEDWKYVAMVIDR 502
QY 744 LLIIFTMFAIATIAVLL 762
Db 503 IFLWLFIIVCFLTIGLFL 521

RESULT 14

US-08-487-596-2

Sequence 2, Application US/08487596

Patent No. 6440681

GENERAL INFORMATION:

APPLICANT: Eliot, Kathryn J.

APPLICANT: Ellis, Steven B.

APPLICANT: Harpold, Michael M.

TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND

TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL

TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: CA

COUNTRY: USA

ZIP: 92101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,596
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US94/02447
FILING DATE: 08-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,503
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,154
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9951
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 529 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-487-596-2

Query Match 21.0%; Score 848.5; DB 4; Length 529;

Best Local Similarity 36.7%; Pred. No. 1.1e-73;

Matches 183; Conservative 87; Mismatches 154; Indels 75; Gaps 10;

QY 309 GYH---EKRLHLLDLPYNTLERPVNLNESDPLQSLFGLTLMLQIIDVDEKNQLLVNWLK 365
Db 53 GSHTETEDRLFKHLFRGYNRWARPVPTSDVIVRFGLSAQIIDVDEKNQMTTNWLK 112
QY 366 LEWMDNLRWNTSDYGVKDLRIPPHRIKPKDVLNMSADEGFDGTQYQTNVVRNNGSCL 425
Db 113 QEWSDYKLRNPNADFGNITSLRVPSEMIWIPDIVLYNNADGEFAVTHMTKAHLFSTGTVH 172
QY 426 YVPPGIFKSTCKIDITWFFDDQRCCKMFGSWTYDGFQDLQDQDETGGDISSYVLNGEW 485
Db 173 WVPPIYKSCSIDVTFFPDQCNCKMFGSWTYDRAKIDLEQEQT-VDLKDYWESGEW 231
QY 486 ELGVPCKRNEIYNNCCPEYIDITPAIIRRTLYFFNLIIPCVLIASMLLGTLP 545
Db 232 AIVNATGTYNSKKYDCAEYIPDVTYAFVIRRLPFTYINLIIPCLLSCLTVLVFLPS 291
QY 546 DSCEKLSLGTILLSTLVFLNMVAETMPATSDAVPL----- 581
Db 292 DCGEKITCLISVLLSTVFLNLIIPSTSLVPLIGEYLLFTMFVLSIVITVFLN 351
QY 582 -----WIRIVLCWLPWILRMSRPGRLILEFTTPCSDTSERKHQILSDV 628
Db 352 VHRSPSTHTMPHWRGALLGCVPRWLLMNRPPPPVEL---CHPLRLKLSPSYHWLESNV 408
QY 629 ELKERSKSLANVLIDDDFRHNCR-PMTGP-GTLPHPAFYRTVYGGDDSGISGIGS 686
Db 409 DAEERE-----VVVEEDRWACAGHAPSVGTL-----CSHGLHSGASGPKAE 452
QY 687 TRMPDA---VTHHTCIKSSTEYELGLILKEIRITDQLRKDDCNDIANDKFAAMVDR 743

Db 453 ALLQEGELLSPH-----MOKALEGVHYIADHLRSEDADSSVKEDWKYVAMVIDR 502

QY 744 LCLIIFTMFAILATIALL 762

Db 503 IFLWLFIIIVCFGLTGFL 521

RESULT 15

US-08-660-451A-2
; Sequence 2, Application US/08660451A
; Patent No. 6524789
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 06/07/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9370B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 529 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-660-451A-2

Query Match 21.0%; Score 848.5; DB 4; Length 529;
Best Local Similarity 36.7%; Pred. No. 1.1e-73;
Matches 183; Conservative 87; Mismatches 154; Indels 75; Gaps 10;
QY 309 GYH---EKRLHDLDPNTLERPVNESDPLQLSFGTLQIIDVDEKNQLLVNWLK 365
Db 53 GSHTETEDLFKHLFRGYNRWARPVNTSDVVIVRFGLSIAQLIDVDEKNQMMTTNVWLK 112
QY 366 LEWDMNLRWNTSDYGVKDLRIPPHRIWKPDVLMNSADEGFGDGTOTNVVVRNNGSCL 425
Db 113 QEWSYKLNWNPADFGNTSLRVPSEMIWIPDIVLYNNRADGEFATHMTKALHFTSTGVH 172
QY 426 YVPPGIFKSTCKIDITWFFDDQRCMKFGSWTYDGFQDLQLODETGGDISSYVLNGEW 485
Db 173 WYPPAIYKSSCSIDYTFEFPDQCNCKMKFGSWTYDKAKIDLQMEQT-VDLKDYWESGEW 231

QY 486 ELLGVPGKRNEIYVNCPEPIDITFAIIIRRTTYFFENLIIPCVLITASMALLGFTLPP 545
Db 232 AIVNATGYNSKKYDCCAEIYPDVYAFVIRRLPLFTYINLIIPCLLISCLTVLVYLP 291
QY 546 DSGEKLSLGVITILLSTVFLNVAETMPATSDAVPL----- 581
Db 292 DCGEKITLCISVLLSLTVFLLEIITFIIPSTLVIPLIGEYLLFTWIFVTLSTIVIVVLN 351
QY 582 -----WIRIVFLCWLPMILRMSRPRPLILEFFPTPCSDTSSERKHOILSDV 628
Db 352 VHRSPSTHTPHWVRGALLGCVPRWLLMNRPPVEL---CHPLRLKLSPSYHWLESNV 408
QY 629 ELKERSKSLANVLIDIDDDFRHNCR-PWTPG-GTLPHPAPYRYVGGDDSGSGTSGS 686
Db 409 DAEERE-----VVVEEDRWACAGHVPASVGTL-----CSHGHLHSGASGPKAE 452
QY 687 TRMPDA---VTHHTCIKSTVEYELGLILKEIRFITDOLRKDDCEDNDIAWKAAMVVD 743
Db 453 ALLQEGELLSPH-----MOKALEGVHYIADHLRSEDADSSVKEDWKYVAMVIDR 502
QY 744 LCLIIFTMFAILATIALL 762
Db 503 IFLWLFIIIVCFGLTGFL 521

Search completed: August 13, 2003, 15:43:09
Job time : 25.5314 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:21:20 ; Search time 73.6446 Seconds
(without alignments)
2698.100 Million cell updates/sec

Title: US-09-303-232-2
Perfect score: 4043
Sequence: 1 MKNQLKLTVEVDDDELMLAV.....MFAITATVLLSAPHIIVS 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4014.5	99.3	807	5 Q8T7V5	Q8T7V5 drosophila
2	2388.5	59.1	482	5 Q8T5P5	Q8T5P5 drosophila
3	1988	49.2	545	5 Q9VW19	Q9VW19 drosophila
4	1850	45.8	496	5 Q9XZ13	Q9XZ13 drosophila
5	1625.5	40.2	494	5 Q8T7S2	Q8T7S2 drosophila
6	1622.5	40.1	494	5 Q8T7S3	Q8T7S3 drosophila
7	1620.5	40.1	494	5 Q8T7S1	Q8T7S1 drosophila
8	1611	39.8	523	5 Q8T7R9	Q8T7R9 drosophila
9	1609	39.8	501	5 Q8XZ14	Q8XZ14 drosophila
10	1602	39.6	509	5 Q8T7S0	Q8T7S0 drosophila
11	1502	37.2	391	5 Q9NKD2	Q9NKD2 drosophila
12	1310.5	32.4	554	5 Q9VL79	Q9VL79 drosophila
13	1235	30.5	525	5 Q8IPE2	Q8IPE2 drosophila
14	1186	29.3	273	5 Q9VJT9	Q9VJT9 drosophila
15	1185.5	29.3	502	11 Q9JHD6	Q9JHD6 mus musculus
16	1168	28.9	511	13 Q03481	Q03481 gallus gall

17	1140	28.2	335	5 Q9NKD1	Q9NKD1 drosophila
18	1015	25.1	480	5 Q8I932	Q8I932 caenorhabdi
19	1009.5	25.0	461	5 P91197	P91197 caenorhabdi
20	977	24.2	554	5 Q62083	Q62083 caenorhabdi
21	968.5	24.0	542	5 Q18556	Q18556 caenorhabdi
22	902	22.3	537	5 Q8MUR0	Q8MUR0 apis mellif
23	897	22.2	515	5 Q46133	Q46133 locusta mig
24	888.5	22.0	537	5 Q9U941	Q9U941 myzus persi
25	888	22.0	567	5 Q9VC74	Q9VC74 drosophila
26	883.5	21.9	523	5 Q46128	Q46128 heliothis v
27	882.5	21.8	552	5 P91765	P91765 myzus persi
28	876	21.7	568	5 Q9NFR5	Q9NFR5 drosophila
29	875	21.6	545	5 Q96631	Q96631 heliothis v
30	861.5	21.3	531	5 Q96632	Q96632 heliothis v
31	859	21.2	536	5 Q8T0Y9	Q8T0Y9 alysia cal
32	854	21.1	540	5 Q46134	Q46134 locusta mig
33	854	21.1	595	5 P91764	P91764 myzus persi
34	851	21.0	509	5 Q9NFX8	Q9NFX8 myzus persi
35	849	21.0	497	5 Q46135	Q46135 locusta mig
36	849	21.0	509	5 Q8MM21	Q8MM21 aphid gossy
37	847.5	21.0	512	11 Q91X60	Q91X60 mus musculu
38	843	20.9	533	5 Q8WRS1	Q8WRS1 chilo suppr
39	843	20.9	536	5 Q8T9S0	Q8T9S0 alysia cal
40	840	20.8	783	5 Q9W366	Q9W366 drosophila
41	839	20.8	559	5 Q46132	Q46132 locusta mig
42	837	20.7	517	5 Q96633	Q96633 heliothis v
43	833	20.6	795	5 Q18394	Q18394 drosophila
44	829.5	20.5	219	5 Q8T5F4	Q8T5F4 drosophila
45	827.5	20.5	499	11 Q8VHH6	Q8VHH6 mus musculu

ALIGNMENTS

RESULT 1

Q8T7V5	Q8T7V5	PRELIMINARY;	PRT;	807 AA.
ID	Q8T7V5;			
AC	Q8T7V5;			
DT	01-JUN-2002 (Tremblrel. 21, Created)			
DT	01-JUN-2002 (Tremblrel. 21, Last sequence update)			
DT	01-MAR-2003 (Tremblrel. 23, Last annotation update)			
DE	Nicotinic acetylcholine receptor Dalp5a5 subunit.			
GN	NACR-ALPHA-34E OR NACRALPHA-34E OR BG:DS05899.4 OR BG:DS05899.5 OR CG4498 OR CG16878.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21969411; PubMed=11973307;			
RA	Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;			
RT	"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalp5a5, Dalp5a6 and Dalp5a7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing.";			
RT	Genetics 160:1519-1533(2002).			
RL	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.			
CC	EMBL; DALP5A6 AND DALP5A7, IN DROSOPHILA MELANOGASTER IDENTIFY A FLYBASE; FBGN0028875; NACR-ALPHA-34E.			
DR	InterPro; IPR006201; Neur_chan.			
DR	InterPro; IPR006202; Neur_chan_LBD.			
DR	InterPro; IPR006029; Neu_channel_memb.			
DR	Pfam; PF02931; Neur_chan_LBD; 1.			
DR	Pfam; PF02932; Neur_chan_memb; 1.			
DR	TIGRFAMs; TIGR00860; Lic; 1.			
DR	PROSITE; PS00236; NEUOTR_ION_CHANNEL; 1.			
KW	Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;			
TR	Transmembrane.			
SQ	SEQUENCE 807 AA; 91223 MW; C8B4F6B34287C8C8 CRC64;			

OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RP	[1]
RN	SEQUENCE FROM N.A.
RX	MEDLINE=21969411; PubMed=11973307;
RA	Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT	"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
RT	Dalpa5, Dalpa6 and Dalpa7, in Drosophila melanogaster Identify a
RT	New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
RT	Mediated A-to-I Pre-mRNA Editing.";
RL	Genetics 160:1519-1533(2002).
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR	EMBL; AY036613; AAK67256.1; -.
DR	FlyBase; FBgn0028875; nAChR-alpha-34E.
DR	InterPro; IPR006201; Neur_channel.
DR	InterPro; IPR006202; Neur_chan_LBD.
DR	Pfam; PF02931; Neur_chan_LBD; 1.
DR	PROSITE; PS00236; NEUROTR_IOM_CHANNEL; 1.
DR	Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW	Transmembrane.
KW	SEQUENCE 482 AA; 54445 MW; A4B95B921CA33F05 CRC64;
SQ	Query Match 59.1%; Score 2388.5; DB 5; Length 482;
	Best Local Similarity 98.3%; Pred. No. 1.6e-197;
	Matches 457; Conservative 4; Mismatches 3; Indels 1; Gaps 1;
QY	1 MKNAQLKLTVEDDDELWLAVLRAHCSNFSSTSTRTTSSNQRNQQLTTLPRLSTKH 60
DB	1 MKNAQLKLTVEDDDELWLAVLRAHCSNFSSTSTRTTSSNQRNQQLTTLPRLSTKH 60
QY	61 HSNITASEOHNSQQOEPASKEDVANHGSRNDQOTHLOQLDSSNMLSPKATAAATAAGDEA 120
DB	61 HSNITASEOHNSQQOEPASKEDVANHGSRNDQOTHLOQLDSSNMLSPKATAAATAAGDEA 120
QY	121 TTQOPTNIRLCARRKQRRLRRRRKRPATPNETDIKKQOQLSMPFPKTRKSTDYSTPAAT 180
DB	121 TTQOPTNIRLCARRKQRRLRRRRKRPATPNETDIKKQOQLSMPFPKTRKSTDYSTPAAT 180
QY	181 TSCPATYMQCRASDNFEFPIPSHRDRVSTATFAWLHVLOVLLVLSQWLHVQOORSVL 240
DB	181 TSCPATYMQCRASDNFEFPIPSHRDRVSTATFAWLHVLOVLLVLSQWLHVQOORSVL 240
QY	241 LFRRIASTTAFISYLGSAQAQKNSSSSSS - SSNSNNSSSTQILNGLNKHISWIFLLIYL 299
DB	241 LFRRIASTTAFISYLGSAQAQKNSSSSSS - SSNSNNSSSTQILNGLNKHISWIFLLIYL 300
QY	300 NLSAKVCLAGYHEKRLHLLDPYNTLTERPVLNESDPLQLSFGLTLMQIIDVDEKNQLLY 359
DB	301 NLSAKVCLAGYHEKRLHLLDPYNTLTERPVLNESDPLQLSFGLTLMQIIDVDEKNQLLY 360
QY	360 TNNWLKLEWNDMNLRWNTSDYGGYKDLRIPPHRLTWKPDVLMYNSADEGFDGTYQTNVVVR 419
DB	361 TNNWLKLEWNDMNLRWNTSDYGGYKDLRIPPHRLTWKPDVLMYNSADEGFDGTYQTNVVVR 420
QY	420 NNGSCLVYPGIFKSTCKIDITWPFDDQRCMKFGSWTYDGFQL 464
DB	421 NNGSCLVYPGIFKSTCKIDITWPFDDQRCMKFGSWTYDGFQV 465

RESULT 3	
Q9VW19	
ID	Q9VW19
AC	PRELIMINARY; PRT; 545 AA.
DT	Q9VW19;
DT	01-MAY-2000 (TREMblrel. 13, Created)
DT	01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT	01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE	CG32538 protein.
GN	NACR-ALPHA-18C OR CG8082 OR CG8109 OR CG32538.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

RESULT 6

Q8T7S3 PRELIMINARY; PRT; 494 AA.

AC Q8T7S3; 729 DIANDKFAAMVVDRLCLIFTMFAITATVLLSAPHIIV 769
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor Dalpha6 subunit variant type I.
GN NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21969411; PubMed=11973307;
RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
RT Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
RT Mediated A-to-I Pre-mRNA Editing.";
RL Genetics 160:1519-1533(2002).
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF321445; AAM13392.1; -;
DR FlyBase; FBgn0032151; nacr-alpha-30D.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_chan_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 494 AA; 56095 MW; B46BEDA63A92942 CRC64;

Query Match 40.1%; Score 1622.5; DB 5; Length 494;
Best Local Similarity 61.2%; Pred. No. 2.3e-131;
Matches 319; Conservative 46; Mismatches 77; Indels 79; Gaps 7;

QY 291 SWIFLLIYLNLSAKVCLAGYHEKRLHDLDPYNTLERPVNLSDFGLTLMOIID 350
DB 10 SLFVLLIFLAIKESC-QGPKHKLNLHLLSTYNTLERPVANSEPLEVKFGLTLQOIID 68
QY 351 VDEKNOLLVTNWKLEWDMNLNWTSDYGGVKDLRIPHRWKPDVLMYNSADGFGD 410
DB 69 VDEKNOLLITNWLNLWENDYNLRWNETEYGGVKDLRITPNKWLKPDVLMYNSADGFGD 128
QY 411 TYOTNVVVRNNGSCLVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGFOLDLQLOD 470
DB 129 TYHTNIVVHNGSCLVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGFOLDLQLOD 188
QY 471 ETGGDISVYLVNGEWELLVGPKRNIYVNCCEPEYDITFAIIIRRTLYFFNLIIPC 530
DB 189 EDGGDISFITNGEWYLLAMPKKNITVYACCEPEYVDITFTIQRIRRTLYFFNLIIPC 248
QY 531 VLIASMAILGFTLPDPSGKLSLGVITLLSLTVFLNVAETPATSDAVPL----- 581
DB 249 VLISSMAILGFTLPDPSGKLSLGVITLLSLTVFLNVAETLPQVSDAIPLLGTYFNCIM 308
QY 582 -----WIRIVFLCWLPLWLRMSRPRPLILEFFTPPC 613
DB 309 FWVASSVLTVVVLYNHRHTADITHMPPIKSVFLQWLPLWLRMRGPRGKI----- 359
QY 614 SDTSSEKQIOLS-----DVELKERSKSLANVLDIDDDFRNCRPWTGGTLPHPNPFY 569
DB 360 -----TRKTLILSNRMKELKERSKSLANVLDIDDDFRHTI----- 398
QY 670 RTVYGGDDSGSIGPIGSTRPAV-THTTCIKSSTEYELGLILKEITFITDOLRKDECN 728
DB 399 -----SGSQTAGSSASFGRPTVEEHHTAI-GCNKDLHLILKELQFITARMKADDEA 452

RESULT 7

Q8T7S1 PRELIMINARY; PRT; 494 AA.

AC Q8T7S1; 729 DIANDKFAAMVVDRLCLIFTMFAITATVLLSAPHIIV 769
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor Dalpha6 subunit variant type
DE III.
GN NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21969411; PubMed=11973307;
RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
RT Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
RT Mediated A-to-I Pre-mRNA Editing.";
RL Genetics 160:1519-1533(2002).
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF321447; AAM13394.1; -;
DR FlyBase; FBgn0032151; nacr-alpha-30D.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_chan_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 494 AA; 56113 MW; 48327537229573FF CRC64;

Query Match 40.1%; Score 1620.5; DB 5; Length 494;
Best Local Similarity 61.0%; Pred. No. 3.5e-131;
Matches 318; Conservative 49; Mismatches 75; Indels 79; Gaps 7;

QY 291 SWIFLLIYLNLSAKVCLAGYHEKRLHDLDPYNTLERPVNLSDFGLTLMOIID 350
DB 10 SLFVLLIFLAIKESC-QGPKHKLNLHLLSTYNTLERPVANSEPLEVKFGLTLQOIID 68
QY 351 VDEKNOLLVTNWKLEWDMNLNWTSDYGGVKDLRIPHRWKPDVLMYNSADGFGD 410
DB 69 VDEKNOLLITNWLNLWENDYNLRWNETEYGGVKDLRITPNKWLKPDVLMYNSADGFGD 128
QY 411 TYOTNVVVRNNGSCLVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGFOLDLQLOD 470
DB 129 TYHTNIVVHNGSCLVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGFOLDLQLOD 188
QY 471 ETGGDISVYLVNGEWELLVGPKRNIYVNCCEPEYDITFAIIIRRTLYFFNLIIPC 530
DB 189 EDGGDISFITNGEWYLLAMPKKNITVYACCEPEYVDITFTIQRIRRTLYFFNLIIPC 248
QY 531 VLIASMAILGFTLPDPSGKLSLGVITLLSLTVFLNVAETPATSDAVPL----- 581
DB 249 VLISSMAILGFTLPDPSGKLSLGVITLLSLTVFLNVAETLPQVSDAIPLLGTYFNCIM 308
QY 582 -----WIRIVFLCWLPLWLRMSRPRPLILEFFTPPC 613
DB 309 FWVASSVLTVVVLYNHRHTADITHMPPIKSVFLQWLPLWLRMRGPRGKI----- 359

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Qy 614 SPTSSERKHQILS-----DVELKERSKSLANVLNVDIIDDHFRHNCRPMPTGGTLPHPNPAFY 669
Db 360 -----TRKTIILSNRMKEKLSKSLANVLNVDIIDDHFRHTI-----398
Qy 670 RTVYGQDDGSGIGSTRMPDAV-THTCTIKSSSTEVELGLILKEIRFITDOLRKKDECN 728
Db 399 -----SGSQTAGSSASGFRPTTVEEHHTAI-GCNHKDLHLILKELOFITARMRKADDEA 452
Qy 729 DIANDWFAAMVDRCLLIIFTMFAILATIAVLSAPHIIV 769
Db 453 ELIGDWFAAMVDRFCLVFTLTITATVTVLSAPHIIV 493

RESULT 8
Q8T7R9
ID 08T7R9 PRELIMINARY; PRT; 523 AA.
AC
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor Dalpha6 subunit variant type V.
GN NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
OS Drosophila melanogaster (Fruit fly)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21969411; PubMed=11973307;
RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
RT Dalphas, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
RT Mediated A-to-I Pre-mRNA Editing.";
RL Genetics 160:1519-1533(2002).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF321449; AAMI3396.1;
DR FlyBase; FBgn0032151; nACR-alpha-30D.
DR InterPro; IPR006201; Neur_chan_memb.
DR InterPro; IPR006202; Neur_chan_LBD.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_LBD; 1.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 523 AA; 59110 MW; 1C200AF74F87F841 CRC64;

Query Match 39.8%; Score 1611; DB 5; Length 523;
Best Local Similarity 58.2%; Pred. No. 2.5e-130;
Matches 320; Conservative 46; Mismatches 76; Indels 108; Gaps 7;

Qy 291 SWIFLLIYNLSAKVCLAGYHEKRLHLLDLPYNTLPRVLNESDPLQSLFGLTLMQIID 350
Db 10 SLFVLLIPLAIKESQ-QGPKHLLNLLSTYNTLPRVANESEPLEVKEFGLTQQIID 68

Qy 351 VDEKNOLLVTNWLKLENDNMLRNWNTSDYGVGKDLRIPPHRWKPDVLMYNSADEGFDG 410
Db 69 VDEKNQILTTNWLNLENDNMLRNWNETEYGVGKDLRITPNKLRKPDVLMYNSADEGFDG 128

Qy 411 TYQTNVVRNNGSLYVPPGIFKSTCKIDITWFFDDQRCMKFGSWTYDGFOLDLQID 470
Db 129 TYHNVVVRNNGSLYVPPGIFKSTCKIDITWFFDDQRCMKFGSWTYDGNQLDLVNS 188

Qy 471 ETGGDISYVLNGEWELGVPGKRNHYYNCCPEYIDITFAIIRRTLYFFNLIIPC 530
Db 189 EDGGLSDFITNGEWYLLAMPKKNKTIYACCPYVDITFTIQIRRTLYFFNLIIPC 248

Qy 531 VLIASMLLGLTLPDSDGKLSLGTIILSLTVFLNVAESMPTTSDAVPLIGVITLLSL 308
Db 582 -----WIR 584
Qy 309 TVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLTVVVLNHHRTADHEMPWIK 368
Qy 585 IVFLCWLPLWILMSRPGRLILEPTTPCSDTSSERKHQILS-----DVELKERSKSLLA 640
Db 369 SVFLQWLPLWILMRGPRKI-----TRKTIILSNRMKELEKERSKSLLA 414
Qy 641 NVLDIDDDHFRHNCRPMPTGGTLPHPNPAFYRTVYGQDDGSGIGSTRMPDAV-THTCTI 699
Db 415 NVLDIDDDHFRHTI-----SGSQTAGSSASGFRPTTVEEHHTAI 453
Qy 700 KSSTEYELGLILKEIRFITDOLRKKDECNDIANDWFAAMVDRCLLIIFTMFAILATIA 759
Db 454 -GCNKHDLHLILKELQFITARMRKADDEAELIGDWFAAMVDRFCLVFTLTITATV 512
Qy 760 VLSAPHIIV 769
Db 513 VLSAPHIIV 522

RESULT 9
Q9XZ14
ID 09XZ14 PRELIMINARY; PRT; 501 AA.
AC
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Putative nicotinic acetylcholine receptor alpha 7-2 subunit.
OS Heliothis virescens (Noctuid moth) (Owllet moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Heliothis.
OX NCBI_TaxID=7102;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte T., Oellers N., Adamczewski M.;
RT "Putative alpha subunits of insect nicotinic acetylcholine receptors
RT more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than
RT to other insect nicotinic acetylcholine receptor alpha subunits.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF143847; AAD32698.1;
DR InterPro; IPR006201; Neur_chan_memb.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_chan_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 501 AA; 56704 MW; 43CB0DC3960C78AB CRC64;

Query Match 39.8%; Score 1609; DB 5; Length 501;
Best Local Similarity 60.8%; Pred. No. 3.5e-130;
Matches 319; Conservative 57; Mismatches 65; Indels 84; Gaps 10;

Qy 295 LLIYLNLSAKVCLAGYHEKRLHLLDLPYNTLPRVLNESDPLQSLFGLTLMQIIDVDEK 354
Db 10 LLLLPVSEQ-----GPHEKRLNLLNALLNYNTLPRVANESEPLEVKEFGLTQQIIDVDEK 65

Qy 355 NQLLVTVNWLKLENDNMLRNWNTSDYGVGKDLRIPPHRWKPDVLMYNSADEGDTYQT 414
Db 66 NOLLITNLSLEWYNDYLNLRWNSDYGVGKDLRITPNKLRKPDVLMYNSADEGDTYQT 125

Qy 415 NVVVRNNGSLYVPPGIFKSTCKIDITWFFDDQRCMKFGSWTYDGFOLDLQIDETGG 474
Db 126 NVVVRSGSLYVPPGIFKSTCKIDITWFFDDQRCMKFGSWTYDGNQLDLVLEKAGG 185

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Db 129 TYHTNIVKHNSCLYVPPGIFKSTCKIDITWFPDDQHCCKMFGSWTYDGNQLDLVLS 188
QY 471 ETGGDISSVLVNGEWELGV-PGK-----RNEIYYNCCPPYDITFAII 515
Db 189 EDGGLSDFITNGEWLVYHAGKEEYDSLRLPRTICRYHLYYT-NSSPYI----- 239
QY 516 RRTLYFFNLIIPCVLIASM-----ALLGFTLPDPSGE----- 549
Db 240 ----ILFFQFN-----CAMCANLIDGPTGLHIAAGFRETADAGNYTIINSISKPCRRVHA 292
QY 550 ----KLSLG-----VTILSLTVFLNKNVAETMPA 574
Db 293 DNVGCCSVRYHTILKRYSLKYPGRTIDHYQCRABRVTLISLTVFLNVAETLPQ 352
QY 575 TSDAVPL-----WIRIVFLCWLWILRM 597
Db 353 VSDAIPLLGTYFCINFWVSSVLTVVVLYVNYHRTADIHMPWIKSVFLQWLWILRM 412
QY 598 SRPGRPLILEPTTPCSDTSSERKHOILS-----DVELKERSKSLANVLDDDFRHC 653
Db 413 GRPGRKI-----TRKTILLSNRKMKELKERSKSLANVLDDDFRHTI 458
QY 654 RPTWGGTLPHNPAFYRTVYGGDGSIGPGICSTMPDAV-THHTCIKSSTYEYGLLILK 712
Db 459 -----SGSQTAGSSASFGRTTVEHHTAI-GCNHKLHLILK 496
QY 713 EIRFITDQLRKDDCCNDIANDKFAVMYVDRCLLIIFTMFAITATIAVLISAPHIIV 769
Db 497 ELQFITARMKADDEALIGDKWFAVMYVDRCLLIIFTIAIVTVLLSAPHIIV 553
RESULT 13
Q8IPE2
ID Q8IPE2 PRELIMINARY; PRT; 525 AA.
AC Q8IPE2
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE CG4128-PC.
GN NACRALPHA-30D.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA April J.F., Adayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.H.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celnik S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Ananides P.G., Brandon R.C., Rogers Y.,
RA Banson J., An H., Baldwin D., Banson J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattel B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.I., Bergman C., Bernman B., Carlson J.W., Celnik S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Flybase:
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003626; AAN10709.1;
SQ SEQUENCE 525 AA; 60135 MW; CF95283C56EA90A9 CRC64;

Query Match 30.5%; Score 1235; DB 5; Length 525;
Best Local Similarity 47.5%; Pred. No. 7.4e-98;
Matches 270; Conservative 53; Mismatches 103; Indels 142; Gaps 15;
QY 291 SWIFLLIYLNLSAKVCLAGYHEKRLHLLDLPYNTLRLPVLNESPLOLSFGLTLMOIID 350
Db 10 SLFVLLIFLAIKESC-OGPHEKRLNHLSTYNTLRLPVLNESPLOLSFGLTLMOIID 68
QY 351 VDEKNQLLVNWKLEWNNMLRWNTSDYGGVKDLRIPPHRIKRPDVLNYSADGDFDG 410
Db 69 VDEKNQLLVNWKLEWNNMLRWNTSDYGGVKDLRIPPHRIKRPDVLNYSADGDFDG 128
QY 411 TYOTNVVNRNGSCLYVPPGIFKSTCKIDITWFPDDQHCCKMFGSWTYDGNQLDLVLS 470
Db 129 TYHTNIVKHNSCLYVPPGIFKSTCKIDITWFPDDQHCCKMFGSWTYDGNQLDLVLS 188
QY 471 ETGGDISSVLVNGEWELGV-PGK-----RNEIYYNCCPPYDITFAII 515
Db 189 EDGGLSDFITNGEWLVYHAGKEEYDSLRLPRTICRYHLYYT-NSSPYI----- 239

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OY 516 RRTLYEFNLIIPCVLISM-----ALLGFTLPDPDSCEKLS----- 552
Db 240 ---ILFFQFN---CAMCANLIDGPTGLHIAAGFRETDAGRNTYTIINSKPCRRVHA 292
OY 553 -----LGVTI-----LLSLTVFLNVA 569
Db 293 DNVGCCSYRTHYTHILKRSYKUGPIGHTIDHYHQCRAESTYFNCIMFWASSVVLTVV 352
OY 570 ---ETMPATSDAVPLWIRIVFLCWLPLWLRMRPRGLPILFPTTPCSDTSSERKHQILS 626
Db 353 LNYHRTADIHEMPWPWKSFLVFLWPLWLRMRGRKTI-----TRKTILLS 398
OY 627 ---DVELKRSKSLANVLIDDDPHRNCPRMTPPGTLPHPAFYTVYVGGDDGSIG 682
Db 399 NRMKELELKRSKSLANVLIDDDFRHTI-----SGSQTAIG 437
OY 683 PIGSTRMPDAY-THTCTIKSSTVEYELGLILKEIRFITDOLRDKDCNDIANDWKFAMV 741
Db 438 SSASFGRPRTVEEHTAI-GCNKDLHLILKELOFITARMKRKADDEALIGDWKFAAMV 496
OY 742 DRLCLIIPTFAILATVLSAPHIIV 769
Db 497 DRFCILVETFTIATVTLVSAPHIIV 524

RESULT 14
O9VJT9 PRELIMINARY; PRT; 273 AA.
AC O9VJT9
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE CG4498 protein.
GN NACR-ALPHA-34E OR NACRALPHA-34E OR BG:DS05899.4 OR BG:DS05899.5 OR
OS CG4498 OR CG16878.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

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RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector R., Turner E., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattel B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome."
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome."
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RN Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AE003642; AAF53374.2;
DR HSSP; P58154; 119B.
DR FlyBase; FBgn028875; nACR-alpha-34E.
DR InterPro; IPR008201; Neur_chan.
DR InterPro; IPR006029; Neur_chan_LBD.
DR Pfam; PF02931; Neur_chan_memb.
DR Pfam; PF02932; Neur_chan_LBD; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
SQ SEQUENCE 273 AA; 31655 MW; CA95F19953E37248 CRC64;
Query Match 29.3%; Score 1186; DB 5; Length 273;
Best Local Similarity 57.2%; Pred. No. 5e-94;
Matches 243; Conservative 13; Mismatches 17; Indels 152; Gaps 7;
Oy 346 MQIIDVDEKNOLLVTNVWLKLEWMDMLRWNTSYGGVKDLRIIPHRITWKPDVLMYNSAD 405
Db 1 MQIIDVDEKNOLLVTNVWLKLEWMDMLRWNTSYGGVKDLRIIPHRITWKPDVLMYNSAD 60
Oy 406 EGPDTGTQTNVVRNNGSCLVPPGIFKSTCKIDITWPPDDQCEMKFGSWTYDGFOLD 465
Db 61 EGPDTGTQTNVVRNNGSCLVPPGIFKSTCKIDITWPPDDQCEMKFGSWTYDGFV- 119
Oy 466 LQLODEGTGDISYVLNGEWELLGVPGKRNIYYNCCPEPIDITFAIIIRRTLYFPFN 525
Db 120 -----W--FSPVPGKRNIYYNCCPEPIDITFAIIIRRTLYFPFN 158

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OY 526 LIIPCVLIASALLGFTLPDPSGEKLSGLGVTILLSLVFLNVAETMPATSDAVPLMIRI 585
DB 159 LIIPCVLIASALLGFTLPDPSGEKLSGLT-----YFNCIMFMVASSVSTI----- 205
OY 586 VFLCWLWILRMSRPGRLILEPTTPCSDTSSEKHKQILSDVELKERSKSLANVLDI 645
DB 206 -----LILNY----- 210
OY 646 DDDFRHNCRPMTEGTLPHNPAFYRTVYVGDDGSGIGSTRMPDAVTHHTCIKSSTEY 705
DB 211 -----HH-----RNADTH 218
OY 706 ELGLILKEIRFTDQRLKDECDNDIANDWKFAMVVDRLCLIIFTMFATIAVLISAP 765
DB 219 EM-----SEWLKDDCEDNDIANDWKFAMVVDRLCLIIFTMTIATIAVLISAP 268
OY 766 HIIVS 770
DB 269 HIIVS 273

RESULT 15
O9JHD6 PRELIMINARY; PRT; 502 AA.
ID O9JHD6;
AC Q9JHD6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor subunit alpha 7.
GN CHRNAT7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/21bg;
RX MEDLINE=97189245; PubMed=9037516;
RA Stitzel J.A.; Farnham D.A.; Collins A.C.;
RT "Linkage of strain-specific nicotinic receptor alpha 7 subunit
restriction fragment length polymorphisms with levels of alpha-
bungarotoxin binding in brain.";
RL Brain Res. Mol. Brain Res. 43:30-40(1996).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/21bg;
RA Stitzel J.A.;
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF225980; AAF35885.1;
DR MGD; MGI:99779; Chrna7.
DR InterPro; IPR006201; Neur_Channel.
DR InterPro; IPR008202; Neur_Channel_LBD.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_LBD; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_IOM_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 502 AA; 56617 MW; C9353E5136D620E3 CRC64;

Query Match 29.38; Score 1185.5; DB 11; Length 502;
Best Local Similarity 46.68; Pred. No. 1.3e-93;
Matches 243; Conservative 79; Mismatches 115; Indels 85; Gaps 12;

OY 297 IYLNLSA---KVCILAGVYHKKRLHLLDLPYTLRPPVNLNEDPLQLSGLTLMQIIDVDE 353
DB 8 IWLALAAALLHVSLOGEFQRLYKELVKNPLRPNVANDSQPLTVYVFSLSLIQIMDVDE 67
OY 354 KQLLVTVNWKLWMDMLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413
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DB 68 KNOVLTNTNWLQMSWTDHYLQNNMSEYPGVKNVRFPDQGIWKPDILLYNSADERDATFH 127
OY 414 TNVVRNNGSLVYPPGIFKSTCKIDITWFPDDQRCMEKFGSWTYDGFOLDLQLODETG 473
DB 128 TNVLVNASGHCOYLPQGIKFSYCIDVRWFPDDQCKLFGSGWSYGLDLOMQE--- 184
OY 474 GDISSYVLNGEWELLLGVPGRKNEYIYNCCEPEYIDITFAIIIRRTLYYFNLIPCVLI 533
DB 185 ADISSYIPNGEWDLMGIPGRNKEFYECCKEYPDVTYVTVMRRRTLYYGLNLLIPCVLI 244
OY 534 ASMALLGFTLPDPSGEKLSGLGVTILLSLVFLNVAETMPATSDAVPL----- 581
DB 245 SALALLVFLLPADSGEKISLIGITVLLSLVFLMLLVAEIMPATSDVPLIAQYFASTMIIV 304
OY 582 -----WIRIVFLCWLPLILRMSRPG-----RPLILEFFPTP 612
DB 305 GLSVVTVIVLYRHHHPDGGKMPKWTIRIILNKCANFLMKRFGEDKVRPACQHKPRR- 363
OY 613 CSDTSSEKHKQILSDVELKERSK-SLLANVLDIDDDFR-----HNCRPMTPGGTLPHNPA 667
DB 364 CS-----LASVELSAGAGPPSSNGNLLYI--GFRGLEGMHCAP--TP----- 401
OY 668 FYRTVYCGDDGSI-GPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFTDQRLKDD 726
DB 402 -----DSGVVCGRLACSPTHDEHLMHGTHPSDGDPLAKILEEVRYIANRFRCODE 452
OY 727 CNDIANDWKFAMVVDRLCLIIFTMFATIAVLISAPHII 768
DB 453 SEVICSEWKFAACVVDRLCLMAFSVFTIICIGILMSAPNEV 494
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Search completed: August 13, 2003, 15:29:07

Job time : 76.6446 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:14:55 ; Search time 16.1234 Seconds
(without alignments)
2245.843 Million cell updates/sec

Title: US-09-303-232-2
Perfect score: 4043
Sequence: 1 MRNAQLKTEVDDELWLAV.....MFAILATIAVLSAPHIIVS 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1182.5	29.2	502	1	ACH7_MOUSE
2	1179.5	29.2	502	1	ACH7_CHICK
3	1173.5	29.0	502	1	ACH7_RAT
4	1159.5	28.7	502	1	ACH7_HUMAN
5	1157	28.6	499	1	ACH7_BOVIN
6	1104	27.3	498	1	ACH1_CAEEL
7	888	22.0	567	1	ACH1_DROME
8	886	21.9	516	1	ACH1_MANSE
9	873	21.6	557	1	ACH1_SCHGR
10	848.5	21.0	529	1	ACH2_HUMAN
11	845	20.9	503	1	ACH3_HUMAN
12	843.5	20.9	576	1	ACH2_DROME
13	840	20.8	521	1	ACH3_DROME
14	838	20.7	528	1	ACH2_CHICK
15	827.5	20.5	456	1	ACHA_CHICK
16	827.5	20.5	496	1	ACH3_CHICK
17	827	20.5	511	1	ACH2_RAT
18	823	20.4	499	1	ACH3_RAT
19	820.5	20.3	495	1	ACH3_BOVIN
20	820.5	20.3	512	1	ACH3_CARAU
21	815.5	20.2	519	1	ACH4_DROME
22	805	19.9	498	1	ACH4_DROME
23	803	19.9	494	1	ACH6_CHICK
24	801	19.8	457	1	ACHA_BOVIN
25	799	19.8	494	1	ACH6_HUMAN
26	797	19.7	457	1	ACHA_MOUSE
27	794.5	19.7	457	1	ACH2_XENLA
28	792.5	19.6	493	1	ACH6_RAT
29	791.5	19.6	538	1	ACH8_CAEEL
30	789	19.5	457	1	ACHA_RAT
31	789	19.5	470	1	ACHP_CHICK
32	787	19.5	491	1	ACHN_CHICK
33	786.5	19.5	456	1	ACHA_BRARE

34	785	19.4	461	1	ACHA_TORMA	P02711	torpedo mar
35	783	19.4	495	1	ACHN_RAT	P12392	rattus norv
36	782.5	19.4	500	1	ACHN_RAT	P12390	rattus norv
37	782	19.3	502	1	ACHN_HUMAN	P17787	homo sapien
38	780	19.3	482	1	ACHA_HUMAN	P02708	homo sapien
39	780	19.3	627	1	ACH4_HUMAN	P43681	homo sapien
40	779.5	19.3	622	1	ACH4_CHICK	P09482	gallus gall
41	779.5	19.3	461	1	ACHA_TORCA	P02710	torpedo cal
42	773.5	19.1	457	1	ACH1_XENLA	P22456	xenopus lae
43	772	19.1	464	1	ACHO_RAT	P12391	rattus norv
44	769.5	19.0	459	1	ACHN_CARAU	P19370	carassius a
45	768	19.0	630	1	ACH4_RAT	P09483	rattus norv

ALIGNMENTS

RESULT 1
ACH7_MOUSE
ID ACH7_MOUSE STANDARD; PRT; 502 AA.
AC P49582;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
GN CHRNA7 OR ACRA7
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Brain;
RX MEDLINE=95324936; PubMed=7601470;
RA Orr-Urtreger A., Seldin M.F., Baldini A., Beaudet A.L.;
RT "Cloning and mapping of the mouse alpha 7-neuronal nicotinic
acetylcholine receptor.";
RL Genomics 26:399-402(1995).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
MEMBRANE.
CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

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EMBL; L37663; AAC42053.1; -
PIR; A57175; A57175.
MGD; MGI:99779; Chna7.
InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006201; Neur_channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PRO0252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUOTR_ION_CHANNEL; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
Transmembrane; Multigene family.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 502 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT DOMAIN 23 230 ALPHA-7 CHAIN.
FT EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 231 255 POTENTIAL.
FT TRANSMEM 262 280 POTENTIAL.
FT TRANSMEM 296 317 POTENTIAL.
FT DOMAIN 318 469 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 470 490 POTENTIAL.
FT DISULFID 150 164 BY SIMILARITY.
FT DISULFID 212 213 ASSOCIATED WITH RECEPTOR ACTIVATION
FT (BY SIMILARITY).
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 502 AA; 56631 MW; C9312E5226D120E3 CRC64;

Query Match 29.2%; Score 1182.5; DB 1; Length 502;
Best Local Similarity 45.8%; Pred. No. 2.8e-75;
Matches 239; Conservative 80; Mismatches 118; Indels 85; Gaps 10;

QY 297 IYLNLSA---KVLGAGYHEKRLHLLDPYNTLPRVPLNESDPLQSLFGLIMLIQIDYDE 353
DB 8 IWLALAAALLHVSQGEFQRLYKELVKNYNPLERPVANDSQPLVYFSLQLQIMDYDE 67
QY 354 KNOVLTVNWLKLENDNMLRNTSDYGVKDLRTPPHRIWKPDVLMYNSADEGFGTYQ 413
DB 68 KNOVLTVNWLKLENDNMLRNTSDYGVKDLRTPPHRIWKPDVLMYNSADEGFGTYQ 127
QY 414 TNVVRNNGSCLYVPPGIFKSTCKIDITWFFDDQRCQEMKFGSWTYDGFQDLQLODETG 473
DB 128 TNVLRNAGHCQYLPPIGIFKSTCKIDITWFFDDQRCQEMKFGSWTYDGFQDLQLODETG 184
QY 474 GDISSVYLVNGEWELGVGCKRNEIYNNCPPEYIDITFAIIRRTLYFFNLIIPCVLI 533
DB 185 ADISSYIFNGEWMGLGIFGCKRNEIYNNCPPEYIDITFAIIRRTLYFFNLIIPCVLI 244
QY 534 ASMALIGETLPDSEKISLGVITLLSLTVFLNVAETMPATSDAVPL----- 581
DB 245 SALALVFLPADSEKISLGVITLLSLTVFLNVAETMPATSDVPLIAYFASTMIIV 304
QY 582 -----WIRIVLCWLPWILMRSPG-----RPLILEFPPTP 612
DB 305 GLSVVTVTVILRYHHDPDGGKMPKWTIRILLNCAWFLMKRPGEDKVRPACQHKPR- 363
QY 613 CSDTSSERKHQILSDVELKRSKSLANVLIDDDFRHNCRPMPGGLPHNPAFYRT 672
DB 364 CS-----LASVELSAGAG-----PPTSNGNLV--IGFRGL 392
QY 673 YGQ-----GDGSI-GPIGSTRMPDAVTHHTCIKSTYEYELGLILKEIRFTDQLRKDE 726
DB 393 EGMHCAPTDSGVCCRLACSPHDEHLMHGTHPSDGDPLAKILEEYRIANRRCQDE 452
QY 727 CNDIANDKFRAMVVDRLCLIFTMFAITLAVLLSAPHII 768
DB 453 SEVICSEKFAACVVDRLCLMAFSVFTICTIGILMSAPNFV 494

RESULT 2
ACH7_CHICK
ID ACH7_CHICK STANDARD; PRT; 502 AA.
AC P22770;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91097796; PubMed=1702646;
RA Couturier S., Bertrand D., Matter J.M., Hernandez M.C., Bertrand S.,
RA Millar N., Valera S., Barks T., Ballivet M.,
```

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RT "A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is
RT developmentally regulated and forms a homo-oligomeric channel blocked
RL by alpha-BTX.";
RN Neuron 5:847-856(1990).
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90315158; PubMed=2369519;
RA Schoeffer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.;
RT "Brain alpha-bungarotoxin binding protein cDNAs and MABs reveal
RT subtypes of this branch of the ligand-gated ion channel gene
RT superfamily.";
RL Neuron 5:35-48(1990).
RP SEQUENCE OF 1-18 FROM N.A.
RC STRAIN=White leghorn; TISSUE=Erythrocyte;
RX MEDLINE=93049204; PubMed=1425587;
RA Matter-Sadzinski L., Hernandez M.C., Rostocil T., Ballivet M.,
RA Matter J.M.;
RT "Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor
RT promoter develops during morphogenesis of the central nervous
RL system.";
RL EMBO J. 11:4529-4538(1992).
RP SEQUENCE OF 24-47.
RC TISSUE=Brain;
RX MEDLINE=85270494; PubMed=3860855;
RA Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A.,
RA Ray N., Raftery M.A.;
RT "Brain and muscle nicotinic acetylcholine receptors are different but
RT homologous proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
RN [5]
RP MUTAGENESIS OF LEU-270.
RX MEDLINE=92049732; PubMed=1719423;
RA Recaf F., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C.,
RA Hussy N., Bertrand S., Ballivet M., Changeux J.-P.;
RT "Mutations in the channel domain alter desensitization of a neuronal
RT nicotinic receptor.";
RL Nature 353:846-849(1991).
RN [6]
RP MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC.
RX MEDLINE=93024917; PubMed=1383829;
RA Galzi J.-L., Devillers-Thiery A., Hussy N., Bertrand S.,
RA Changeux J.-P., Bertrand D.;
RT "Mutations in the channel domain of a neuronal nicotinic receptor
RT convert ion selectivity from cationic to anionic.";
RL Nature 359:500-505(1992).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DEVELOPMENTAL STAGE: ALPHA-7 TRANSCRIPTS TRANSCIENTLY ACCUMULATE
CC IN THE DEVELOPING OPTIC TECTUM BETWEEN E5 AND E16.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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CC -----
DB EMBL; X52295; CAA36543.1; -.
DR EMBL; X68246; CAA48317.1; -.
DR EMBL; X68586; CAA48576.1; -.
DR PIR; JN0113; JN0113.
DR PDB; 1KC4; 17-APR-02.
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FT CARBOHYD 46 46 (BY SIMILARITY).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 447 447 N -> F (IN REF. 2).
FT CONFLICT 469 469 P -> R (IN REF. 2).
SQ SEQUENCE 502 AA; 56410 MW; 00996674EC7B9A56 CRC64;

Query Match 29.0%; Score 1173.5; DB 1; Length 502;
Best Local Similarity 45.6%; Pred. No. 1.2e-74;
Matches 238; Conservative 80; Mismatches 119; Indels 85; Gaps 10;

QY 297 IYLNLSA---KVLACGHEKLLHLDLPYTLRPPVNLSPDLQSLFGLTLMQIIDVE 353
DB 8 IWLALAAHLSLQGEQRRLYKELVKNYPLRPVANDSQPLTVYFSLQLQIMDVE 67

QY 354 KNOLLVTNVLKLEWDMNLRWNTSDYGGVKKLRIPPHRIWKPDVLMVNSADEGFGTYQ 413
DB 68 KNQVLTNIWLOMSWTHYLQWNSYPGVKNRFPDQGIWKPDILLNYSADERFATFH 127

QY 414 TNYVVRNNGSLYPPPGIFKSTCKIDITWFFPDQRCMKFGSWTYDGFQDLQDQETG 473
DB 128 TNLVNASGHCOYLLPPGIFKSSCYIDVRWFFDVQCKLFGWSYGGWSLDLQMQE--- 184

QY 474 GDSSYVLNGEWELLGVPKNEIYNYCCPEYDITFAIIRRTLYFFNLIPCVLI 533
DB 185 ADISSYIPNGWDLGIPGKNEKFEYCECKPEYPDVTYVTMTTRRTLYGLNLIPCVLI 244

QY 534 ASMALGFTLPDSCGKLSGLVTLLSLTVFLNVAETMPATSDAVPL----- 581
DB 245 SALALLVFLLPADSGEKISLIGITVLLSLTVFLNVAETMPATSDVPLIAQYFASTMIIV 304

QY 582 -----WIRIVFLCWLPLWLRMSRPG-----RPLILEFFPTP 612
DB 305 GLSVVTVTVILRYHHDPDGGKMPKWKTRILLNLCAMFLMRKPGEDKVRPACQHKPR- 363

QY 613 CSDFSSERKHOILSDVELKRSKSLANVLDDDDPHNCRPMTGGTLPHNFAFYTV 672
DB 364 CS-----LASVELSAGAG-----PPTSGNGLLY--IGFGL 392

QY 673 YGQ-----GDGSI-GPTGSRMPDAVTHHTCIKSTSEYELGLIKETFRITDQLRKDE 726
DB 393 EGMHCAPTDSGVVCGRLACSPTHDEHLMHGAHPSDGDPLAKILEEVRYIANNRCODE 452

QY 727 CNDIANDWKFAAMVDRCLIFTFMFAIATIAVLLSAPHII 768
DB 453 SEVICSEWKAACVVDPLCLMAFSVFTICTIGILMSAPNEV 494

RESULT 4
ACH7_HUMAN STANDARD; PRT; 502 AA.
AC P36544; Q15826; Q96RH2; Q99555; Q9BXH0;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
GN CHRNA7 OR NACHRA7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94195283; PubMed=8145738;
RA Peng X., Katz M., Gerzanich V., Anand R., Lindstrom J.;
RT "Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit
RT from the SH-SY5Y cell line and determination of pharmacological
RT properties of native receptors and functional alpha 7 homomers
RT expressed in xenopus oocytes.";
RL Mol. Pharmacol. 45:546-554(1994).
RN [2]

SEQUENCE FROM N.A.
TISSUE-Hippocampus;
RA Logel J., Drebjng C., Barnhart M., Antle C., Leonard S.;
RN Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
MEDLINE=97062879; PubMed=8906617;
RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
RA Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
RT 2-beta 4 nicotinic acetylcholine receptor subunits and functional
RT expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
RT beta 4 subunits.";
RL J. Mol. Neurosci. 7:217-228(1996).
[4]
SEQUENCE FROM N.A.
MEDLINE=97162233; PubMed=9009220;
RA Groot Kormelink P.J., Luyten W.H.M.L.;
RT "Cloning and sequence of full-length cDNAs encoding the human neuronal
RT nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and
RT expression of seven nAChR subunits in the human neuroblastoma cell
RT line SH-SY5Y and/or IMR-32.";
RL FEBS Lett. 400:309-314(1997).
[5]
REVISONS.
RP Groot Kormelink P.J., Luyten W.H.M.L.;
RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE FROM N.A.
TISSUE=Epidermal keratinocytes;
RA Arredondo J., Grando S.A.;
RT "Cloning cholinergic receptors in human keratinocytes.";
RN Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
[7]
SEQUENCE OF 17-502 FROM N.A.
TISSUE=Brain;
RA Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M.T.,
RA Lee J., Iian J., Giordano T.;
RT "Cloning and sequence of the human a7 nicotinic acetylcholine
RT receptor.";
RL Drug Dev. Res. 30:252-256(1993).
[8]
SEQUENCE OF 24-502 FROM N.A.
TISSUE=Retina;
RA MEDLINE=94245214; PubMed=8188270;
RA Chini B., Raimondi E., Elgoyhen A.B., Moralli D., Balzaretta M.,
RA Heinemann S.F.;
RT "Molecular cloning and chromosomal localization of the human alpha 7-
RT nicotinic receptor subunit gene (CHRNA7).";
RL Genomics 19:379-381(1994).
[9]
SEQUENCE OF 118-129 FROM N.A.
MEDLINE=21818878; PubMed=11829490;
RA Riley B., Williamson M., Collier D., Wilkie H., Makoff A.;
RT "A 3-Mb map of a large segmental duplication overlapping the alpha7-
RT nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14.";
RL Genomics 79:197-209(2002).
[10]
MASS SPECTROMETRY.
RP TISSUE=Breast cancer;
RX MEDLINE=21829512; PubMed=11840567;
RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
RA Zvelebil M.J.;
RT "Cluster analysis of an extensive human breast cancer cell line
RT protein expression map database.";
RL Proteomics 2:212-223(2002).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE AChR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
```

CC CC SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- MASS SPECTROMETRY: MW=54157.68; METHOD=MALDI.

CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

CC -----

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CC -----

DR EMBL; X70297; CAA49778.1; -

DR EMBL; U40583; AAA83561.1; -

DR EMBL; U62436; BAB40114.1; -

DR EMBL; Y08420; CAA69697.1; -

DR EMBL; AF385585; AAK68111.1; -

DR EMBL; L25827; -; NOT_ANNOTATED_CDS.

DR EMBL; Z23141; CAA80672.1; -

DR EMBL; AF332758; AAK19515.1; -

DR PIR; G02259; G02259.

DR PIR; I37185; ACHUA7.

DR Genew; HGNC:1960; CHRNA7.

DR MM; 118511; -

DR GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. . . ; TAS.

DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. . . ; TAS.

DR GO; GO:000187; P:activation of MAPK; TAS.

DR GO; GO:0006832; P:small molecule transport; TAS.

DR InterPro; IPR006029; Neu_channel_memb.

DR InterPro; IPR006202; Neur_chan_LBD.

DR InterPro; IPR006201; Neur_channel.

DR Pfam; PF02931; Neur_chan_LBD; 1.

DR Pfam; PF02932; Neur_chan_memb; 1.

DR PRINTS; PR00252; N2IONCHANNEL.

DR TIGRFAMs; TIGR00860; LIC; 1.

DR PROSITE; PS00236; NEUOTR_ION_CHANNEL; 1.

DR PostSynaptic membrane; Ionic channel; Glycoprotein; Signal;

KW Transmembrane; Multigene family.

FT SIGNAL 1 22

FT CHAIN 23 502

FT BY SIMILARITY.

FT NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,

FT ALPHA-7 CHAIN. (POTENTIAL).

FT EXTRACELLULAR (POTENTIAL).

FT POTENTIAL.

FT POTENTIAL.

FT POTENTIAL.

FT CYTOPLASMIC (POTENTIAL).

FT POTENTIAL.

FT BY SIMILARITY.

FT ASSOCIATED WITH RECEPTOR ACTIVATION

FT (BY SIMILARITY).

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT A -> G (IN REF. 1 AND 7).

FT S -> N (IN REF. 2 AND 6).

FT S -> P (IN REF. 2 AND 6).

FT S -> S (IN REF. 8).

FT A -> G (IN REF. 1).

FT RMACS -> AWPAP (IN REF. 8).

FT CONFLICT 409 413

FT CONFLICT 502 AA; 58449 MW; D94B3A482EAA0E42 CRC64;

FT SEQUENCE

Query Match 28.7%; Score 1159.5; DB 1; Length 502;

Best Local Similarity 45.1%; Pred. No. 1.le-73;

Matches 237; Conservative 82; Mismatches 115; Indels 91; Gaps 12;

QY 297 IYNLSAK---VCLAGYHERKRLHLDLDYPNTLIERPVNLSDPLQLSFGTLMOIIDVDE 353

Db 8 VTLAALASLHVSQGEFQKLYKELVKNYPLRPVANDSQPLTVVLSLSLQIMDVDE 67

QY 354 KNOYLTNVWLKLEWDMNLRWNTSDYGGVKDLRIPPHRTWKPDVLMYNSADESGFDCTYQ 413

Db 68 KNOYLTNTIWLQMSWTDDYLOWNVSEYPGVKTRFPDQGIWKPDILLYNSADERFDATEH 127

QY 414 TNVVRNNGSCLYVPPGIFKSTCKIDITWFPDQDRCMKFGSWTVYDGFOLDLQLODQETG 473

Db 128 TNVLVNSSGHCQYLPPIGFKSSCYIDVRWPFQVQCKLAFKFGWSYGSWGLDLMQMB--- 184

QY 474 GDISSYVLNCEWELLGVPGKRNELIYNCCPEPIDITFAIIIRRTLYYFNLIIPCVLI 533

Db 185 ADISGYIPNCEWDLVGPGRSERFECCKEYPDVTFVTMRRTLYYGLNLLIPCVLI 244

QY 534 ASMALGFTLPDPSGKLSIGVTLLSLTVFLNVAETMPATSDAVPL----- 581

Db 245 SALALLVFLPADSGEKISLIGITVLLSLTVFLLVAEIMPATSDSVPLIAQYFASPMIIV 304

QY 582 -----WIRIVFLCWLPMILRMSRPG-----RPLILEFTTTP 612

Db 305 GLSVVTVTVIYQYHHHDPDGGKMPKWTRVILLNWCAMFLRMKRPGEKVRP-ACQHKQR 363

QY 613 CSDTSSERKHQILSDVELKERSKSLANVLDIDDDFRH---NCRWMTGGTLPHPNPAF 668

Db 364 CSLASVE-----MSAVAPPASNGNLLY-----IGRGLDGVHCV-TP----- 401

QY 669 YRTVYGGDDSGISGPIGSTRMPDAVTH-----HTCIKSSTEYELGLILKEIRFTDOLRK 723

Db 402 -----DSGVV-----CGRMACSPHDEHLLHGGOPPEGDPDLAKLILEVRYIANRFR 449

QY 724 DDECNDIANDKFAAMVVDRLCLIIIFTFMFAILATIAVLLSAPHII 768

Db 450 QDESEAVCSBWKFAACVVDRLCLMAFSVFTIICITGILMSAPNFV 494

RESULT 5

ACH7_BOVIN

ID ACH7_BOVIN STANDARD; PRT; 499 AA.

AC P54131;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.

GN CHRNA7.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).

RC TISSUE=Adrenal medulla;

RA MEDLINE=95346009; PubMed=7620615;

RA Garcia-Guzman M., Sala F., Sala S., Campos-Caro A., Stuehmer W.,

RA Gutierrez L., Criado M.;

RT "Alpha-Bungarotoxin-sensitive nicotinic receptors on bovine

RT chromaffin cells: molecular cloning, functional expression and

RT alternative splicing of the alpha 7 subunit.";

RL Eur. J. Neurosci. 7:647-655(1995).

CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN

CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND

CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA

CC MEMBRANE.

CC -1- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-

CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY

CC SIMILARITY). HOMO-OLIGOMER OF THE SHORT FORM GIVES RISE TO

CC UNFUNCTIONAL CHANNELS, AS DOES COEXPRESSION OF BOTH LONG AND SHORT

CC FORMS OF THE RECEPTOR.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=2;

CC Name=Long;

CC IsoId=P54131-1; Sequence=Displayed;

CC Name=Short;

CC IsoId=P54131-2; Sequence=VSP_000075;

CC -1- TISSUE SPECIFICITY: AT LEAST IN CHROMAFFIN CELLS.

CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

CC -----

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DR EMBL; X93604; CAA63802.1; --
 DR InterPro; IPR006029; Neu_chan_memb.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR InterPro; IPR006201; Neur_chan_memb.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family; Alternative splicing.
 FT SIGNAL 1 19
 FT CHAIN 20 499
 FT DOMAIN 20 227
 FT TRANSMEM 28 252
 FT TRANSMEM 259 277
 FT TRANSMEM 293 314
 FT TRANSMEM 315 466
 FT TRANSMEM 467 487
 FT DISULFID 147 161
 FT DISULFID 209 210
 FT CARBOHYD 43 43
 FT CARBOHYD 87 87
 FT CARBOHYD 130 130
 FT VARSPLIC 262 290
 FT SEQUENCE 499 AA; 56002 MW; AEE5D0B3820D42D5 CRC64;

Query Match 28.6%; Score 1157; DB 1; Length 499;
 Best Local Similarity 46.4%; Pred. No. 1.7e-73;
 Matches 235; Conservative 76; Mismatches 122; Indels 74; Gaps 10;

QY 305 VCLAGYHEKRLHLLDLPYNTLPRVNLNESPQLSGLTLMQIIDVDEKNQLLVTVNL 364
 DB 16 VSLQGEFQRKLYKDLVKNYNPLRPVANDSLPTVYFSLQLQIMDYDEKNQVLTVNL 75
 QY 365 KLEWDMNLRWNTSDYGVKDLRPPHRIKWPDLVMTNSADEGFGDTGYOTNVVYRNGSC 424
 DB 76 QMTWTDHYLQWNASEYFGVKTVPDGOIWKPDILLNSADEREDATFTNVLNMSGHC 135
 QY 425 LYVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGFQDLQQLQDETGGDISYVLNGE 484
 DB 136 QYLPPIGIFKSSCYIDVRWFPDVOQCKLFGSWSYGGNSLDLQWQE--ADISGYIPNGE 192
 QY 485 WELGVGPKRNEIYNCCPEYIDITAIIRRTLYFFNLIITPCVLIASMLLGGTLP 544
 DB 193 WDLVGLGKSEKEFYECCKEPPDVTETVSTRRTLYGLNLLPCVLIASALLVFLLP 252
 QY 545 PDSGEKLSLGVITLLSTVFLNVAETMPATSDAVPL----- 581
 DB 253 ADSGEKLSLGVITLLSTVFLNVAETMPATSDVPLIAQYFASTMIIVGLSVVTVIVL 312
 QY 582 -----WIRIVLCWPLWILRMSRGPRLILEFPTTSCDTSERKHQLSD 627
 DB 313 QYHHDPDGGKMPKWTWVLLNCAWFLRMKRPQ-----EDKVRPAQHNRRCSS--LAS 365
 QY 628 VELKE-RSSKSLANVLIDIDDDFR-----HNCPRMTPGTLPHNPAFTVYVGGDDGSI- 681
 DB 366 VEMSAVAGPATNGNLLYI--GFGLDTHCAP--TP-----DSGVVC 404
 QY 682 GPIGSTRMPDAVTHHTCKISTEYELGLILKEIFITDQLRKDCDNDIANDWKFAMVY 741
 DB 405 GRVACSTPHDEHLLHAGQSEGDPLAKILEEVYIAHRFCQDESAVCSWKFAACV 464

QY 742 DRLCLIIFTFAIATIAVLASAPHII 768
 DB 465 DRLCLMAFSVFTILCTIGILMSAPNFV 491

RESULT 6

ACHI_CAEEL STANDARD; PRT; 498 AA.
 AC P48180;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acetylcholine receptor like protein, alpha-type chain precursor.
 GN F25G6.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;
 OC Rhabditiidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RC MEDLINE=96196478; PubMed=9627624;
 RA Ballivet M., Alliod C., Bertrand S., Bertrand D.;
 FT "Nicotinic acetylcholine receptors in the nematode Caenorhabditis
 FT elegans.";
 FT J. Mol. Biol. 258:261-269(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Nelson J., Wohlmann P.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: POSSIBLE ACETYLCHOLINE RECEPTOR.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC
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DR EMBL; X83887; CAA58764.1; --
 DR PIR; S68588; S68588.
 DR HSP; P58154; 119B.
 DR WormPep; F25G6.3; CE09639.
 DR InterPro; IPR006029; Neu_chan_memb.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR InterPro; IPR006201; Neur_chan_memb.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
 KW Transmembrane; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 498
 FT DOMAIN 20 230
 FT TRANSMEM 231 252
 FT TRANSMEM 261 279
 FT TRANSMEM 295 314
 FT TRANSMEM 315 472
 FT TRANSMEM 473 493
 FT DISULFID 147 161
 FT DISULFID 211 212
 FT CARBOHYD 43 43
 FT CARBOHYD 93 93

POTENTIAL.
 ACETYLCHOLINE RECEPTOR LIKE PROTEIN,
 ALPHA-TYPE CHAIN.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 POTENTIAL.
 POTENTIAL.
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 POTENTIAL.
 BY SIMILARITY.
 ASSOCIATED WITH RECEPTOR ACTIVATION
 (BY SIMILARITY).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).

DR Pfam: PF02931; Neur_chan_LBD; 1.
DR Pfam: PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 567
FT DOMAIN 22 240
FT TRANSMEM 241 264
FT TRANSMEM 272 290
FT TRANSMEM 306 325
FT DOMAIN 326 513
FT TRANSMEM 514 532
FT DISULFID 149 163
FT DISULFID 222 223
FT CARBOHYD 45 45
FT CARBOHYD 233 233
FT VARIANT 538 538
FT CONFLICT 108 108
SQ SEQUENCE 567 AA; 64019 MW; 08EIF721FB2A92AC CRC64;
Query Match 22.0%; Score 888; DB 1; Length 567;
Best Local Similarity 35.2%; Pred. No. 1.3e-54;
Matches 196; Conservative 91; Mismatches 168; Indels 102; Gaps 10;
QY 291 SWIFLLIYLLNS-AKVCAGYHEKRLHLLDPYNTLPRVNLNESDPLQLSFGLTLMQII 349
DB 3 SYLFAVFTALHTGGLGPAKRLYDLSNRLIRPVGNNSDRIVTKMGLRLSLI 62
QY 350 DYDEKNQLLVTVNWLKLEWDMNLRWNTSDYGGVXDLRIPPHRWKPDVLMVNSADEGDF 409
DB 63 DYNLKNQINTVWQEQENDYKLNWPDYGGVDTLHVPSEHILPDLVLNNADGVE 122
QY 410 GYQYVNVVNRNGSLVPPGIFKSTCKIDITWFFDDQRCMKGWSYDFQDL--- 466
DB 123 VTIMTKAILHRTGKVKWPKPAIYKSCFEDVEYFPDEQTCFMKFGSWTYDGYMVDLRL 182
QY 467 -QLQD---ETGDSLVVNGEWELLVGPGRNELIYNCCPEYKIDITFAIIIRRTLY 521
DB 183 KOTASDNIEVGIDQDYIYISWEDIMRVPAVRNEKFYSCCEEPYLDIVFNLTLRKTLF 242
QY 522 YFNLIIICVLIASMALLFTLPDPSGKSLGVTLLSLTVFLNNVAETPATSDAVPL 581
DB 243 YTVNLIICVGSFSLVFLPSDSGKISLISLISLTVFFLLAEIIPPTSLTVPL 302
QY 582 -----WIRIVFLCWLPIWLRMSRGRPL 604
DB 303 LGKYLFTMMLVTLVVVYIAVLNVNFRSPVTHRMAPWVQRLFIQLPKLLCIERPKR-- 360
QY 605 ILEFPTTCDSTSRKQHLSDV-ELKERSKSLANVLDIDDDFRHNCRPMTPGGTLP 663
DB 361 -----EEPEEQPPEVLTVDVHLPP-----DVDKFNVDKRFSGDYGP 400
QY 664 HNPAYR-----TVYGGDD-----GSIGPTGSTRMPDAVTH 695
DB 401 ALPASHRFDLAAAGGSAHCAFPPLPSLPGADDDLFSPSLGNGDISPCCPAAAAA 460
QY 696 HFCIKSST-----EYELGLILKEIRFITDLRKDDCNDIANDWFAAMVDRCLLIIFT 750
DB 461 AAADLSPTFEKPYAREMKEITGSRFIAHQVANKDKFSEVEDWYKAVMLDRMFLWIFA 520
QY 751 MFALITATIAVLISAPIH 767
DB 521 IACVVGTAIIILQAPSL 537
PRT; 516 AA.
STANDARD;
ID ACH1_MANSE STANDARD; PRT; 516 AA.

RESULT 8

ACH1_MANSE

ID

AC P91766;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acetylcholine receptor protein, alpha-like chain precursor (MARAL).
GN ARAL.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Spingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98424077; PubMed=9753155;
RA Eastham H.M., Lind R.J., Eastlake J.L., Clarke B.S., Townner P.,
RA Reynolds S.E., Wolstenholme A.J., Wonnacott S.;
RT "Characterization of a nicotinic acetylcholine receptor from the
RT insect Manduca sexta";
RL Eur. J. Neurosci. 10:879-889(1998).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC
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CC
CC EMBL: Y09795; CAA70928.1;
DR InterPro: IPR006029; Neur_chan_memb.
DR InterPro: IPR006202; Neur_chan_LBD.
DR InterPro: IPR006201; Neur_chan.
DR Pfam: PF02931; Neur_chan_LBD; 1.
DR Pfam: PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 21
FT CHAIN 22 516
FT DOMAIN 22 243
FT TRANSMEM 244 264
FT TRANSMEM 274 294
FT TRANSMEM 306 326
FT DOMAIN 327 465
FT TRANSMEM 466 486
FT DISULFID 149 163
FT DISULFID 222 223
FT CARBOHYD 45 45
FT CARBOHYD 132 132
FT CARBOHYD 233 233
SQ SEQUENCE 516 AA; 58720 MW; E7A71E8C45D13BD2 CRC64;
Query Match 21.9%; Score 886; DB 1; Length 516;
Best Local Similarity 36.6%; Pred. No. 1.5e-54;
Matches 199; Conservative 65; Mismatches 141; Indels 138; Gaps 9;
QY 298 YLN---LSAKVCLAGYHEKRLHLLDPYNTLPRVNLNESDPLQLSFGLTLMQIIDVDEK 354
DB 8 YLHGVLVLFATGAGNPDARLYDLSNRLIRPVGNNSDRIVTKMGLRLSLI 67
QY 355 NQLLVTVNWLKLEWDMNLRWNTSDYGGVXDLRIPPHRWKPDVLMVNSADEGFGDTQT 414
DB 68 NQIMTTLNWEQSWDYKLSWEPREYGGVEMLHVPDHDHWRPDIYLYNNADGNFEVTLAT 127

```
QY 415 NVVNRNGSLVPPGIFKSTCKIDITWFFDQRCCKMFGSWTYDGFQDLQDDETG 474
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 KATLNYGRVWEPPIAYKSSCEIDVEYFPDQTCVMKFGSWTYDGFQDLRHIDEVRG 187
QY 475 -----DISSVYLVGEWELLGVGGRNEIYVNCPEPIDITFAIIIRRLIYFFNL 526
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 188 TNVELGVLDSEFYTSVEMDILEYPAVRNEKFYTCDEPYLDITFNITMRKTLFTVNL 247
QY 527 IIPCVLIASMLLGLTLPDGSKEKLSGVTLISLTVFLNVAETMPATSDAVPL----- 581
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 248 IIPCMGISFTLVLYLPDSGKEKLSISILISLTVFFLLAEIIPPTSLVPLLGKVF 307
QY 582 -----WIRIVFLCWLPMILRMSRPGRLILEFP 609
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 308 LFTMILDTFSICVTVVNLNVHFRSPQHTMSPVVRFVHVLPRLLVMRRP----- 358
QY 610 TTPCSDTSSERKHOILSDVELKERSSKILLANVLIDIDDFRHNCRPMTPCGTILPHNPAFY 669
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 359 -----HYRLD-----PHRSRFA 370
QY 670 RTVYGOG-----DDGSIGPIGSTRMP-----DAVTH-HTCIKSS 702
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 371 GLVTGAGETLWDGSGVGPVAPPVPPCAPPLAPACAPAEAPALCDALRRHRC----- 426
QY 703 TEVELGILKEIRFITDQLRKDDCNDIANDWKFAMVVDRLCLLIIFTMFAILATIAVLL 762
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 427 --PELHKAIDGINIADQTRKEESTRVKEDWKVYAMVLDLPFLWIIFLAVVVGSAIGIL 484
QY 763 SAP 765
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 485 QAP 487

RESULT 9
ID ACHI_SCHGR STANDARD; PRT; 557 AA.
AC P23414;
AT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acetylcholine receptor protein, alpha-L1 chain precursor.
OS Schistocerca gregaria (Desert locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
OX NCBI_TaxID=7010;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91092263; PubMed=1702381;
RA Marshall J., Buckingham S.D., Shingai R., Lunt G.G., Goosey M.W.,
RA Darlison M.G., Sattelle D.B., Barnard E.A.;
RT "Sequence and functional expression of a single alpha subunit of an
RT insect nicotinic acetylcholine receptor.";
RL EMBO J. 9:4391-4398(1990).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC -----
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CC -----
DR EMBL; X55439; CAA39081.1; -
DR PIR; S12359; S12359.
DR InterPro; IPR006029; Neu_channel_memb.
```

```
DR InterPro; IPR006029; Neu_chan_LBD.
DR InterPro; IPR006201; Neur_channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 557 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-L1
FT EXTRACELLULAR.
FT DOMAIN 24 244
FT TRANSMEM 245 266
FT TRANSMEM 274 294
FT TRANSMEM 308 329
FT DOMAIN 330 500
FT TRANSMEM 501 523
FT DISULFID 151 165
FT DISULFID 224 225
FT CARBOHYD 47 47
FT CARBOHYD 235 235
FT DOMAIN 382 400
FT DOMAIN 406 422
SQ SEQUENCE 557 AA; 63026 MW; 168389C887DFDF3E CRC64;

Query Match 21.6%; Score 873; DB 1; Length 557;
Best Local Similarity 36.8%; Pred. No. 1.4e-53;
Matches 197; Conservative 90; Mismatches 174; Indels 74; Gaps 8;

QY 293 IFLLIYLNLSAKVCLAGYHEKRLHLLDLPNTLERPVNESDPLQLSFGTLMQIIDVD 352
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 MLLLLLLLLLHPAAANPDAAKRLYDLLSNVNLIRPVSNTDVLVKGRLSLQIDLN 67
QY 353 EKNOLLVTNVWLKLEWDMNLWNTSDYGVGKOLRIIPHRIPKDPVLMYNSADGFGTY 412
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 LKQILTTNVWLEHEWQDHKFRWDPAEYGVGTLYSEHILWPLDIVLYNNADGEYVVT 127
QY 413 QTNVVRNGSLVPPGIFKSTCKIDITWFFDQRCCKMFGSWTYDGFQDL-----QL 468
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 MTRAVLHHTGKVVWTPPAIFKSCSIDVRYFPDQTCFMKFGSWTYDGFQDLKHINQK 187
QY 469 QDE-----TGGDISYVLNGEWELGVGGRNEIYVNCPEPIDITFAIIIRRLIYFF 524
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 188 YDNKVKVGDILREYVPSVEMDILGVAERHEKYPCCAEPYPDIFENITLRRKTLFTV 247
QY 525 NLIIPCVLIASMLLGLTLPDGSKEKLSGVTLISLTVFLNVAETMPATSDAVPL--- 581
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 248 NLIIPCVGISYLSVLYLPADSGEKIALCISILLSQTMFLFLLISEIIPSTSLALPLGK 307
QY 582 -----WIRIVFLCWLPMILRMSRPGRLILE 607
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 308 YLLFTWVLVGLSVVITWVLNVHVRKPSHKMAPVRKVFIRRLPKLLMRVPEQLL--- 364
QY 608 FPTTPCSDTSSERKHOILSDVELKERSSKILLA-----NLVIDDDFRHN----- 652
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 365 -----ADLASKRLLRHAHNSKLSAAAAAASSSAASSPSDLRHHHLHQHQHHL 418
QY 653 --CRPMPGCTLPHNPAFYTVYVGQDGSIGPIGSTRMPDPAVTHHTCIKSSYEYELGLI 710
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 419 QLHHLQRPGGCNGLIHSATNR--FG-GSAGAGFGLPSVVGDLGSLSDVATRKRYFELEKA 475
QY 711 LKETRFITDOLRKDDCNDIANDWKFAMVVDRLCLLIIFTMFAILATIAVLLSAP 765
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 476 IHNVLFIQNHMQRODEDAEDQDMGFMVAVLDRLFLWIFTIASIVGTFAILCEAP 530

RESULT 10
ID ACHI_SCHGR STANDARD; PRT; 529 AA.
AC Q15822; Q9HQA03;
DT 01-NOV-1997 (Rel. 35, Created)
```


RX MEDLINE-91114756; PubMed-1989896;
 RA Mihovilovic M., Roses A.D.;
 RT "Expression of mRNAs in human thymus coding for the alpha 3 subunit
 of a neuronal acetylcholine receptor.";
 RL Exp. Neurol. 111:175-180(1991).
 [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE-97062879; PubMed-8908617;
 RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
 Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
 RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
 2-beta 4 nicotinic acetylcholine receptor subunits and functional
 expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
 beta 4 subunits.";
 RL J. Mol. Neurosci. 7:217-228(1996).
 [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE-97162233; PubMed-9009220;
 RA Groot Kormelink P.J., Luyten W.H.M.L.;
 RT "Cloning and sequence of full-length cDNAs encoding the human neuronal
 nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and
 expression of seven nAChR subunits in the human neuroblastoma cell
 line SH-SY5Y and/or IMR-32.";
 RL FEBS Lett. 400:309-314(1997).
 [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE-99118870; PubMed-9921897;
 RA Rempel N., Heyers S., Engels H., Slegers E., Steinlein O.K.;
 RT "The structures of the human neuronal nicotinic acetylcholine receptor
 beta2- and alpha3-subunit genes (CHRNA2 and CHRNA3).";
 RL Hum. Genet. 103:645-653(1998).
 [6]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE-21342809; PubMed-11450844;
 RA Lev-Lehman E., Bercovich D., Xu W., Stockton D.W., Beaudet A.L.;
 RT "Characterization of the human beta4 nAChR gene and polymorphisms in
 CHRNA3 and CHRNA4.";
 RL J. Hum. Genet. 46:362-366(2001).
 [7]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE-22388257; PubMed-12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [8]
 RP SEQUENCE OF 30-503 FROM N.A.
 RX TISSUE=Brain;
 RA Anand R., Lindstrom J.;
 RT Submitted (JUN-1990) to the EMBL/GenBank/DBJ databases.
 [9]
 RP SEQUENCE OF 6-493 FROM N.A.
 RX TISSUE=Epidermal keratinocytes;
 RA Arredondo J., Grando S.A.;
 RT "Cloning cholinergic receptors in human keratinocytes.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE
 CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P32297-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P32297-2; Sequence=VSP_000073;
 CC Note=No experimental confirmation available;
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M86383; AAC84176.1; -;
 CC EMBL; M37981; AAA59942.1; -;
 CC EMBL; U62432; AAB40110.1; -;
 CC EMBL; Y08418; CAA69695.1; -;
 CC EMBL; AJ007783; CAA07682.1; -;
 CC EMBL; AJ007784; CAA07682.1; JOINED.
 CC EMBL; AJ007785; CAA07682.1; JOINED.
 CC EMBL; AJ007786; CAA07682.1; JOINED.
 CC EMBL; BC001642; AAH01642.1; -;
 CC EMBL; BC002996; AAH02996.1; -;
 CC EMBL; BC000513; AAH00513.1; -;
 CC EMBL; AF385584; AAK68110.1; -;
 CC EMBL; X53559; CAA37625.1; -;
 CC PIR; A37040; A37040.
 CC PIR; A53956; A53956.
 CC Genew; HGNC:1957; CHRNA3.
 CC MIM; 118503; -;
 CC GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. . . ; TAS.
 CC GO; GO:004889; F:nicotinic acetylcholine-activated cation-se. . . ; TAS.
 CC GO; GO:0005215; F:transporter activity; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC GO; GO:0006832; P:small molecule transport; TAS.
 CC InterPro; IPR006039; Neu_chan_memb.
 CC InterPro; IPR006202; Neur_chan_LBD.
 CC InterPro; IPR006201; Neur_chan_memb.
 CC Pfam; PF02931; Neur_chan_LBD; 1.
 CC Pfam; PF02932; Neur_chan_memb; 1.
 CC PRINTS; PR00252; NRIONCHANNEL.
 CC TIGRfams; TIGR00860; LIC; 1.
 CC PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 CC Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 CC Transmembrane; Multigene family; Alternative splicing; Polymorphism.
 CC SIGNAL 1 29
 CC CHAIN 30 503
 CC NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 CC ALPHA-3 CHAIN
 CC EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 30 238
 CC TRANSMEM 239 263
 CC TRANSMEM 271 289
 CC TRANSMEM 305 326
 CC DOMAIN 327 475
 CC TRANSMEM 476 495
 CC TRANSMEM 157 171
 CC DISULFID 221 222
 CC ASSOCIATED WITH RECEPTOR ACTIVATION
 CC (BY SIMILARITY).
 CC CARBOHYD 53 53
 CC CARBOHYD 170 170
 CC VARSPLIC 1 5
 CC MALAV -> MGSGPL (in isoform 2).
 CC /FTid=VSP_000073.

FT VARIANT 21 21 L -> LL
 FT CONFLICT 5 13 /FTID-VAR_013240A
 FT CONFLICT 11 14 VSLPALSP -> CRA (IN REF. 1).
 FT CONFLICT 100 100 LSPG -> CRA (IN REF. 1).
 FT CONFLICT 132 133 DD -> TT (IN REF. 1).
 FT CONFLICT 235 235 I -> S (IN REF. 1).
 FT CONFLICT 430 430 L -> V (IN REF. 1).
 SQ SEQUENCE 503 AA; 57309 MW; 8A9BEC5D71AEC7D6 CRC64;

Query Match 20.9%; Score 845; DB 1; Length 503;
 Best Local Similarity 35.2%; Pred No. 1, le-51;
 Matches 178; Conservative 97; Mismatches 166; Indels 64; Gaps 6;

QY 295 LLIYLNLSAKVCLAGYHEKRLHLDLPYNTLRLPVLNEDPLQLSFGTLTMOIIVDVK 354
 DB 17 LLLLSL-LPVARSEAEHRLFERLFEDYIIRPVANVSDPVIIHFVMSQLVKVDEV 75

QY 355 NOLLVNTWKLKLEWMDNLRWNTSDYGGVKDLRIPHRIRWKPDLVLYNSADEGFDGTQT 414
 DB 76 NQIMETNLWLKQINDYKUKWPSDYGGAEFMRVPAQKIWKPDVLYNNVAGDFQVDDKT 135

QY 415 NYVVRNNGSCLVPPGIFKSTCKIDITWPPDDQRCMKFGSWTDGFDOLDLQLODETGG 474
 DB 136 KALLKTYGVTWIPPAIFKSSCKIDVYPPDYQNCYMKFGSWDKAKIDLVLIG-SSM 194

QY 475 DISSVNLGEWELGVPGKRNIIYNCPEPIDITFAIIIRRLIYFFNLIIPCVLIA 534
 DB 195 NLKDYWESGEWAIIRKAPGYKHDIKYNCCBEIYPIDTYSYIRRLPLFTVNLIIPLCLIS 254

QY 535 SMALLGFTLPPDSGKLSGVTLISLTVFLNVAETMPATSDAVPL----- 581
 DB 255 FTVLVFLYPSDGEKVTLCISVLLSLTVFLVLTITPSTSLVPLIGEYLLFTWIFVT 314

QY 582 -----WIRVFLCWLPLWILMSRPGRLPILEFPPTPCSDTS 617
 DB 315 LSIVITVFLNVHYRTPTHTPMSWKTVFLNLLPRV-----FWTRPTSNEG 362

QY 618 SERKHQILSDVELKERSKSLANVLDDDDFRHCRPMTPGTLPHPNPAFRTVYGGQD 677
 DB 363 NAKQRPRLYGAELSNLNCFSRAES-----KGCKEGYPCQDGMCGYCHRRIRKISNF 413

QY 678 DGSIGPIGSTRMPDVAHTHTCKSTPEYELGLILKEIRFTDQLRKDDDCNDIANDWKA 737
 DB 414 SANLFRSSSESDAVLS-----LSALSPKIAQSVKVIENAKQAENKAIQDDWKV 469

QY 738 AMVDRLCLIIFTFAILATIAVLL 762
 DB 470 AMVIDRFLWVFLVCLILGTAGLFL 494

RESULT 12

ACH2_DROME STANDARD; PRT; 576 AA.
 AC ACH2_DROME
 AC P17644; Q9VC73;
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acetylcholine receptor protein, alpha-like chain 2 precursor.
 GN NACR-ALPHA-96AB OR ACR96AB OR ACR96AB OR CG5844.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Head;
 RX MEDLINE=90301489; PubMed=2114015;
 RA Baumann A., Jonas P., Gundelfinger E.D.;
 RT "Sequence of D alpha 2, a novel alpha-like subunit of Drosophila
 RT nicotinic acetylcholine receptors.";
 RL Nucleic Acids Res. 18:3640-3640(1990).

RNA SEQUENCE FROM N.A.
 RC TISSUE-Head;
 RX MEDLINE=90353591; PubMed=2117557;
 RA Jonas P., Baumann A., Merz B., Gundelfinger E.D.;
 RT "Structure and developmental expression of the D alpha 2 gene
 RT encoding a novel nicotinic acetylcholine receptor protein of
 RT Drosophila melanogaster.";
 RL FEBS Lett. 269:264-268(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90360975; PubMed=1697262;
 RA Sawruk E., Schloss P., Betz H., Schmitt B.;
 RT "Heterogeneity of Drosophila nicotinic acetylcholine receptors: SAD,
 RT a novel developmentally regulated alpha-subunit.";
 RL EMBO J. 9:2671-2677(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Mikos G.D.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laso P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley; TISSUE=Head;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuncio J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBI databases.
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC MEMBRANE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: CNS IN EMBRYOS.

Search completed: August 13, 2003, 15:26:10
Job time : 19.1234 secs

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DR EMBL; AJ250359; CAB59624.1; -.
DR EMBL; AF051909; AAC06012.1; -.
DR EMBL; M14808; AAA48565.1; -.
DR EMBL; M14809; AAA48564.1; -.
DR PIR; I50150; I50150.
DR PIR; S00376; ACCHAN.
DR InterPro; IPR006029; Neu_channel_memb.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006201; Neur_channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane.
FT SIGNAL 1 20
FT CHAIN 21 456
FT DOMAIN 21 229
FT TRANSMEM 230 254
FT TRANSMEM 262 280
FT TRANSMEM 296 315
FT DOMAIN 316 427
FT TRANSMEM 428 446
FT DISULFID 147 161
FT DISULFID 211 212
FT CARBOHYD 160 160
FT CONFLICT 33 33
SQ SEQUENCE 456 AA; 52183 MW; 0B31B6EABD7B4D42 CRC64;

Query Match 20.5%; Score 827.5; DB 1; Length 456;
Best Local Similarity 34.6%; Pred. No. 1.6e-50;
Matches 176; Conservative 92; Mismatches 130; Indels 111; Gaps 12;

QY 293 IFLLIYLNLSAKVCLAGYHEKRLHLDLDYNTLPRVPLESDPLQLSFGTLMQIIDVD 352
Db 6 VLLIFSAAGPALCYE--HETRLVDLDFREYSKVVPRPVENHRDAVVVTVGLIQLINVD 63
QY 353 EKNQLLVNTVMKLEWDMNLRWTSYGGVKDLRIPIPHRIWKDPDVLVMSADEGFDGTY 412
Db 64 EVNQIVTIVNRLKQWTDINLKQNPDDYGGVKQIRIPSDDIWRPDLVLYNNADGFAIVK 123
QY 413 QTNVVRNNGSCLVPPGIFKCKIDITWPEPDQRCMKFGSWTYDGFOLDLQLODET 472
Db 124 YTKVLLHTGKITWTPPAIFKSYCEIIVTFPQQNCMKLGTWTYDGTWVVPINPESDR 183
QY 473 GGDISSYVLNGEWELLGVPGKRNEIYYNCCPE-PYIDITFAIIIRRTLYFFNLIIPCV 531
Db 184 -PDLNFMESGEWYMKDYRGWKHWYVYACCPDTPYDITYHFLMQRLPLFYIVNVIIPCL 242
QY 532 LIASWALLGFTLPDPSGKLSGLVTILLSLVFLNMVAETMPATSDAVPL----- 581
Db 243 LFSFLTGFVFLPTDSGEKMTLSVLLSLVFLVIVELIPSTSSAVPLIGKYMLETMW 302
QY 582 -----WIRIVELCWLPLWIL---RMSRPGRLILEPFTT 611
Db 303 FVIASIIITIVINTHRSPSTHTMPWPWRKIFIDTIPNIMFFSTMKRPSR----- 353
QY 612 PCSDTSSERKHQIISDVDELKERSKSLIANVLDIDDDFRHNCRPMTFGGTLPHNPAFYRT 671
Db 354 -----DKPKKIFAEDIDISEISKQ-----GPPVNV--FY-- 382
QY 672 YVGQDDGSGIGPISGRMPDVAHTHTCIKSSTYELGLILKEIRFITDQLRKDDECDNIA 731
Db 383 -----SPL--TKNPD-----VKNAIE-----GIKYIAETMKSDQESSNAA 415
QY 732 NDWKFAAMVDRLCLIIFTMEFAILATIAV 760
Db 416 DEWKFVAMVLDHLLVIFMLVCIIGTLAV 444
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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:21:45 ; Search time 28.7606 Seconds
(without alignments)
2574.698 Million cell updates/sec

Title: US-09-303-232-2
Perfect score: 4043
Sequence: 1 MKNAQKLFEVDDDELWLAV.....MFAILATIAVLISAPHIIVS 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1182.5	29.2	502	2 A57175	nicotinic acetylch
2	1179.5	29.2	502	2 JN0113	nicotinic acetylch
3	1173.5	29.0	502	2 T01378	nicotinic receptor
4	1168	28.9	511	2 JH0173	alpha-bungarotoxin
5	1160.5	28.7	502	1 ACH0A7	nicotinic acetylch
6	1155.5	28.6	502	2 G02359	alpha 7 neuronal n
7	1104	27.3	498	2 S68588	nicotinic acetylch
8	1009.5	25.0	461	2 T25671	hypothetical prote
9	988	24.4	560	2 T19622	hypothetical prote
10	968.5	24.0	542	2 T19862	hypothetical prote
11	889	22.0	567	1 ACFFA1	nicotinic acetylch
12	873	21.6	557	1 S12359	nicotinic acetylch
13	845	20.9	503	2 A53956	nicotinic acetylch
14	843.5	20.9	576	1 ACFFA2	nicotinic acetylch
15	841	20.8	521	1 ACFFNN	nicotinic acetylch
16	840	20.8	502	2 A37040	nicotinic acetylch
17	838	20.7	528	1 ACCH2N	nicotinic acetylch
18	828	20.5	511	2 A40110	nicotinic acetylch
19	827.5	20.5	456	1 ACCHAN	nicotinic acetylch
20	824	20.4	499	2 A24572	nicotinic acetylch
21	820.5	20.3	495	2 S60589	acetylcholine rece
22	820.5	20.3	512	2 B37014	nicotinic acetylch
23	817	20.2	494	2 T09289	nicotinic acetylch
24	806.5	19.9	500	2 S12899	nicotinic acetylch
25	805	19.9	498	2 G02421	nicotinic acetylch
26	802.5	19.8	457	1 ACHUA1	nicotinic acetylch
27	801	19.8	457	1 ACBOA1	nicotinic acetylch
28	794.5	19.7	457	2 A28529	nicotinic acetylch
29	794	19.6	457	2 A24383	nicotinic acetylch

30	792.5	19.6	445	2 T49458	acetylcholine rece
31	789	19.5	457	2 S13872	nicotinic acetylch
32	789	19.5	470	2 A39218	nicotinic acetylch
33	787	19.5	491	1 ACCHNN	nicotinic acetylch
34	785	19.4	503	2 JH0174	nicotinic acetylch
35	783	19.4	461	2 I50548	acetylcholine rece
36	782	19.3	495	2 B35721	nicotinic acetylch
37	782	19.3	502	2 S10505	nicotinic acetylch
38	780	19.3	627	2 JC4021	nicotinic acetylch
39	779.5	19.3	559	2 E89134	protein F2566.4 [1
40	779.5	19.3	622	1 ACCHAN	nicotinic acetylch
41	779	19.3	461	1 ACRTA1	hypothetical prote
42	776	19.2	468	2 T24724	nicotinic acetylch
43	775.5	19.2	625	2 A26456	nicotinic acetylch
44	773.5	19.1	457	2 S08162	nicotinic acetylch
45	773	19.1	565	2 T23843	hypothetical prote

ALIGNMENTS

RESULT 1

A57175
nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Aug-1999
C:Accession: A57175
R:Orr-Urtreger, A.; Seidlin, M.F.; Baldini, A.; Beaudet, A.L.
Genomics 26, 399-402, 1995
A:Title: Cloning and mapping of the mouse alpha7-neuronal nicotinic acetylcholine rec
A:Reference number: A57175; MUID:95324936; PMID:7601470
A:Accession: A57175
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-502 <ORR>
A:Cross-references: GB:L37663; NID:g790853; PID:AA2053.1; PID:g790854
C:Superfamily: acetylcholine receptor
C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprote
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pr
F:231-254/Domain: transmembrane #status predicted <TR1>
F:262-280/Domain: transmembrane #status predicted <TR2>
F:296-317/Domain: transmembrane #status predicted <TR3>
F:470-488/Domain: transmembrane #status predicted <TR4>
F:46,90,133/Binding site: carboxylate (Asn) (covalent) #status predicted
F:365,413,427/Binding site: phosphate (Ser) (covalent) #status predicted
F:415/Binding site: phosphate (Thr) (covalent) #status predicted
F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 29.2% ; Score 1182.5; DB 2; Length 502;
Best Local Similarity 45.8% ; Pred. No. 5.1e-77;
Matches 239; Conservative 80; Mismatches 118; Indels 85; Gaps 10;

QY	297	IYLNLSA---KVCAGYHEKRLHLLDPYNTLPRVNLNEDSPQLSFGTLNQIIVDVE	353
DB	8	IWLALAAALHVSLSQGEFQRRLKELVKNPLRPVANDSQPLTVYFSLSLQIIVDVE	67
QY	354	KNOLLVTNVWLKLEWDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFCGTQY	413
DB	68	KNQVLTNTNWLQMSWTDHYLQWNMSEYPGVKNVRFPGQIWKPDILLYNSADRFDFATFH	127
QY	414	TNVVVRNNGSCLYVPFGIFKSCIKDITWFFPDQRCMEKFGSWTYDGFOLDLOQDET	473
DB	128	TNVLVNASGHCQVLPPIGPKSSCYIDVRWFFDVQCKLAFGWSYGSWLDLQMQE---	184
QY	474	GDTSIVLVNGEWELLGVPGRNEIYNCCPEPIDITFAIIIRRTLYYFNLIIPCVLI	533
DB	185	ADISSYIPNGEWELMGIPGRNEKFECKPEYCDVTYVTMRRRTLYYGNLLIIPCVLI	244
QY	534	ASWALLGFTLPDPSGKLSIGVTILLSLTVFLNVAETMPATSDAVPL-----	581
DB	245	SALALLVFLLPADSGEKISIGITVLLSLTVFLLVAEIMPATSDSVPLIAQYFASTMIIV	304

QY 582 -----WIRIVFLCWLPLWLRMSRPG-----RPLILEPPTP 612
DB 305 GLSVVVTIVLYRHHHDPGKMPKWTIRIILNMCWFLMRKPGEDKVRACQHKPRR- 363
QY 613 CSDTSSERKHOLLSDELKERSKSLANVLIDDDFRHRCRPMPTGGTLPHPAFYRTV 672
DB 364 CS-----LASVELSAGAG-----PPTSNGNLLY--IGFRGL 392
QY 673 YGQ-----GDGSI-GPIGSTRMPDAVTHHTCIKSTSEYELGLILKEIRFITDQLRKDD 726
DB 393 EGMHCAPTDSGVCGRLACPTDHEHLMHGTHPSDGDPLAKILEEYRYANRRCODE 452
QY 727 CNDIANDKFAAMVDRCLLIFTFMAILATIAVLLSAPHII 768
DB 453 SEVICSEKFAACVYDRCLLMAFSVFTIICITIGILMSAPNEV 494

RESULT 2
JN0113
nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken
N:Alternate names: alpha-bungarotoxin-binding protein alpha chain
C:Species: Gallus gallus (chicken)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1999
C:Accession: JN0113; JH0172; S28018; B25738; S26566
R:Contourier, S.; Bertrand, D.; Matter, J.M.; Hernandez, M.C.; Bertrand, S.; Millar, N.; Neuron 5, 847-856, 1990
A:Title: A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is developmentally regulated in the chick embryo
A:Reference number: JN0113; MUID:91097796; PMID:1702646
A:Accession: JN0113
A:Molecule type: DNA
A:Residues: 1-502 <COU>
A:Cross-references: GB:X68586; NID:g287756; PIDN:CAA48576.1; PID:g287757
A:Experimental source: white leghorn; brain
R:Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.; Neuron 5, 35-48, 1990
A:Title: Brain alpha-bungarotoxin binding protein cDNAs and MAb reveal subtypes of this receptor
A:Reference number: JH0172; MUID:90315158; PMID:2369519
A:Accession: JH0172
A:Molecule type: mRNA
A:Residues: 1-502 <SCH>
A:Cross-references: EMBL:X52295; NID:g63077; PIDN:CAA36543.1; PID:g63078
A:Experimental source: brain
R:Matter-Sadzinski, L.; Hernandez, M.C.; Roztocil, T.; Ballivet, M.; Matter, J.M.; EMBO J. 11, 4529-4538, 1992
A:Title: Neuronal specificity of the alpha7 nicotinic acetylcholine receptor promoter determined by a 5' deletion analysis
A:Reference number: S28018; MUID:93049204; PMID:1425587
A:Accession: S28018
A:Molecule type: DNA
A:Residues: 1-18 <MAS>
A:Cross-references: EMBL:X68246; GB:S49751; NID:g65319; PIDN:CAA48317.1; PID:g65320
A:Experimental source: white leghorn; erythrocyte
R:Conti-Tronconi, B.M.; Dunn, S.M.J.; Barnard, E.A.; Dolly, J.O.; Lai, F.A.; Ray, N.; Proc. Natl. Acad. Sci. U.S.A. 82, 5208-5212, 1985
A:Title: Brain and muscle nicotinic acetylcholine receptors are different but homologous
A:Reference number: A94055; MUID:85270494; PMID:3860855
A:Accession: B25738
A:Molecule type: protein
A:Residues: 24-25, 'ET', 28-41, 'X', 43-45, 'X', 47 <CON>
A:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localized to the neuromuscular junction
C:Genetics:
A:Introns: 19/1; 65/3; 80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3
C:Superfamily: acetylcholine receptor
C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein; F.1-23/Domain: signal sequence #status predicted <SIG>
F.24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predicted <TR1>
F.231-254/Domain: transmembrane #status predicted <TR2>
F.262-280/Domain: transmembrane #status predicted <TR3>
F.296-317/Domain: transmembrane #status predicted <TR4>
F.470-488/Domain: transmembrane #status predicted <TR5>
F.46-90,133/Binding site: carbonyl site: phosphate (Ser) (covalent) #status predicted <TR6>
F.365,367,413,427,465/Binding site: phosphate (Thr) (covalent) #status predicted <TR7>
F.415/Binding site: phosphate (Thr) (covalent) #status predicted <TR8>
F.442/Binding site: phosphate (Tyr) (covalent) #status predicted <TR9>

Query Match 29.2%; Score 1179.5; DB 2; Length 502;
Best Local Similarity 45.7%; Pred. No. 8.3e-77;
Matches 237; Conservative 80; Mismatches 127; Indels 75; Gaps 9;
QY 295 LLIYLNLSA---KVCLAGYHEKRLHLLDDPNTLERPVNLNEDPQLQLSFGTLMOIIV 351
DB 6 LMLNLLAAGLVRESLOGEFQKLYKELLKNYLERPVANDSQPLVFTLUSLMOIIV 65
QY 352 DEKNOLLVTNWLKLEWDMNLRWNTSDYGVKDLRIPPHRIWKPDVLMYNSADEGFGDT 411
DB 66 DEKNQVLTNTWLQMYTDHYLOWNVSEYGVKNVRFDPGLWKPDILLYNSADERFDT 125
QY 412 YQTNVVRNNGSCLYVPGIFKSTCKIDITWFFPDQRCCKEMKFGSWTYDGFOLDLQDE 471
DB 126 FHTNVLVNSSGHCQYLPPIGIFKSSCYIDVRWFFDQVCKNLKFGSWTYDGFOLDLQDE 184
QY 472 TGGDISSVVLNGEWELLGVPGKRNLIYVNCCEPIYDITFAIIIRRTLYFFNLIIPCV 531
DB 185 --ADISGYISNGEWDLVGIPGKRTSEFYECCKEYPDITFTVTMRRRTLYYGLNLIIPCV 242
QY 532 LIASMAILGFTLPDPDSGEKLSLGVITLLSLVFLNVAETMPATSDAVPL----- 581
DB 243 LISALALLVFLPADSGEKISLIGIVILLSLVFLVLAIEIMPATSDSPLIAQYFATMI 302
QY 582 -----WIRIVFLCWLPLWLRMSRPGRLIILEFTPTPCS 614
DB 303 IVGLSVVVTIVLYRHHHDPGKMPKWTIRIILNMCWFLMRKPG-----EDKVRPAC 357
QY 615 DTSSERKHOLLSDELKERSKSL-ANVLIDDDFRH-----NCRPMPTGGTLPHPAFY 669
DB 358 QHKQRRCSS--LSSMEMMVTVSQOCSNGNMLYI--GFRGLDGVHCTPTTDSGVI----- 406
QY 670 RTVYGQDGSIGTIGSTRMPDAVTHHTCIKSTSEYELGLILKEIRFITDQLRKDDCND 729
DB 407 -----CGRMTCPTTEENLLHSGHSEGGDPLAKILEEYRYANRFRDQDEEA 455
QY 730 IANDWKFAAMVDRCLLIFTFMAILATIAVLLSAPHII 768
DB 456 ICNEWKFAASVDRCLLMAFSVFTIICITIGILMSAPNEV 494

RESULT 3
T01378
nicotinic receptor alpha 7 chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
C:Accession: T01378
R:Seguela, P.; Wadiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W.
J. Neurosci. 13, 596-604, 1993
A:Title: Molecular cloning, functional properties, and distribution of rat brain alpha 7 nicotinic receptor cDNA
A:Reference number: Z14310; MUID:93147931; PMID:7678857
A:Accession: T01378
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-502 <SEG>
A:Cross-references: EMBL:S53987; NID:g264770; PIDN:AAB25224.2; PID:g5705903
A:Experimental source: brain
C:Superfamily: acetylcholine receptor

Query Match 29.0%; Score 1173.5; DB 2; Length 502;
Best Local Similarity 45.6%; Pred. No. 2.2e-76;
Matches 238; Conservative 80; Mismatches 119; Indels 85; Gaps 10;
QY 297 IYLNLSA---KVCLAGYHEKRLHLLDDPNTLERPVNLNEDPQLQLSFGTLMOIIV 353
DB 8 IWLALAAALLHVSLOGEFQRLYKELVKNYLERPVANDSQPLVYFSLQLQIMDVDE 67
QY 354 KNQLLVNTNWLKLEWDMNLRWNTSDYGVKDLRIPPHRIWKPDVLMYNSADEGFGTYQ 413
DB 68 KNQVLTNTWLQMSWTDHYLOWNMSEYGVKNVRFDPGQIMKPDILLYNSADERFDT 127
QY 414 TNVVRNNGSCLYVPPGIFKSTCKIDITWFFPDQRCCKEMKFGSWTYDGFOLDLQDETG 473


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Db 128 TNYLVNASHGCOYLPGIEKSSCYIDVRNPPFDVQCKLAFGWSYGGWGLDLQMOE---184
QY 474 GDSSVYNGEWELLLGVPGRKNEYIYNCCPEYIDITFEAIIIRRTLYYFNNLIIPCVLI 533
Db 185 ADSSYIPNGEWMOLGIPGRNKEFTYECCKEPPYDVTYITMRRRTLYYGLNLLIPCVLI 244
QY 534 ASMALGFTLPDPSGKLSGLVITLLSLTVFLNNVAETMPATSDAVPL-----581
Db 245 SALALLVFLLPADSGEKISGLITVLLSLTVFLMLVAEIMPATSDSVPLIAQYFASTMIIIV 304
QY 582 -----WIRIVFLCWLWILRMSRPG-----RPLIERPTTP 612
Db 305 GLSVVVTVIVLRYHHDDPGKMPKWTRIILLNCAWFLRMKPGDKVPCOHPKRR- 363
QY 613 CSDTSERKHQILSDVELKERSKSLLANVLDIDDDFRHNCRPMTPGGTLPHPNPAFTV 672
Db 364 CS-----LASVELSAGAG-----PPTSGNLLY-IGFRGL 392
QY 673 YGQ-----GDGSI-SPIGSTRMPDAVTHHTCKSTYELGLILKEIRITDOLRKDE 726
Db 393 EGMHCAPTDPDSGVVCGRLACSPTHDEHLMHGAHPSDGDPDLAKILEVRYIANRRCODE 452
QY 727 CNDIANDWKFAAMVVDRLCLIIITMFAILLATIAVLLSAPHII 768
Db 453 SEVICSEWKPACVDPDPLMAFVFTIICITGILMSAPNFV 494

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RESULT 4

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JH0173
alpha-bungarotoxin-binding protein alpha-2 chain precursor - chicken
C:Species: Gallus gallus (chicken)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Aug-1999
C:Accession: JH0173
R:Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
Neuron 5, 35-48, 1990
A:Title: Brain alpha-bungarotoxin binding protein cDNAs and MAbS reveal subtypes of this
A:Reference number: JH0172; MUID:90315158; PMID:2369519
A:Accession: JH0173
A:Molecule type: mRNA
A:Residues: 1-511 <SCH>
A:Cross-references: GB:X52296; NID:g63081; PIDN:CAA36544.1; PID:g63082
A:Experimental source: brain
A:Note: this sequence is similar to acetylcholine receptor alpha chains
C:Comment: Alpha-bungarotoxin binding proteins are localized to extrasynaptic pseudodend
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-510/Product: alpha-bungarotoxin binding protein alpha-2 chain #status predicted <AE
F:239-262/Domain: transmembrane #status predicted <TM1>
F:270-288/Domain: transmembrane #status predicted <TM2>
F:304-323/Domain: transmembrane #status predicted <TM3>
F:479-496/Domain: transmembrane #status predicted <TM4>
F:54/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Query Match 28.98; Score 1168; DB 2; Length 511;
Best Local Similarity 44.28; Pred. No. 5.7e-76;
Matches 238; Conservative 83; Mismatches 117; Indels 100; Gaps 12;

QY 285 NGLKSHWIFLLYLNLSAKVCLAGYHEKRLLDLDLPYNTLRRPVLNEDPLQSLGLT 344
Db 12 SGJCLWASLFLSFF-----KVSQGESQRRLYDLRLNRYNRLRPVNMDSQPIVVELQLS 66
QY 345 LMQIIDVDENKQLLVTVNWLKLEWMDNLRWNTSDGVGVKDLRLPHRIPKPDVLMYNSA 404
Db 67 LLQIIDVDENKQVLITNWLQMTWVDIYLSWDQYEPGVQVNLRFPSQDIWVPDILLYNSA 126
QY 405 DEGFDTGYQTNVVRNNGSCLYPPGIFKSTCKIDITWFPDQRCMKFGSWTYDGQQL 464
Db 127 DERFDAFTHTNVLNYSQCOYIPPGILKSTCVIYDNRWFFPDVQKDLKFGSWTHSWLI 186
QY 465 DLQLODTGDDISYVLNGEWELLLGVPGRKNEYIYNCCPEYIDITFAIIRRTLYYFF 524

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Db 187 DLQMLE---ADISNYISNGEWDLVGVPGKRNELYYECKEPPYDVTYITMRRRTLYYGL 243
QY 525 NLIIPCVLIASMALGFTLPDPSGKLSGLVITLLSLTVFLNNVAETMPATSDAVPL---581
Db 244 NLIIPCVLISGLALLVFLLPADSGEKISGLITVLLSLTVFLMLVAEIMPATSDSVPLIAQ 303
QY 582 -----WIRIVFLCWLWILRMSRPG-----RPL 604
Db 304 YFASIMVIVGLSVVVTVVLVQLFHHDPPQAGKMPWRVIRVILLNCAWFLRMKPGENIKPL 363
QY 605 ILFEPPTPCSDTSERKHQILSDVELKERSKSLLANVLDIDDDFRHNCRPMTPGGTLPHP 664
Db 364 SCAY-----SYRHPHPSLKNTM-----NVL-----PG-----H 387
QY 665 NPAFYRTVYG-----QGDD--GSIQIGSTRMPDAVTHHTCKIS--STEYELGLI 710
Db 388 QPSNGNNIYSHYTMENPCCQPNNDLGSKSKITCPLSED--NEHVOKKALMDTIPVIVKI 445
QY 711 LKSEIRFITDOLRKDDCNDIANDWKFAAMVVDRLCLIIITMFAILLATIAVLLSAPHII 768
Db 446 LEEVQFIAMFRFRQDEGEETCEWKFAAAVIDRLCLVAFTLFAICTFTILMSAPNFI 503

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RESULT 5

ACHUA7

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nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human
N:Alternate names: cholinergic nicotinate receptor alpha-7 chain
C:Species: Homo sapiens (man)
C>Date: 12-Aug-1996 #sequence_revision 31-Jan-1997 #text_change 22-Jun-1999
C:Accession: I37185; A54194; S60309
R:Peng, X.; Katz, M.; Gerzanich, V.; Anand, R.; Lindstrom, J.
Mol. Pharmacol. 45, 546-554, 1994
A:Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from th
omers expressed in Xenopus oocytes.
A:Reference number: I37185; MUID:94195283; PMID:8145738
A:Accession: I37185
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-502 <PEN>
A:Cross-references: EMBL:X70297; NID:g495606; PIDN:CAA49778.1; PID:g496607
A:Experimental source: brain neuroblastoma cell line SHSY-5Y
R:Chini, B.; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzarotti, M.; Heinemann, S.
Genomics 19, 379-381, 1994
A:Title: Molecular cloning and chromosomal localization of the human alpha-7-nicotini
A:Reference number: A54194; MUID:94245214; PMID:8188270
A:Accession: A54194
A:Molecule type: mRNA
A:Residues: 24-363,'S',365-374,'A',376-408,'AWPAP',414-502 <CHI>
A:Cross-references: GB:223141; NID:g457736; PIDN:CAA80672.1; PID:g457737
A:Experimental source: retina
C:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is locali
C:Genetics:
A:Gene: GDB:CHRNA7
A:Cross-references: GDB:I38751; OMIM:118511
A:Map position: 15q14-15q14
A:Note: defects in this gene have been associated with mental retardation and schizop
C:Complex: the functional receptor molecule is a heteropentamer with two alpha chains
C:Superfamily: acetylcholine receptor
C:Keywords: brain; glycoprotein; heteropentamer; ion channel; neurotransmitter recept
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pr
F:231-254/Domain: transmembrane #status predicted <TR1>
F:262-280/Domain: transmembrane #status predicted <TR2>
F:296-317/Domain: transmembrane #status predicted <TR3>
F:470-488/Domain: transmembrane #status predicted <TR4>
F:46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:150-164/Disulfide bonds: #status predicted
F:362,413/Binding site: phosphate (Ser) (covalent) #status predicted
F:415/Binding site: phosphate (Thr) (covalent) #status predicted
F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

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Query Match 28.78; Score 1160.5; DB 1; Length 502;
Best Local Similarity 45.18; Pred. No. 1.9e-75;

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[illegible]

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Db 362 TRPNRH-----SESLIRNIKNEHLSRANSFDACRLNQYIMTOSVS----- 404
QY 667 AFYRTVYGGDDG--SIGPIGSTRMPDAVTHHTCIKSSTYEYELGLTLKEIRFTDQLRKD 724
Db 405 -----NGLTSLGSIPTSMISSNGTTDVSQATLILLHRIYHEKLVITKRMIEG 453
QY 725 DECNDIANDKFAAMVDRCLLIITFMFAILATIAVLLSAPHII 768
Db 454 DKEEQACNNKFAAMVDRCLLYVFTIIVSTIGIFWSAPYIV 497

RESULT 8
T25671
hypothetical protein D2092.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T25671
R:Gattung, S.; Maggi, L.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid D2092.
A:Reference number: Z20067
A:Accession: T25671
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-461 <GAT>
A:Cross-references: EMBL:U88167; PIDN:AAB42223.1; GSPDB:GN00019; CESP:D2092.3
A:Experimental source: strain Bristol N2; clone D2092
C:Genetics:
A:Gene: CESP:D2092.3
A:Map position: 1
A:Introns: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2
C:Superfamily: acetylcholine receptor

Query Match 25.0%; Score 1009.5; DB 2; Length 461;
Best Local Similarity 39.4%; Pred. No. 1.2e-64;
Matches 209; Conservative 80; Mismatches 126; Indels 115; Gaps 10;

QY 283 ILNGLNKHWFLLIYLNLSAKVLAGYHEKRLLDLPYNTLERPVNESDPLQLSFG 342
Db 2 IFNLINS-----ILSLVITHSNLCGSAETKLTDLKGYNPLRPVQNSQPLEVKIK 56
QY 343 LTLMLQIIDYDEKNOILLVNNWKLKLENDNMLRWNTSDYGVKDLRIP--PHRIWKPDLML 400
Db 57 LFLQQLLDVDERKQIVSVNAWLSYTFDHLKQWPKYGGIQQDIRPFGSSDHIWKPDLVL 116
QY 401 YNSADEGFGDTQTNNVVRNNGSCLYVPPGIFKSTCKIDITWFPDDORCEMKFGSWTYD 460
Db 117 YNSAEDFSTFKSNLLTHTGTWVWIPGVKLVQCLDVTWFPDDQVCEMKFGSWTH 176
QY 461 GFOLDLQLODETGG-----DISSVVLNGEWELLVGPGRNEIYVNCPCPEYIDITFAIIR 516
Db 177 GYALDQLDIDDTNGTQSMDLSTYLVNGEQVISTNAKRVVSYVYKCCPEYPTVNYVLR 236
QY 517 RRTLYFFNLIIPCVLIASWALLGFTLPDSEKLSLGVTTILLSLTVFLNVAETMPATS 576
Db 237 RRTLYGFNLIIPSLIISMAILGEMFPDAGEKITLEVTILLAIIVFFLSVMSEMTPTPS 296
QY 577 DAVPL-----WIRVFLCMLPWILRMSR 599
Db 297 EAVPLIGVFSCMLVSVASVFTIIVNLHFRSADSHENPLVRVRYLLEFLPWLFWSR 356
QY 600 PGRPLILEPTTPCSDTSSERKHQILSDVELKERSKSLLANVLDIDDDFRNCRPMTPT 658
Db 357 PG-----YKFVKANVIDSTDKMPK--KPKNPL 381
QY 659 GTPLHNPAPFYTVYGGDDGSGIGPIGSTRMPDANTHTCIKSSTYEYELGLTLKEIRFIT 718
Db 382 DCNLPNSHAGY-----EAQILLHSV-----HT-----ELRRVY 410
QY 719 DQLRDKDECDNDIANDKFAAMVDRCLLIITFMFAILATIAVLLSAPHII 768
Db 411 AFYNKEEHDERIQTDWRFAAMVDRCLLFTFVIFVISILATMSAPHII 460
```

RESULT 9

T19622

hypothetical protein C31H5.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C:Accession: T19622

R:Kershaw, J.

submitted to the EMBL Data Library, April 1997

A:Reference number: Z19153

A:Accession: T19622

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-560 <WIL>

A:Cross-references: EMBL:Z93778; PIDN:CAB07843.1; GSPDB:GN00019; CESP:C31H5.3

A:Experimental source: clone C31H5

C:Genetics:

A:Gene: CESP:C31H5.3

A:Map position: 1

A:Introns: 24/1; 70/3; 139/2; 270/1; 299/1; 336/3; 372/2; 456/3

C:Superfamily: acetylcholine receptor

Query Match 24.4%; Score 988; DB 2; Length 560;

Best Local Similarity 37.2%; Pred. No. 5.3e-63;

Matches 214; Conservative 85; Mismatches 152; Indels 124; Gaps 13;

QY 293 IFLLIYLNLSAKVLAGYHEKRLLDLPYNTLERPVNESDPLQLSFGTLMLQIIDVD 352

Db 12 VSLIWEKCSKVITGTGDHERRLYAKLAENYNKLARPVNRESEAVVLLGMDYQQIILDID 71

QY 353 ERNQLLVTVNWLKLENDNMLRWNTSDYGVKDLRIPPHRIWKPDLVMTNSADEGPDGY 412

Db 72 EXHQIMNSNVWLMRMSWTDLWTDPSEFGNIKEVRLPINNIWKPDLVLLNSVDQPDSTW 131

QY 413 QTNVVRNNGSCLYVPPGIFKSTCKIDITWFPDDORCEMKFGSWTYDGFOLDLQLODET 472

Db 132 PYNAVVLVTGNTWTPPAIIRSCAIDIAIFPDTOHCTMKFGSWTYSGFTDL---INT 188

QY 473 GGDISYVLNGEWELLVGPGRNEIYVNCPCPEYIDITFAIIRRTLYFFNLIIPCVL 532

Db 189 TISPATYKPGEWELLVGLTSQSIFFYECPCPEYDVTFTVSIIRRTLYVGNLLPCML 248

QY 533 IASMAILGFTLPDSEKLSLGVTTILLSLTVFLNVAETMPATSDAVPLWIRVFLC--- 589

Db 249 ISSALLSFTLPADCGEKLNLGVTIPMSLCVFEMVAEAMPQTSALPL-IQIFYSCIMF 307

QY 590 -----WLPWILRMSRPGRLILEPPTTPC 613

Db 308 QVGASVVAIVIALNFHRSPEQYKPMKFKLTLGLGLWLPGLLGMERPD---VLELSVHGA 364

QY 614 SDTSSERKHQ-----IL-----SDVELKERSKSL 638

Db 365 HYASDNKKQROYLLIEVERHILTRPNNGHSAVDKAVHLDSLSTGNPHSDAKKSSPSKPT 424

QY 639 LANVLD-----IDDDF-RHNC-----RPMTPG-GTLPH-----NPAFYRTVYG 674

Db 425 SASIMGTGLPTTOMGALDSSINKYTKTRPLENGSATINHKSSPOINPINNNIYK 484

QY 675 QGDDGSGIGSTRMPDANTHTCIKSSTYEYELGLTLKEIRFITDOLRDKDECDNDIANDW 734

Db 485 CANN-----QKTQFEDRHFH-----ILNELRVISARVKEEAHMAHALQADM 525

QY 735 KFAAMVDRCLLIITFMFAILATIAVLLSAPHII 769

Db 526 MFASRVDRVCFALSAFLMCTAISYNAPHLFV 560

RESULT 10

T19862

hypothetical protein C40C9.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T19862

R;Hemby, C.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19188
A:Accession: T19862
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-542 <WIL>
A:Cross-references: EMBL:Z70266; PIDN:CAA94206.1; GSPDB:GN00028; CESP:C40C9.2
A:Experimental source: clone C40C9
C:Genetics:
A:Gene: CESP:C40C9.2
A:Map position: X
A:Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1; 49
C:Superfamily: acetylcholine receptor

Query Match 24.0%; Score 968.5; DB 2; Length 542;
Best Local Similarity 38.7%; Pred. No. 1.3e-61;
Matches 208; Conservative 79; Mismatches 144; Indels 107; Gaps 12;
QY 312 EKRLHLLDPYNTLERPVNESDPLQSLFGLTLMQIIDVDEKNQLLVNWLKLEWDM 371
DB 30 EYRLADLRNIDYPERVANASEPLVSVKIIYQQIILDVDEKNQVITLVAVIEYQWTDY 89
QY 372 NLRWNTSDYGVKDLRIP--PHRIWKPDVLMYNSADEGFDGTOTVNVVRNNGSLVPP 429
DB 90 KKWDPSEYGGIKDIRIPGNANALWKPDVLYNSADENFSTPTVNTVWSYTGVDLVQVPP 149
QY 430 GIFKSTCKIDITWFPDQRCMKFGSWTYDGFQDLQLO-----DETGDDISSYVLN 482
DB 150 GILKLSCKIDITWFPDQRCMKFGSWTYSGNFDLRINGPEGKNISDEGIDVQVYVQN 209
QY 483 GEWELLVGPKRNEIYVNCPEYIDITFAIIRRTLYFFNLIIPCVLIASMALLGFT 542
DB 210 GWNLLAVAPRAHETNIF--EQYPSLFYLIQRTLYGLNLIIPSFLISLMTVLGFT 267
QY 543 LPDPSGEKLSGVITILLSVFLNMVAETMPATSDAVPL-----LDIDDDF--RHN-CRPM 581
DB 268 LPDAGEKIYLEITILLSVGFLLSNVADMTPTSEAVPLGLIIFSGAFSCCMVVSAS 327
QY 582 -----WIRIVLCWLPILMRSPGRPLILEFTTPCSDTSSE 619
DB 328 VFTVLVNLNHRKPETHMSPLRELLIWLPLMLRRPGKTF-----NCTHLKAE 381
QY 620 RKHQILSDVELKE-----RSSKSLANV-----LDIDDDF--RHN-CRPM 656
DB 382 KAEKAKQSGIKNGVGGKPTDSDVHPSEGLSMKNIKLGRQQTIDFYEYFVQHNLMPV 441
QY 657 TPGGTLPHNPAFYRTYVGGDGSIGPIGSTRMPDAVTHHTCIKSTSEY-----ELGLI 710
DB 442 APSEMTPE-----RVTY-----SKVMAESYVEDVWTELKYNKQKACLELKN 483
QY 711 LKEIRFTDQLRKDECDNDANDWKFAAMVVDRLCLIIFTWFAIATIAVLLSAPHII 768
DB 484 SSQTRAMRKMEEDERDEQAANDWKFAAMVVDRCCLITFSVFIVWTCGIMFSSPHLI 541

RESULT 11

ACFAI
nicotinic acetylcholine receptor alpha-1 chain precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jun-2002
C:Accession: S00381; A38801
R;Bossy, B.; Ballivet, M.; Spierer, P.
EMBO J. 7, 611-618, 1988
A:Title: Conservation of neural nicotinic acetylcholine receptors from Drosophila to ver
A:Reference number: S00381; MUID:88283626; PMID:2840281
A:Accession: S00381
A:Molecule type: DNA
A:Residues: 1-567 <BOS>
A:Cross-references: GB:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576
A:Accession: A38801
A:Molecule type: mRNA
A:Residues: 1-567 <B02>

A:Cross-references: EMBL:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576
A:Note: 538-Tyr was also found
C:Genetics:
A:Gene: FlyBase:NAcr-alpha-96Aa
A:Cross-references: FlyBase:FBgn0000036
A:Map position: 3R 96A
A:Introns: 64/3; 79/3; 116/2; 176/3; 330/2; 401/1; 499/3
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membra
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-567/Product: nicotinic acetylcholine receptor alpha-like chain #status predicted
F:22-240/Domain: extracellular #status predicted <EXT>
F:240-264/Domain: transmembrane #status predicted <TM1>
F:272-290/Domain: transmembrane #status predicted <TM2>
F:306-325/Domain: transmembrane #status predicted <TM3>
F:326-513/Domain: intracellular #status predicted <INT>
F:514-532/Domain: transmembrane #status predicted <TM4>
F:545-233/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:149-163,222-223/Disulfide bonds: #status predicted

Query Match 22.0%; Score 889; DB 1; Length 567;
Best Local Similarity 35.2%; Pred. No. 6.7e-56;
Matches 196; Conservative 91; Mismatches 168; Indels 102; Gaps 10;
QY 291 SWIFLLIYLNLS-AKVCAGYHEKRLHLLDPYNTLERPVNESDPLQSLFGLTLMQII 349
DB 3 SVLFAAVFIATLHATGATGLAMPDAKRLYDLDLSNRYLRIRPVGNNSDRLTVMKURLSOLI 62
QY 350 DVEKKNOLLVTNVWLKLEWDMNLRWNTSDYGVKDLRIPPHRIWKPDVLMYNSADEGFD 409
DB 63 DVNLKNOIMTWNVEQEWNDYKLNWPDYGGVDTLHVPSEHWHHPDIVLYNNADNYE 122
QY 410 GTYQTNVVVRNNGSLVPPGIFKSTCKIDITWFPDQRCMKFGSWTYDGFOLDL--- 466
DB 123 VTIMTKAILHHTGKVVWKPPAIYKSFCEIDVEYFPFDEQTCFMKFGSWTYDGYMVDLRHL 182
QY 467 -QLOD-----ETGGDISYVLNGEWELLVGPKRNEIYVNCPEYIDITFAIIRRTLY 521
DB 183 KQTADSDNIEVGIDLDQYIISVEMDIMRVPVAVRNEKEYSCCEPYLDIVNLTLRRRTLF 242
QY 522 YFNLIIPCVLIASMAILGFTLPDPSGEKLSGLVITILLSVFLNMVAETMPATSDAVPL 581
DB 243 YTVNLIIPCVGISFLSVLVEPLSDSGEKISLCISILLSLTVFPLLLAEIIPPTSLVPL 302
QY 582 -----WIRIVLCWLPILMRSPGRPL 604
DB 303 LGKYLFTMLVTLVVVVTIAVLNVNPRSPVTHRMAPVQVRLFIQILPKLICIERPKK-- 360
QY 605 ILEFPTTPCSDTSERKHOILSDV-ELKERSKSLANVLDIDDDFRHNCRPMTPPGTLP 663
DB 361 -----EPEEDQPEVLTVDYHLPP-----DVDFVNVDSKRFSGDYGIP 400
QY 664 HNPAYR-----TVYQGDD-----GSIGPIGSTRMPDAVTH 695
DB 401 ALPASHRFDLAAAGGISAHCAFAEPPLPSSLLPLGADDDLFSPSLNGDISGCCPAAAAA 460
QY 696 HTCIKST-----EYELGLILKEIRFTDQLRKDECDNDANDWKFAAMVVDRLCLIFT 750
DB 461 AAADLSPTFKPYAREMEKTIIEGSRFIAQHVKNKDKFESVEEDWKVYAMVLDRLMFLWIFA 520
QY 751 MFAIATIAVLLSAPHI 767
DB 521 IACVVGTAIIILQAPSL 537

RESULT 12

S12359
nicotinic acetylcholine receptor alpha-L1 chain precursor - desert locust
C:Species: Schistocerca gregaria (desert locust)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C:Accession: S12359
R;Marshall, J.; Buckingham, S.D.; Shingai, R.; Lunt, G.G.; Goosey, M.W.; Darlison, M.
EMBO J. 9, 4391-4398, 1990

A;Title: Sequence and functional expression of a single alpha subunit of an insect nicotinic acetylcholine receptor
A;Reference number: S12359; MUID:91092263; PMID:1702381
A;Accession: S12359
A;Molecule type: mRNA
A;Residues: 1-557 <MAR>
A;Cross-references: EMBL:X55439; NID:g10133; PIDN:CAA39081.1; PID:g10134
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-557/Product: nicotinic acetylcholine receptor alpha-L1 chain #status predicted <MAT>
F;245-266/Domain: transmembrane #status predicted <TM1>
F;274-295/Domain: transmembrane #status predicted <TM2>
F;308-329/Domain: transmembrane #status predicted <TM3>
F;501-523/Domain: transmembrane #status predicted <TM4>
F;47,235/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 21.6%; Score 873; DB 2; Length 557;
Best Local Similarity 36.8%; Pred. No. 9.2e-55;
Matches 197; Conservative 90; Mismatches 174; Indels 74; Gaps 8;
QY 293 IFLLIYLNLSAKVCLAGYHEKRLHLLDPPYNTLRLPVLNESDPLQLSFGLTLMQIIDVD 352
Db 8 MLLLLLLLLHHPAAAPDAKRLYDLSNRYLRPVSNNTDTVLKGLRLSQLIDLN 67
QY 353 EKQOLLVTNVWLKLEWDMNLRWNTSDYGVKDLRPPHRIKPDVLMYNSADEGDTY 412
Db 68 LKQILLTNNWLEHWDHFRDPAEYGGVTELYPSEHILPDIVLYNADGEVVT 127
QY 413 QTNVVRNNGSLYVPGIFKSTCKIDITWPPDDQRCMKFGSWTYDGFQDL---QL 468
Db 128 MTKAVLHHTGKVVTTPAIFKSCSIDVRYFPDQOTCFMKFGSWTYDGDQIDKHNQK 187
QY 469 QDE-----TGGDISYVLNGEWELLGVPGRNEIYVNCPEPYIDITFAIIRRTLYYFF 524
Db 188 YDNKVKVGLDREYVPSVEMDILGVAERHEKYVCCAPYDPIDFENITLRKTELYTV 247
QY 525 NLIIPCVLIASMLLFTLPDPSGEKLSLGVITLLSVTLPLNVAETMPATSDAVPL--- 581
Db 248 NLIVPCVGISYLVFLPADSGEKIALCISILLSTQMPFLITSEIIPSTSLALPLGK 307
QY 582 -----WIRVFLCWLPLWLRMRGRPLILE 607
Db 308 YLFTWVLVGLSVITIMLVNHYRKPSTHKMAPVWKVFIKRLPCLLLMRVPEQL--- 364
QY 608 FPTTPCSDTSERKHQILSDVELKERSKSLA---NVLIDDDFRHN----- 652
Db 365 -----ADLASKRLLRHAHNSKLSAAAAAASSSAASPDLSRHHHLHQHQHHL 418
QY 653 --CRPMTPGTLPHPNPAFYRTVYGGDDGSGIGSTPMPPDVTHHTCIKSTYEYELGLI 710
Db 419 QLHHLQRPGCCNGLHSATNR--FG-GSAGAFGLPSVVGDLGSLSDVATRKYPFELEKA 475
QY 711 LKEIRFTDQLRKDDCNDIANDKAAVMDRLCLLIETMFAIATIAVLLSAP 765
Db 476 IHNVLFIQNHQKODEDAEDQWGFVAMVLDRLFLWIFTIASIVGTFAILCEAP 530

RESULT 13
A53956
nicotinic acetylcholine receptor alpha-3 chain precursor, neuronal - human
C;Species: Homo sapiens (man)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 20-Aug-1999
C;Accession: A53956; S21338
R;Mihovilovic, M.; Roses, A. D.
Exp. Neurol. 111, 175-180, 1991
A;Title: Expression of mRNAs in human thymus coding for the alpha3 subunit of a neuronal
A;Reference number: A53956; MUID:91114756; PMID:1989896
A;Accession: A53956
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-503 <MTH>
A;Cross-references: GB:M37981; NID:g189252; PIDN:AAAS9942.1; PID:g189253
R;Anand, R.; Lindstrom, J.

submitted to the EMBL Data Library, June 1990
A;Description: Nucleotide sequence of the mature human nicotinic acetylcholine receptor
A;Reference number: S21338
A;Accession: S21338
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 30-503 <ANA>
A;Cross-references: EMBL:X53559; NID:g34985; PIDN:CAA37625.1; PID:g34986
C;Genetics:

A;Gene: GDB:CHRNA3
A;Cross-references: GDB:125219; OMIM:118503
A;Map position: 15q24-15q24
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor

Query Match 20.9%; Score 845; DB 2; Length 503;
Best Local Similarity 35.2%; Pred. No. 8.2e-53;
Matches 178; Conservative 97; Mismatches 166; Indels 64; Gaps 6;
QY 295 LLIYLNLSAKVCLAGYHEKRLHLLDPPYNTLRLPVLNESDPLQLSFGLTLMQIIDVDEK 354
Db 17 LLLLLSL-LPVARASEAEHRLFERLPEDYNEIIRPVANVSDPVIHFEVMSQLVKVDEV 75
QY 355 NQLLVTVNLKLEWDMNLRWNTSDYGVKDLRIPHRHWKPDVLMYNSADEGDTGYOT 414
Db 76 NQIMETNLWLKQIWDYKLNWPSDYGAEFMRVPAQKIWKPDIVLYNNAVGDFQVDDKT 135
QY 415 NVVVRNNGSLYVPGIFKSTCKIDITWPPDDQRCMKFGSWTYDGFQDLQLODDETG 474
Db 136 KALKYTGVTWTPAIFKSSCKIDVTFYFPDQNTMKFGSWYKAKIDLVLIG-SSM 194
QY 475 DISSYVLNGEWELLGVPGRNEIYVNCPEPYIDITFAIIRRTLYYFFNLIIPCVLIA 534
Db 195 NLADYEWESGEWAIKAPGYKHKDIKNCCREIYDIPVLSYLRPLFTYTNLIIPCLIS 254
QY 535 SMALLGFTLPDPSGEKLSLGVITLLSVTLPLNVAETMPATSDAVPL----- 581
Db 255 FLTVLVFLYLPDSCGKVTLCISVLLSLTVFLLVITETIPSTSLVPLIGLYLFTMTFVT 314
QY 582 -----WIRVFLCWLPLWLRMRGRPLILEFPTTPCSDTS 617
Db 315 LSIVITVFLNVHYRTPHTMPSWKVTFVLLPLRV-----FMRTPTNEG 362
QY 618 SERKHQILSDVELKERSKSLANVLIDDDFRHNCRPMTPGGTLPHPNPAFYRTVYGGDD 677
Db 363 NAQKPRPLYGAELSNLNCFSRAES-----KGCKEGYPCODGCMGCHHRRIKISNF 413
QY 678 DGSIGIGSTPMPPDVTHHTCIKSTYEYELGLILKEIRFTDQLRKDDCNDIANDKFA 737
Db 414 SANLTRSSSESVDVLS-----LSALSPEIKAEIOSVKYIAENKKAQNEAKETODDKYV 469
QY 738 AMVVDRLCLLIETMFAIATIAVLL 762
Db 470 AMVIDRFLWVTLVLCILTAGLFL 494

RESULT 14
ACFFA2
nicotinic acetylcholine receptor alpha-2 chain precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jun-2002
C;Accession: S11679; S10306; S11084
R;Sawruk, E.; Schloss, P.; Betz, H.; Schmitt, B.
EMBO J. 9, 2671-2677, 1990
A;Title: Heterogeneity of Drosophila nicotinic acetylcholine receptors: SAD, a novel
A;Reference number: S11679; MUID:90360975; PMID:1697262
A;Accession: S11679
A;Molecule type: mRNA
A;Residues: 1-576 <SAW>
A;Cross-references: EMBL:X53583; NID:g8532; PIDN:CAA37652.1; PID:g8533
A;Note: 232-ile was also found
R;Baumann, A.; Jonas, P.; Gundelfinger, E. D.
Nucleic Acids Res. 18, 3640, 1990

A:Title: Sequence of D-alpha-2, a novel alpha-like subunit of Drosophila nicotinic acetylcholine receptor
A:Reference number: S10306; MUID:90301489; PMID:2114015
A:Accession: S10306
A:Molecule type: mRNA
A:Residues: 1-576 <BAU>
A:Cross-references: EMBL:X52274; NID:g7802; PIDN:CAA36517.1; PID:g7803
R:Jonas, P.; Baumann, A.; Merz, B.; Gundelfinger, E.D.
FEBS Lett. 269, 264-268, 1990
A:Title: Structure and developmental expression of the D-alpha-2 gene encoding a novel alpha-2 subunit of Drosophila nicotinic acetylcholine receptor
A:Reference number: S11084; MUID:90353591; PMID:2117557
A:Accession: S11084
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 42-90, 'I', '92-576 <JON>
C:Genetics:
A:Gene: FlyBase:nACR-alpha-96AB
A:Cross-references: FlyBase:FBgn0000039
A:Map position: 3R 96A
A:Introns: 84/3; 136/2; 196/3; 250/1; 445/2; 512/3
A:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
F:1-41/Domain: signal sequence #status predicted <SIG>
F:42-576/Product: nicotinic acetylcholine receptor alpha-2 chain #status predicted <BAT>
F:42-260/Domain: extracellular #status predicted <EXT>
F:261-287/Domain: transmembrane #status predicted <TM1>
F:293-311/Domain: transmembrane #status predicted <TM2>
F:327-348/Domain: transmembrane #status predicted <TM3>
F:349-526/Domain: intracellular #status predicted <INT>
F:527-545/Domain: transmembrane #status predicted <TM4>
F:65,254,570/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:169-183/Disulfide bonds: #status predicted

Query Match 20.9%; Score 843.5; DB 1; Length 576;
Best Local Similarity 34.4%; Pred. No. 1.3e-52;
Matches 193; Conservative 87; Mismatches 170; Indels 111; Gaps 11;

QY 290 HSW-----IFLLIYLNLSAKVCLAGYHEKRLHLLDPYNTLERPVNLNESPQLQSLFGLT 344
DB 18 HIWRCKPLCLLLVLLLCETVQANPDARLKYDYLSSNRLIRPVSNNTDTVLVKGGLR 77
QY 345 LMOIIDVDEKOLLVTNWLKLEWDMNLRNWTSDYGVKDLRIPIPHRIKVPDVLVYNSA 404
DB 78 LSQIDLNLKQDLITNWLHEWQDHFKFDPSEYGVTELYVPSHILWLPDVLVYNSA. 137
QY 405 DEGFDTGYQTNVVRNNSCLYVPPGIFKSTCKIDITWFPDDQRCCKMFGSWTYDGPQL 464
DB 138 DGEYVVTMTKAILHYTKVWVTPPAIFKSCEIDVRYFPDQRCCKMFGSWTYDGPQI 197
QY 465 DL-----QLQD-----ETGDDISSYVLNGEWELLGVPGKRNELIYNCCPEYDITFAIII 515
DB 198 DLKHISQRNDKNKVEIGIDLREYYPSEVDILGVPAERHEKYPCCAEYPIPIFNITL 257
QY 516 RRTLYYFNLIIPCVLIASMALGFTPPDSGKLSLGVITLLSLTVFLANVAETMPAT 575
DB 258 RKTLFYTNLIIPCVGISYLSVLVYLPADSGEKALICISLLSQTWFFLLISLIPST 317
QY 576 SDAPVL-----WIRYIFLCWLPWILRMS 598
DB 318 SLALPLKCYLLFTMLLVGLSVITIIILNTHYRKPSTHKRPWIRSPFIKRLPKLLMR 377
QY 599 RGRPLILEFTPTPCSDTSSEKHOILSDVELKE-----RSKSLANVLIDDDFRNC 653
DB 378 VP-----KDLRLDLANKINYGLKFSKTFGQAL-MDE----- 409
QY 654 RPTPGGLPHNPAFYRTVYGGD-----DGSGTGPICS-----TRMPDA 692
DB 410 MQMNSGGSPSLRRMQGRVAGGCGNMHVTTATNRFSGLVGALGCGGLSTLSGYNGLPV 469
QY 693 VT-----HHTCIKSTSEYELGLILKEIRFTDQKDECDNDIANDKFAAMVDRCL 746
DB 470 LSGLDLSLSDVAARKKYPFELEKAIHNYMFIQHMQRQDEFNADQDQGFVAMVDRFL 529
QY 747 IIFTFAIATAVLLSAPHI 767

DB 530 WLFMIASLVGTFFVILGEAPSL 550
RESULT 15
ACFFNN
C:Species: Drosophila melanogaster
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
C:Accession: S03012; A38064; A26313; A28126; A38759
R:Sawruk, E.; Hermans-Borgmeyer, I.; Betz, H.; Gundelfinger, E.D.
FEBS Lett. 235, 40-46, 1988
A:Title: Characterization of an invertebrate nicotinic acetylcholine receptor gene: t
A:Reference number: S03012; MUID:88296842; PMID:3136037
A:Accession: S03012
A:Molecule type: DNA
A:Residues: 1-521 <SAW>
A:Cross-references: EMBL:X07956; NID:g7602; PIDN:CAA30778.1; PID:g1065712
A:Accession: A38064
A:Molecule type: mRNA
R:Hermans-Borgmeyer, I.; Zopf, D.; Ryseck, R.P.; Hovemann, B.; Betz, H.; Gundelfinger
EMBO J. 5, 1503-1508, 1986
A:Title: Primary structure of a developmentally regulated nicotinic acetylcholine rec
A:Reference number: A26313
A:Accession: A26313
A:Molecule type: mRNA
A:Residues: 1-72, 'V', '74-521 <HER>
A:Cross-references: EMBL:X04016; NID:g7537; PIDN:CAA27641.1; PID:g7538
R:Wadsworth, S.C.; Rosenthal, L.S.; Kammermeyer, K.L.; Potter, M.B.; Nelson, D.J.
Mol. Cell. Biol. 8, 778-785, 1988
A:Title: Expression of a Drosophila melanogaster acetylcholine receptor-related gene
A:Reference number: A28126; MUID:88174720; PMID:2832736
A:Accession: A28126
A:Molecule type: mRNA
A:Residues: 1-521 <WAD>
A:Cross-references: EMBL:M20316
C:Genetics:
A:Gene: arid
A:Cross-references: FlyBase:FBgn0000038
A:Map position: 3L 64B/C
A:Introns: 22/1; 67/3; 119/2; 267/3; 467/3
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membra
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-521/Product: nicotinic acetylcholine receptor nonalpha chain #status predicted <
F:25-236/Domain: extracellular #status predicted <EXT>
F:237-260/Domain: transmembrane #status predicted <TM1>
F:268-285/Domain: transmembrane #status predicted <TM2>
F:302-323/Domain: transmembrane #status predicted <TM3>
F:324-481/Domain: intracellular #status predicted <INT>
F:482-500/Domain: transmembrane #status predicted <TM4>
F:48/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:152-166/Disulfide bonds: #status predicted

Query Match 20.8%; Score 841; DB 1; Length 521;
Best Local Similarity 35.6%; Pred. No. 1.7e-52;
Matches 186; Conservative 95; Mismatches 172; Indels 70; Gaps 9;

QY 291 SWIFLLIYNLSAKVCLAGYHEKRLHLLDPYNTLERPVNLNESPQLQSLTLMQIID 350
DB 7 SWLGSILVLVAFSLVSASEDEERLVRDLFGYKRLIRPVQNMOTKQVGRGLAVQLIN 66
QY 351 VDEKNOLLVTNWLKLEWDMNLRNWTSDYGVKDLRIPIPHRIKVPDVLVYNSADEGFDG 410
DB 67 VNEKNQIMKSNVNLRLWYDQLQWDEADYGGIGVLRPLPPDKVKVPDVLVFNADGNVEY 126
QY 411 TYQTNVVRNNSCLYVPPGIFKSTCKIDITWFPDDQRCCKMFGSWTYDGPQLQL-Q 469
DB 127 RYKSNVLIYPTGELWVPPAIYQSSCTIDVTYFPDQTCIMKFGSWTFNGDQVSLALYN 186
QY 470 DETGDDISSYVLNGEWELLGVPGKRNELIYNCCPEP-YIDITFAIIRRTLYYFNLI 528

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Db 187 NKNFVLSYWKSGTWDIIIEVPAYLN-VYEGDSNHPTETDITFYIIIRKTLFYTVNLIL 245
QY 529 PCVLIASMAIIGFTLPDPDSGEKLSLGTILLSLTVFLNMVAETMPATS----- 576
Db 246 PTVLISFLCVLYFLPAEAGEKVTLGISILLSLVVELLVSKILPPTSLVLPILAKYLLF 305
QY 577 -----DAVPLWIRIVFLCWLPMILRMSRGRPLILEFPPT 611
Db 306 TFIIMTVSILVTVIIINWNFRGPRTHRMPMYIRSIPLHYLPAFLPMKRPKTRLRMMEM 365
QY 612 PCSDTSSERKHQILSDVELKERSS-----KSLLANVLIDDDFRHNC---RPMTPGGTLPH 664
Db 366 PGMSMPAHPHPYSGPAELPKHISATGGKQKMEVMEISDLHHPNCKINRKVNSGEL-- 423
QY 665 NPAFYRTVYQGDGDSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDOLRKD 724
Db 424 -----GLGD---GCRRESSESDSILLSPEASKATE-----AVEFIAEHLRNE 462
QY 725 DECNDIANDKFAAMVVDRLCLIIETMFAILATIIVLLSAPHI 767
Db 463 DLYIQTREDWKYVAMVIDRLQLYIFFIVTTAGTVGILMDAPHI 505
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Search completed: August 13, 2003, 15:30:19
Job time : 30.7606 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2003, 15:14:30 ; Search time 67.5439 Seconds
(without alignments)
1809.483 Million cell updates/sec

Title: US-09-303-232-2

Perfect score: 4043

Sequence: 1 MKNAQLKTEVDDDELWLAV.....MFAILTAVLLSAPHIIVS 770

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4043	100.0	770	21	AA1980
2	1850	45.8	496	21	AA1981
3	1809	39.8	501	21	AA1982
4	1498.5	37.1	327	22	AA1983
5	1407.5	34.8	311	22	AA1984
6	1179.5	29.2	502	18	AA1985
7	1168	28.9	511	18	AA1986
8	1159.5	28.7	502	15	AA1987
9	1159.5	28.7	502	18	AA1988
10	1159.5	28.7	502	21	AA1989
11	1159.5	28.7	502	21	AA1990
12	1159.5	28.7	502	21	AA1991
13	1159.5	28.7	502	21	AA1992
14	1159.5	28.7	502	21	AA1993
15	1159.5	28.7	502	21	AA1994
16	1159.5	28.7	502	21	AA1995
17	1159.5	28.7	502	21	AA1996
18	1159.5	28.7	502	21	AA1997
19	1159.5	28.7	502	21	AA1998
20	1159.5	28.7	502	21	AA1999
21	1159.5	28.7	502	21	AA2000
22	1159.5	28.7	502	21	AA2001
23	1159.5	28.7	502	21	AA2002
24	1159.5	28.7	502	21	AA2003
25	1159.5	28.7	502	21	AA2004
26	1159.5	28.7	502	21	AA2005
27	1159.5	28.7	502	21	AA2006
28	1159.5	28.7	502	21	AA2007
29	1159.5	28.7	502	21	AA2008
30	1159.5	28.7	502	21	AA2009
31	1159.5	28.7	502	21	AA2010
32	1159.5	28.7	502	21	AA2011
33	1159.5	28.7	502	21	AA2012
34	1159.5	28.7	502	21	AA2013
35	1159.5	28.7	502	21	AA2014
36	1159.5	28.7	502	21	AA2015
37	1159.5	28.7	502	21	AA2016
38	1159.5	28.7	502	21	AA2017
39	1159.5	28.7	502	21	AA2018
40	1159.5	28.7	502	21	AA2019
41	1159.5	28.7	502	21	AA2020
42	1159.5	28.7	502	21	AA2021
43	1159.5	28.7	502	21	AA2022
44	1159.5	28.7	502	21	AA2023
45	1159.5	28.7	502	21	AA2024

Human PRO2145 prot
Nicotinic acetylch
Wild-type human al
Human neuronal NAC
Human neuronal nic
V274T variant huma
Mutant human alpha
Mutant human alpha
Mutant human alpha
Drosophila melanog
Drosophila melanog
Caenorhabditis ele
Caenorhabditis ele
Chimeric alpha7/5-
Mature cell surfac
Human neuronal nic
Alpha 2 subunit of
Neuronal nicotinic
Human neuronal NAC
Human neuronal nic
Prostate cancer-as
Drosophila melanog
Neuronal nicotinic
Drosophila melanog
Drosophila melanog
Modified acetylcho
Drosophila melanog
Caenorhabditis ele
Caenorhabditis ele
Drosophila melanog
Modified acetylcho
JTF-38 nAChR alpha
Drosophila melanog
Neuronal nicotinic
Human neuronal NAC

ALIGNMENTS

RESULT 1
AA1980
ID AA1980 standard; Protein; 770 AA.
AC AA1980;
XX
XX
DT 17-FEB-2000 (first entry)
XX
DE D. melanogaster, acetylcholine receptor protein from clone Da7.
DE Acetylcholine receptor; nicotinic; insect; insecticide; screening;
KW neurotransmission; plant protection agent; conductance; AChR.
XX Drosophila melanogaster.
OS
PN DE19819829-A1.
XX
PD 11-NOV-1999.
XX
PF 04-MAY-1998; 98DE-1019829.
XX
PR 04-MAY-1998; 98DE-1019829.
XX
PA (FARB) BAYER AG.
XX
PI Adamczewski M, Oellers N, Schulte T;
XX WPI; 2000-014207/02.
DR N-PSDB; AAZ24475.
XX
PT New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides -

Db 244 NLLIPCVLISGLALVFLPADSGEKLSTGLTIVLSLVFVLLVAEIMPATSDSVPLIAQ 303
 Qy 582 -----WIRIVELWLPWILMSRPG---RPL 604
 Db 304 YFASIMVIGLSVVTVLVLFQHHDPQAGKMPWRVRVILLNWCWFLRMKKGKPKL 363
 Qy 605 ILEFPTPCSTSSERKHOILSDVELKERSKSLANVLDIDDDFRHNCRPMTPGGTLPH 664
 Db 364 SCKY-----SYPKHPSLKNTEM-----NVL-----PG-----H 387
 Qy 665 NPAFRTVYG-----QGDD--GSIGPIGSTRMPDVAHTHTCIKS--STVELGLI 710
 Db 388 QPSNGNMTIYXHTMENPCPNQNDLGSKGITCPLSED--NEHVQKKALMDTIPVIVKI 445
 Qy 711 LKEIRFIDQLRQDECDIANDKFAAMVVDRLCLIFTMFAILATIAVLLSAPHII 768
 Db 446 LEEVQFIAMRRFKQDEGEICSEWKFAAAVIDRCLVAFTLFAICTFTILMSAPNFI 503

RESULT 8

AAW44153
 ID AAW44153 standard; Protein; 502 AA.

XX AC AAW44153;

XX 14-MAY-1998 (first entry)

XX Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.

XX Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
 KW brain tissue; screening; NACHR; antibody.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..23

FT /label= signal

FT Domain 229..256

FT /label= TMD1

FT /note= "transmembrane domain"

FT Domain 262..284

FT /label= TMD2

FT /note= "transmembrane domain"

FT Domain 290..317

FT /label= TMD3

FT /note= "transmembrane domain"

FT Misc-difference 343

FT /note= "encoded by CTS"

FT Domain 462..487

FT /label= TMD4

FT /note= "transmembrane domain"

FT Domain 318..461

FT /label= cytoplasmic_loop

XX WO9420617-A2.

XX 15-SEP-1994.

XX 08-MAR-1994; 94WO-US02447.

XX 08-MAR-1993; 93US-0028031.

XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
 PA (SIBI-) SIBIA NEUROSCIENCES INC.

XX Elliott KJ, Ellis SB, Harpold WM;

XX WPI; 1994-303024/37.

XX N-PSDB; AAV12197.

XX Human neuronal nicotinic acetylcholine receptor subunits and DNA -
 PT also transformed cells useful for screening cpds. which modulate

PT activity of the receptor

PS Claim 7; Page 80-81; 99pp; English.

CC The present sequence represents a human neuronal nicotinic acetylcholine
 CC receptor (NACHR) subunit. The cells expressing the alpha and/or beta
 CC NACHR subunits may be used in a method of screening compounds to
 CC identify any which modulate the activity of human neuronal NACHR.
 CC Subunit specific antibodies may be used to monitor the distribution
 CC and expression density of various subunits in normal vs diseased brain
 CC tissues. Testing of single receptor subunits or specific receptor
 CC subunit combinations with a variety of potential agonists or antagonists
 CC provides information with respect to the function and activity of the
 CC individual subunits and should lead to the identification and design of
 CC compounds that are capable of very specific interaction with one or
 CC more receptor subtypes. The resulting drugs should exhibit fewer
 CC unwanted side effects than drugs identified e.g. screening with cells
 CC that express a variety of subtypes.

XX SQ Sequence 502 AA;

Query Match 28.7%; Score 1159.5; DB 15; Length 502;

Best Local Similarity 45.1%; Pred. No. 1.4e-97;

Matches 237; Conservative 82; Mismatches 115; Indels 91; Gaps 12;

Qy 297 IYLNLSAK---VCLAGYHEKRLLDLPYNTLPRVNLNESPQLQSLGLIMQIIVDE 353

Db 8 VWLALASLLHVSLLQGEFQRLKYLKYNPNLPRPVANDSQPLTVYFSLSLQIMVDE 67

Qy 354 KNOLLVYNWLKLEWDMNLNLTSDYGVKDLRIPPHRIWKPVDVLMVNSADEGPDGYQ 413

Db 68 KQVLTTNIIWLOMSWTDIYLNQNVSEYPGVATVRFPDQGIWKPDLILNSADERDAIFH 127

Qy 414 TNVVRNNGSLYVPPGIFKSTCKIDITWFFPDQRCMKFGSWTYDGFOLDLQDDETG 473

Db 128 TNVLNSSGHCQYLPPIGFKSSCYIDVWFFDVQHKLFSGWSYGLSLDLQWQE--- 184

Qy 474 GDSSVYLVNGEWELLGVPGKRNIEYVNCPCPYIDITFAIIRRTLYFFNLIPCVLI 533

Db 185 ADISGYIPNGEWDLVGIPGKRSERFYECCKEPPDVTFVTVMRRRTLYYGLNLIPCVLI 244

Qy 534 ASMALGFTLPDPSGEKISGLVITLISLTVFLNVAETMPATSDAVPL----- 581

Db 245 SALLLVFLPADSGEKISGLVITLISLTVFLNVAETMPATSDVPLIAQYFASTMIIV 304

Qy 582 -----WIRIVELWLPWILMSRPG-----RPLILEFPTTP 612

Db 305 GLSVVTVIVLQYHHDDPDGKMPKWTVRVILLNWCWFLRMKKGKEDKVRP-ACQHKORR 363

Qy 613 CSDTSSERKHOILSDVELKERSKSLANVLDIDDDFRH-----NCRPMTPGGTLPHNPAF 668

Db 364 CSLASVE-----MSAVAPPASNGNLLY-----IGFRLDGVHCVP-TP----- 401

Qy 669 YRTVYGGDDGSGIGPIGSTRMPDVAHT-----HTCIKSSTVELGLIKELIRFTDQURK 723

Db 402 -----DSGVV-----CGRMACSPTHDEHLLHGQPPGPDILAKILEEYVRIANRRC 449

Qy 724 DDECDIANDKFAAMVVDRLCLIFTMFAILATIAVLLSAPHII 768

Db 450 QDESEAVCSWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNEV 494

RESULT 9

AAW09025

ID AAW09025 standard; Protein; 502 AA.

XX AC AAW09025;

XX 09-APR-1997 (first entry)

XX Neuronal nicotinic acetylcholine receptor alpha-7 subunit.

XX Neuronal nicotinic acetylcholine receptor; NACHR; neurotransmitter;
 KW Neuronal nicotinic acetylcholine receptor; NACHR; neurotransmitter;

CC PRO polynucleotide and protein sequences given in the exemplification of
 XX the present invention.
 SQ Sequence 502 AA;

Query Match 28.7%; Score 1159.5; DB 21; Length 502;
 Best Local Similarity 45.1%; Pred. No. 1.4e-97;
 Matches 237; Conservative 82; Mismatches 115; Indels 91; Gaps 12;

QY 297 IYLNLSAK---VCLAGYHEKRLHLLDPYNTLERPVLNESDPLQLSFLGLTLMQIDYDE 353
 DB 8 VWLALAAALLHVSLOGEFQKLYKELVKNYPLERPVANDSQPLTVYFSLSLQIMDVE 67

QY 354 KNOILLVTNWLKLEWDMNLRWNTSDYGGVKDLRIIPPHRIKWPDLVMTNSADEGFDGYQ 413
 DB 68 KNOVLTNWLQMSWTDHYLQWNVSEYPGVKTVPFPDQGIWKPDILLNSADERFDATEFH 127

QY 414 TNVVRNNGSLYVPPGIFKSTCKIDITWFFDDQRCCKFGSWTYDGFQDLQLODETG 473
 DB 128 TNVLNSSGHCOYLPPGIFKSSCYIDVRWFFDVQHCCLKFGSWYGGWSLDLQMQE--- 184

QY 474 GDISSYVLNGEWELGLVPGKNEIYNNCCPEYIDITFAIIRRTLYFFNLIIPCVLI 533
 DB 185 ADISCIYNGEWDLVGIFGKSERFECKEPEYDVTFTVMRRTLYGLNLLIPCVLI 244

QY 534 ASMLLGTFLPDSGEKLSGLVTILLSTVLNMYAETMPATSDAVPL----- 581
 DB 245 SALALLVLLPADSGEKISLGITVLLSTVFMLLVAEIMPATSDSVPLIAQVFASTMIIV 304

QY 592 -----WIRVFLCWLPIILMRSPG-----RPLILEFPTP 612
 DB 305 GLSVVVTVIVLQYHHHDPDGKMPKWTIVILLNCWFLMRKPGEDKVRP-ACQHKORR 363

QY 613 CSDTSSERKHQILSDVELKRSKSLANVLNIDDDFRH---NCRPMTPGGTLPHPNPAF 668
 DB 364 CSLASVE-----MSAVAPPASGNLLY-----IGFRGLDGVHCV-TP----- 401

QY 669 YRTVYGGQDGSIGPIGSTRMPDAVTH-----HTCIKSSTYEGLILKEIRFTDQURK 723
 DB 402 -----DSGVV-----CGRMACSPTHDEHLHGQPPGDPDLAKILEEVRYIANRRC 449

QY 724 DDECNDIANDKFAAMVVDRLCLIFTFAILATIATVLLSAPHII 768
 DB 450 QDESAVCEWSEKFAACVVDRLCLMAFSVFTICTIGILMSAPNFV 494

RESULT 11
 ID AAB82690 standard; Protein; 502 AA.
 XX AAB82690;
 AC AAB82690;
 DT 15-OCT-2001 (first entry)
 DE Nicotinic acetylcholine receptor alpha7.
 XX Nicotinic acetylcholine receptor; nAChR; human;
 KW acetylcholine binding protein; AChBP; mollusc;
 KW ligand-binding protein; ligand-gated ion channel; crystal;
 KW drug design; protein co-ordinate data; schizophrenia;
 KW Alzheimer's disease; nicotine addiction; Tourette's syndrome;
 KW therapy; nootropic; neuroprotective.
 OS Homo sapiens.
 XX Location/Qualifiers
 FH 108..115
 FT /note= "conserved ligand-binding region, residues
 Trp108 and Tyr115 are essential"
 FT 171..173
 FT /note= "conserved ligand-binding region, residues
 Trp171 and Tyr173 are essential"
 FT 210..217

/note= "conserved ligand-binding region, residues
 Tyr210, Cys212, Cys213 and Tyr217 are
 essential"

WO200158951-A2.
 16-AUG-2001.
 09-FEB-2001; 2001WO-EP01457.
 10-FEB-2000; 2000EP-0200443.
 31-OCT-2000; 2000EP-0203810.
 (TEWE-) STICHTING TECH WETENSCHAPPEN.
 Smit AB, Sixma TK;
 WPI; 2001-497071/54.
 Water-soluble ligand-binding proteins derived from molluscs and analogues
 of ligand-gated ion channels, useful in drug screening assay, where the
 drugs identified can be used in the treatment of Alzheimer's disease or
 schizophrenia

Disclosure; Page 252-254; 260pp; English.

The present sequence is that of the alpha subunit of human
 nicotinic acetylcholine receptor (nAChR). The sequence includes
 regions that are conserved throughout the various nAChR alpha
 subunits and which are essential for ligand binding. The invention
 relates to water-soluble ligand-binding proteins derived from
 molluscs, especially acetylcholine-binding proteins (AChBPs) and
 analogues of ligand-gated ion channels, their crystals, and their
 use for screening ligands of ligand-gated ion channels. The
 water-soluble ligand-binding proteins are capable of forming
 multimers and are amenable to crystallization. The crystal
 structure of AChBP is provided, and can be used to generate 3D
 models of the extracellular ligand-binding domain of ligand-gated
 ion channels and thus for screening of drugs that act on these
 ion channels. Chimeric proteins are provided that are capable of
 binding a ligand of a ligand-gated receptor, and comprise at
 least the amino acids of the AChBP determining solubility of the
 AChBP, in the same positions as in the AChBP, and also comprising
 amino acids determining binding to the ligand. In the chimeric
 proteins, at least the essential amino acids of at least 1 of the
 conserved regions of an nAChR have been substituted for the
 corresponding amino acids, and preferably entire stretches have
 been substituted. New drugs can be developed that selectively
 intervene in neuronal signalling pathways, especially where the
 ligand-gated ion channel is the nAChR, and the related disorder is
 Tourette's syndrome, Alzheimer's disease, addiction to nicotine
 or schizophrenia.

Query Match 28.7%; Score 1159.5; DB 22; Length 502;
 Best Local Similarity 45.1%; Pred. No. 1.4e-97;
 Matches 237; Conservative 82; Mismatches 115; Indels 91; Gaps 12;

QY 297 IYLNLSAK---VCLAGYHEKRLHLLDPYNTLERPVLNESDPLQLSFLGLTLMQIDYDE 353
 DB 8 VWLALAAALLHVSLOGEFQKLYKELVKNYPLERPVANDSQPLTVYFSLSLQIMDVE 67

QY 354 KNOILLVTNWLKLEWDMNLRWNTSDYGGVKDLRIIPPHRIKWPDLVMTNSADEGFDGYQ 413
 DB 68 KNOVLTNWLQMSWTDHYLQWNVSEYPGVKTVPFPDQGIWKPDILLNSADERFDATEFH 127

QY 414 TNVVRNNGSLYVPPGIFKSTCKIDITWFFDDQRCCKFGSWTYDGFQDLQLODETG 473
 DB 128 TNVLNSSGHCOYLPPGIFKSSCYIDVRWFFDVQHCCLKFGSWYGGWSLDLQMQE--- 184

QY 474 GDISSYVLNGEWELGLVPGKNEIYNNCCPEYIDITFAIIRRTLYFFNLIIPCVLI 533
 DB 185 ADISCIYNGEWDLVGIFGKSERFECKEPEYDVTFTVMRRTLYGLNLLIPCVLI 244

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2003, 03:48:31 ; Search time 5045.31 Seconds
(without alignments)
11127.831 Million cell updates/sec

Title: US-09-303-232-1_COPY_372_2681

Perfect score: 2310

Sequence: 1 atgaaaaatgcacaaactgaa.....caccacattattgtctgc 2310

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

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2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	332.2	14.4	1101	29	AL058211 Drosophil
3	331.2	14.3	1007	29	AL073676 Drosophil
4	323.8	14.0	978	29	AL064281 Drosophil

5 281.8 12.2 1201 9 AL530299
6 265 11.5 607 9 AI292581
7 235.2 10.2 922 13 BU915857
8 232.6 10.1 2940 11 AK034228
9 232.6 10.1 3230 11 AK083157
10 228.8 9.9 833 14 CB245337
11 219.6 9.5 755 13 BU702422
12 219.2 9.5 4290 11 AK029177
13 217 9.4 615 14 CB149460
14 215.8 9.3 1864 11 AK053497
15 215.8 9.3 2916 11 AK051730
16 215.8 9.3 3126 11 AK080415
17 207 9.0 3483 11 AK081254
18 207 9.0 4037 11 AK049722
19 207 9.0 4046 11 AK051742
20 206.4 8.9 683 12 BM639954
21 205.4 8.9 908 13 BU149265
22 202.8 8.8 411 12 B1516733
23 202.2 8.8 2010 11 AK080475
24 201.8 8.7 410 12 B1516843
25 200 8.7 658 12 BM711715
26 198 8.6 755 10 AW914206
27 197.2 8.5 1036 13 BX437801
28 196.6 8.5 2513 11 AK033068
29 189.6 8.2 720 14 CA373069
30 180.8 7.8 640 14 CB244439
31 178.8 7.7 1034 13 BX403124
32 172.2 7.5 754 29 CNS02R2B
33 170 7.4 891 9 AI110117
34 169.8 7.4 882 12 B1195149
35 169.8 7.4 4589 11 AK030464
36 168.8 7.3 763 14 CA374163
37 168.4 7.3 600 13 BU919212
38 154.8 6.7 809 10 BG404575
39 153.6 6.6 818 13 BU161024
40 153 6.6 586 13 BX299163
41 152.2 6.6 1201 13 BX421718
42 151.6 6.6 864 9 AU120692
43 150.6 6.5 2342 11 AK009902
44 146.6 6.3 494 9 AA697326
45 146.4 6.3 694 12 B1194994

ALIGNMENTS

RESULT 1

BG632919/c

LOCUS

DEFINITION

EST.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BG632919 885 bp mRNA linear EST 23-APR-2001
GH16126.3prime GH Drosophila melanogaster head pot2 Drosophila
melanogaster cDNA clone GH16126.3 similar to CG4128: FBan0004128
'ion channel' located on: 2L 30D1-30E1;: 04/10/2001, mRNA sequence.

BG632919

BG632919.1 GI:13758409

EST.

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 885)

Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,

Lewis,S. and Rubin,G.M.

BDGP/HMI Drosophila EST Project

Unpublished

Other_ESTs: GH16126.5prime

Contact: Stapleton, M.

BDGP

Lawrence Berkeley National Lab

One Cyclotron Rd, Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu

Based upon the presence of a XhoI site followed by a run of 14 or

more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting Poly-T sequence has been removed. hit genomic AF003511: arm: X [18792641,19136447] estimated-cyto:18A3-18C6: 04/10/2001 plate: GH.161 row: C column: 2 High quality sequence stop: 784.

FEATURES

Location/Qualifiers

1..885

/organism="Drosophila melanogaster"

/mol_type="mRNA"

/db_xref="taxon:7227"

/clone="GH16126"

/sex="male and female"

/dev_stage="adult"

/lab_host="DH5 - alpha"

/clone_lib="GH Drosophila melanogaster head pot2"

/note="Orikan: head; Vector: pot2; Site:1; EcoRI: Site:2; XhoI: Sized fractionated cDNAs were directly ligated into pot2. Plasmid cDNA library."

BASE COUNT 257 a 205 c 181 g 242 t

ORIGIN

Query Match 18.4%; Score 424.8; DB 10; Length 885;

Best Local Similarity 74.6%; Pred. No. 6e-92;

Matches 534; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

QY 1028 TAACCTTAATGCAAAATTCATGATGGACGAGAAATCAATTCCTAGTCACTAATGTGT 1087

DB 884 TAACATCATCTAGATATGATGTCGACGAAGAATCACTGCTTATACGAATATT 825

QY 1088 GGTAAACTGAGTGGACACATGAATCTCCGCTGGAACACCTCCGACTATGGCGAG 1147

DB 824 GGCTCAATGGAATGGAACGATATGAATCTTCGATGGAATTCGAGTGAGTGGTG 765

QY 1148 TTAAGGATCTCGAATACCGCGCATCGATCTGGAAGCGCGTGTGATGATACACA 1207

DB 764 TCGCGGATCTCGAATTCGCGCACATCGCTATGGAACCGGATGATGATGATACACA 705

QY 1208 GTCCGGATGAGGGATTTGACGGCACCTACACAGACGAGTGGTGGCGAACACCGCT 1267

DB 704 GTCCGACGAGGGCTTCGATGGAACGTACGCCACAAATGTGGTTCGCAATATGGGA 645

QY 1268 CGTGTCTATAGTTCCGCGGGGATCTCAAGTCGACGTGCAAGATCGATCATCGTGGT 1327

DB 644 GCTGTCTGTAGTACCGCGAGTATATTAAAGTCAACGTGTAAGATCGACATTAACGTGGT 585

QY 1328 TCCCTTCGATGACACGGGTGCGAGATGAATTCGGCAGTTGGACCTACGACGATTC 1387

DB 584 TTCCATTCGACGATCAGAGATGCTGAATGAATTTGGTTCGTGACCTACGATGGTTTC 525

QY 1388 AGCTGGATTTACAATTACAAGATGAAGTGGCGGTGATATCAGCAGTTACGTCTCAACG 1447

DB 524 AGTTGGACCTCAGTTGCGAGCAGAAAGTGGTGGCGACATTTCTAGCTTTTATAACCAATG 465

QY 1448 CGGAGTGGAACTACTGGGTGTCGCCGCAACGTAACGAGATCTATTACAACTGCTGCC 1507

DB 464 CGGAATGGAGCTGTGAGGTGTCGCCGTAACGAAATGAAATCTACTATAATTTGCTGCC 405

QY 1508 CGGAACCTTATATAGACATCACTTCGCCATCATCATCCGCGGACGACACTGTACTATT 1567

DB 404 CAGAACCTTATTTGACATACATTCGCCATTTTGAATAAGCGCAAAACGTTGTACTATT 345

QY 1568 TCCTTCAACCTGATCATACCTTTGTACTGATGTCCTCCATGGCCCTTGTCTGGATTCACCC 1627

DB 344 TTTTCAATCTGATTTGTCGGTGGCTACTGATCGCTCCATGGCAGCTAGGGTTTACAC 285

QY 1628 TGCGCCGAGATTCGGGTGAAATATATCGCTGGGTGTACCATCTTCTCTCGCTGACCG 1687

DB 284 TGCCACCATGATCTTGGTGAAAGCTTTTCGCTGGAGTTACAAATTTCTATTATCTCGTTACAG 225

QY 1688 TGTTTCTGAATATGTTTGCCGAGACAAATTCGCCGCTACTTCCGATGCGGTGCAATTG 1743

DB 224 TCTTCTCAACATGGTGCCGCAACATGCGGGACCTCCGATGCGGTACCGCTG 169

RESULT 2

CNS000IF

LOCUS

DEFINITION

Drosophila melanogaster genome survey sequence T7 end of BAC # BCR02C08 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION

AL058211

VERSION

AL058211.1

GI:4930650

KEYWORDS

GSS

SOURCE

Drosophila melanogaster (fruit fly)

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

1 (bases 1 to 1101)

Genoscope.

DIRECT SUBMISSION

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial, EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers

1..1101

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone="BACR02C08"

/clone_lib="RPCI-98"

/note="end : T7"

BASE COUNT 277 a 259 c 261 g 283 t 21 others

ORIGIN

Query Match 14.4%; Score 332.2; DB 29; Length 1101;

Best Local Similarity 98.5%; Pred. No. 1.8e-69;

Matches 334; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1053 GGACGAGAAAATCAATTCCTAGTCACTAATGTGTTAACTGGAGTGAACGACAT 1112

DB 113 GGACGAGAAAATCAATTCCTAGTCACTAATGTGTTAACTGGAGTGAACRCAAT 172

QY 1113 GAATTCCTCGTGGAAACACCTCCGACTATGGCGGAGTTAAGGATCTGGGAATACCGCGCA 1172

DB 173 GAATTCCTCGTGGAAACACCTCCGACTATGGCGGAGTTAAGGATCTGGGAATACCGCGCA 232

QY 1173 TCGCATCTGGAAACCGCGCTGATGTACAACAGTCCGATGAGGATTTGACGAC 1232

DB 233 TCGCATCTGGAAACCGCGCTGATGTACAACAGTCCGATGAGGATTTGATGGCAC 292

QY 1233 CTACACAGCAACCTGGTGGTGGCGGAACAACGGCTCGTGTATACGTTCCGCGGGGAT 1292

DB 293 CTACACAGCAACCTGGTGGTGGCGGAACAACGGCTCGTGTATACGTTCCGCGGGGAT 352

QY 1293 CTTCAAGTCGACGTGCAAGATCGACATCAGCTGGTTCCTCCCTTCGATGACACGCGGTGGA 1352

DB 353 CTTCAAGTCGACGTGCAAGATCGACATCAGCTGGTTCCTCCCTTCGATGACACGCGGTGGA 412

QY 1353 GATGAAGTTCGGCAAGTGGACCTACGACGATTCAGCT 1391

```

Db      413 GATGAAGTTCGCAGTTGGACCTACGACGATTCCAGCT 451
|||||
CNS000HJU      1007 bp      DNA      linear      GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR35F05 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION      AL073676.1      GI:4953355
VERSION
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1007)
REFERENCE
AUTHORS
TITLE
JOURNAL
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammosier in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
source
Location/Qualifiers
1..1007
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="BACR35F05"
/clone_lib="RPCI-98"
/note="end : TET3"
BASE COUNT      255 a      246 g      271 t      5 others
ORIGIN
Query Match      14.3%; Score 331.2; DB 29; Length 1007;
Best Local Similarity 98.2%; Pred. No. 3.1e-69;
Matches 333; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY      1053 GCACGAGAAAATCAATTGCTAGTCACCTAAATGTTGGTTAAACCTGGAGTGAACGACAT 1112
|||||
Db      125 GCACGAGAWAAATCAATTGCTAGTCACCTAAATGTTGGTTAAACCTGGAGTGAACACNAT 184
|||||
QY      1113 GAATCTCCGCTGGAACACCTCCGACTATGGCGGAGCTTAAGGATCTGCGAATACCCCGCA 1172
|||||
Db      185 GAATCTCCGCTGGAACACCTCCGACTATGGCGGAGCTTAAGGATCTGCGAATACCCCGCA 244
|||||
QY      1173 TCGCATCTGGAAGCCGGAGCTGCTGATGTACACAGTCCGGATGAGGGATTTGATGGCAC 1232
|||||
Db      245 TCGCATCTGGAAGCCGGAGCTGCTGATGTACACAGTCCGGATGAGGGATTTGATGGCAC 304
|||||
QY      1233 CTACACAGACGACGTTGGTGGCGGAACAACGGCTGCTGTATACGTTCCGCGGGGAT 1292
|||||
Db      305 CTACACAGACGACGTTGGTGGCGGAACAACGGCTGCTGTATACGTTCCGCGGGGAT 364
|||||
QY      1293 CTTCAAGTCGACGTTCAAGATCGACATCACGTGGTTCCCTTCGATGATACCAAGCGGTGCGA 1352
|||||
Db      365 CTTCAAGTCGACGTTCAAGATCGACATCACGTGGTTCCCTTCGATGATACCAAGCGGTGCGA 424
|||||

RESULT 4
CNS0006F9      978 bp      DNA      linear      GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR13K21 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION      AL064281      GI:4944356
VERSION
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 978)
REFERENCE
AUTHORS
TITLE
JOURNAL
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammosier in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
source
Location/Qualifiers
1..978
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="BACR13K21"
/clone_lib="RPCI-98"
/note="end : TET3"
BASE COUNT      249 a      221 c      236 g      260 t      12 others
ORIGIN
Query Match      14.0%; Score 323.8; DB 29; Length 978;
Best Local Similarity 99.1%; Pred. No. 1.9e-67;
Matches 336; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY      1053 GCACGAGAAAATCAATTGCTAGTCACCTAAATGTTGGTTAAACCTGGAGTGAACGACAT 1112
|||||
Db      117 GCACGAGAAAATCAATTGCTAGTCACCTAAATGTTGGTTAAACCTGGAGTGAACG-CAT 175
|||||
QY      1113 GAATCTCCGCTGGAACACCTCCGACTATGGCGGAGCTTAAGGATCTGCGAATACCCCGCA 1172
|||||
Db      176 GAATCTCCGCTGGAACACCTCCGACTATGGCGGAGCTTAAGGATCTGCGAATACCCCGCA 235
|||||
QY      1173 TCGCATCTGGAAGCCGGAGCTGCTGATGTACACAGTCCGGATGAGGGATTTGACGGCAC 1232
|||||
Db      236 TCGCATCTGGAAGCCGGAGCTGCTGATGTACACAGTCCGGATGAGGGATTTGATGGCAC 295
|||||
QY      1233 CTACACAGACGACGTTGGTGGCGGAACAACGGCTGCTGTCTATACGTTCCGCGGGGAT 1292
|||||
Db      296 CTACACAGACGACGTTGGTGGCGGAACAACGGCTGCTGTCTATACGTTCCGCGGGGAT 355
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QY      1293 CTTCAAGTCGACGTTCAAGATCGACATCACGTGGTTCCCTTCGATGATACCAAGCGGTGCGA 1352
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|||||
356 CTTCAAGTCGAGTCGCAAGATCGATCAGTGGTTCCTCCCTTCGATGACCGGTCGA 415
|||||
1353 GATGAAGTTCGCGAGTTGGACCTAGCAGCGATTCCAGCT 1391
|||||
416 GATGAAGTTCGCGAGTTGGACCTAGCAGCGATTCCAGGT 454
|||||

RESULT 5
AL530299.
LOCUS
DEFINITION
AL530299 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
cDNA clone CS0DD007YP05 5-PRIME, mRNA sequence.
ACCESSION
AL530299.2 GI:31068132
VERSION
AL530299.2
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12793792.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
7646.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DD007CH030PL&cluster=7646.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DD007CH03QPL.
Location/Qualifiers
1. 1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DD007YP05"
/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 258 a 326 c 319 g 273 t 25 others
ORIGIN
Query Match 12.2%; Score 281.8; DB 9; Length 1201;
Best Local Similarity 59.8%; Pred. No. 3e-57;
Matches 503; Conservative 5; Mismatches 322; Indels 11; Gaps 2;

QY 905 CTGCTAAAGTTGCCCTAGCAGGATATCATGAAAGAGACTGTGTACACGATCTTTGGATC 964
|||||
170 CTCCTCAGCGTGTCCCTGCAAGCGAGTCCAGAGGAGCTTTACAGGAGCTGGTCAAGA 229
|||||
QY 965 CTTATAATACACTAGAACGTCCTGCTTCAATCAATCGGACCGGTTTACAAATTAAGCTTTG 1024
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230 ACTACAATCCCTTGGAGAGCCGCTGGCCCAATGACTCGCAACCACTACCGCTACTCTT 289
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QY 1025 GTTTAACTTTAATGCAAAATATTCGATGTGGACGAGAAAAATCAATTCGTAGTCACTAATG 1084
|||||
290 CCTGAGCCCTCTGCAGATCATGGAGTGTGATGAGAGAACCAAGTTTAAACCACCAACA 349
|||||
QY 1085 TGTGGTTAAACTGGAGTGAACGACATGAATCTCCGCTGGGAGAACCTCCGACTATGGCG 1144
|||||
350 TTTGGCTGCAAAATGTCTTGGACAGATCACTATTATACAGTGGAAATGTGTGAGAAATATCCAG 409
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1145 GAGTTAAGGATCTGCGGAATACCCGCCATCGCATCTGGAAGCGGACGCTGCTATGATCA 1204
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|||||
410 GGGTGAAGACTTTTCGTTTCCAGATGGCCAGATTGGAAACAGACATTCCTCTCTATA 469
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1205 ACAGTGGGATGAGGATTTTGGCGCAGCTACACAGCAAGAGTGGTGGTGGCGGAACAACG 1264
|||||
470 ACAGTGGTGTAGGCGCTTTGACGCCACATTCACACATACCGTGTGGTGAATTCCTCTG 529
|||||
1265 GCTCGTGTCTATACGTTCCGCGGGGATCTTCAAGTCGACGTCGAAGATCGACATCAGCT 1324
|||||
530 GGCATTGGCAGTWCCTGCCCTCCAGGACATATTCAAGAGTTCCCTGCTACATCGATGACGCT 589
|||||
1325 GGTTCCTCCCTTCATGACACAGCGGTGGAGATGAAGTTCCGAGTGTGGACCTAGCAGCGAT 1384
|||||
590 GGTTCCTCCCTTCATGTCGACGACTGCAAACTGAAAGTTTGGGTCCTGGTCTTACGGAGGCT 649
|||||
1385 TCCAGCTGGATTACAAATTACAAAGATGAAACTGGCGGTGATATACAGCAGTTACGTGCTCA 1444
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650 GGTCTTGGATCTGCAGATGCAGAGGCA-----GATATCAGTGCCTATATCCCA 700
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1445 ACGGGAGTGGGAACCTACTGGTGTGCCCGGCAAAAGTAAACGAGATCTATTACAACGTGT 1504
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701 ATGGAGAATGGACCTAGTGGGAATCCCGGCAAGAGGAGTGAAGGTCTATAGTCTCT 760
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1505 GCCCGGAACCTTATATAGACATCACCCTCGCCCATCATCATCCGCGCACGACACTGTACT 1564
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761 GCAAGAGCGCTTACCCCGATGTACCTTCACAGTGACCATGCGCGCAGACGCTCTACT 820
|||||
1565 ATTCTTCAACCTGATACATCCTTGTGTACTGATTCCTCATGCTCCCTGCTTGGCTCGGATCA 1624
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821 ATGGGCTCAACCTGCTGATCCCTGTGTGCTCATCTCCGCTCGCCCTGCTGGTGTTC 880
|||||
1625 CCTCGCGCGCAGATTC--GGGTGAAATAATTATCGTGGTGGTGTGTACCATCTTCTCTCTCT 1682
|||||
881 TCGTTCCTCGACATTCGCGGGGAGAGATTTTCCCTKGGGATAACAGTGTACTCTCTCT 940
|||||
1683 GACCGTGTTCGATATGTTGCCGAGACATCCGCGTACTTCCGATCGCGTGCCTATT 1742
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941 TACCGTCTTCATGCTGCTGCTGCTGAGATCATGCCCCCAACATCCGATTCGTTACCAIT 1000
|||||
1743 G 1743
|
1001 G 1001

RESULT 6
AL5302581
LOCUS
DEFINITION
AL5302581 607 bp mRNA linear EST 23-APR-2001
GH15518.5prime GH Drosophila melanogaster head pot2 Drosophila
melanogaster cDNA clone GH15518 5 similar to CG4128: FBan0004128
'ion channel', located on: 2L 30D1-30E1:: 04/10/2001, mRNA sequence.
ACCESSION
AL5302581
VERSION
AL5302581.1 GI:3941988
KEYWORDS
EST.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 607)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G. M.
BDGP/HMI Drosophila EST Project
Unpublished
Other_ESTs: GH15518.3prime
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AB003626: arm:2L [9617316,9882551]
estimated-cyto:30C7-30F4: 04/10/2001
Plate: GH.155 row: B column: 6

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```
High quality sequence stop: 521
POLYA=No.
FEATURES
  source
    Location/Qualifiers
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        /mol_type="mrna"
        /db_xref="taxon:7227"
        /clone="GH15518"
        /sex="male and female"
        /dev_stage="adult"
        /lab_host="DH5 - alpha"
        /clone_lib="GH Drosophila melanogaster head pot2"
        /note="Organ: head; vector: pot2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pot2. Plasmid cDNA library."
BASE COUNT 157 a 151 c 162 g 137 t
ORIGIN
  Query Match 11.5%; Score 265; DB 9; Length 607;
  Best Local Similarity 71.4%; Pred. No. 3.1e-53;
  Matches 349; Conservative 0; Mismatches 140; Indels 0; Gaps 0;
  QY 909 TAAAGTTTCCTAGCAGGATATCATGAAAGAGACTGTTACAGATCTTTTGGATCCTTA 968
  Db 106 TAAAGAAAGCTGTCAAGGACCTCATGAAAGCCCTGCTGAACCATCTGCTGTCCACCTA 165
  QY 969 TAATACACTAGAACCTCCCGTTCTCAATGAATCGGACCGTTTACAAATTAAAGCTTTGGTTT 1028
  Db 166 CAATACGCTGGAGCGACCGCTGGCCCAATGAATCGGAGCCCTGGAGGTTAAGTTCGGACT 225
  QY 1029 AACTTTAATGCAAAATATCGATGTGGACGAGAAAATCAATTTGCTAGTCACCTAAATGTGTG 1088
  Db 226 GACGCTGCACGACATCATCGCTGGACGAGGAATCAGCTTCTCATAACGAATCTTTG 285
  QY 1089 GTTAAACCTGGAGTGAAGCAGATGAATCTCCGCTGGACACCTCCGACTATGCGGGAGT 1148
  Db 286 GCTTTCGTTGGAGTGAAGCACTACATCTCGCTGGGAATGAACCGGAATACGCGGGGT 345
  QY 1149 TAAGGATCTGCGAATACCGCCGCATCGCATCTGGAAGCGCGAGCTGCTGATGTACAACAG 1208
  Db 346 CAAGGATCTACGAATCACGCCCAACAAAGCTGTGGAAGCCGCGCTCATGTACAACAG 405
  QY 1209 TCGGATGAGGATTTGACGCAACCTACACAGACAGAGTGTGTGGCGGAACAAACGGCTC 1268
  Db 406 CGCGATGAGGATTCGATGGCAGCATATCACACAGCGTGTGGTCAACACATGGCGGCAG 465
  QY 1269 GTGTCTATACGTTCCGCGGGGATCTTCAAGTCGACGTGCAAGATCGACATCACCTGGT 1328
  Db 466 TTGTCTGACGTGCCCCCTGGTATCTTCAAGAGCACATGCAAGATGGACATCACCTGGT 525
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  VERSION
  KEYWORDS
  SOURCE
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  1 (bases 1 to 922)
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AUTHORS
TITLE
JOURNAL
COMMENT

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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ORIGIN

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ACCESSION	AK034228		
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REFERENCE	1	Carninci, P. and Hayashizaki, Y.	
AUTHORS			
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
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TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
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AUTHORS			
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
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AUTHORS			
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409 (6821), 685-690 (2001)		
MEDLINE	21085660		

11217851			
5			
REFERENCE			
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
JOURNAL	Nature 420, 563-573 (2002)		
REFERENCE	6 (bases 1 to 2940)		
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN) Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)		
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ location/Qualifiers		
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HTC; CAP trapper.
Mus musculus (house mouse)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, H., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
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3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
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4
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yananaka, I., Saito, T., Okazaki, Y., Gojohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Balderelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S. and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
PUBMED
11217851

5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4290)

ADACHI, J., AIZAWA, K., AKIMURA, T., ARAKAWA, T., BONO, H., CARNINCI, P., FUKUDA, S., FURUNO, M., HANAGAKI, T., HARA, A., HASHIZUME, W., HAYASHIDA, K., HAYATSU, N., HIRAMOTO, K., HIRAO, T., HIROZANE, T., HORI, F., IMOTANI, K., ISHII, Y., ITOH, M., KAGAWA, I., KASUKAWA, T., KATO, H., KAWAI, J., KOJIMA, Y., KONDO, S., KONNO, H., KUNDA, M., KOYA, S., KURLHARD, C., MATSUYAMA, T., MIYAZAKI, A., MURATA, M., NAKAMURA, M., NISHI, K., NOMURA, K., NUMAZAKI, R., OHNO, M., OHSAKI, N., OKAZAKI, Y., SAITO, R., SAITO, H., SAKAI, C., SAKAI, K., SAKAZUME, N., SANO, H., SASAKI, D., SHIBATA, K., SHINAGAWA, A., SHIRAKI, T., SOGABE, Y., TAGAMI, M., TAGAWA, A., TAKAHASHI, F., TAKAKU-AKAHIRA, S., TAKEDA, Y., TANAKA, T., TOMARU, A., TOYA, T., YASUNISHI, A., MURAMATSU, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
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Homo sapiens  
ORGANISM  
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AUTHORS  
1 (bases 1 to 615)  
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
Kim,Y.S.  
21C Frontier Korean EST Project 2001  
Unpublished  
Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
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High quality sequence stop: 615.  
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with tabacco acid pyrophosphatase (TAP). The deapped  
intact mRNA was ligated with DNA-RNA linker including  
EcoRI site by treatment of T4 RNA ligase and the first  
strand cDNA was synthesized from oligo dT-selected mRNA by  
priming with dr-tailed vector. The dr-tailed vector was  
adjusted to have about 60nt. The cDNA vector was  
circularized with E. coli DNA ligase after digestion of  
EcoRI which site is also included in vector. An RNA strand  
converted to a DNA strand by Okayama-Berg method. The  
obtained cDNA vectors were used for transformation of  
competent cells E. coli Top10F by electroporation method.  
The cDNA libraries constructed by this method are  
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RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.

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AK053497.1 GI:26343494
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AK053497.1
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HTC; CAP trapper.
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Mus musculus (house mouse)
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Mus musculus
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REFERENCE
1 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
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11042159
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3
AUTHORS
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
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Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
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4
AUTHORS
Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamataka,I.,
Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
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Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
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Sato,K., Schonbach,C., Seva,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Toyooka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
MEDLINE
11217851
PUBMED
11217851
REFERENCE
5
AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1864)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
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Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
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Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
Riing, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.,
and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2916)

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hori, F., Imotani, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Soabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: <http://fantom.gsc.riken.go.jp/>.

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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SUMMARIES

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2	881	38.1	984	23	ABL27131
3	776.2	33.6	3144	23	ABL27130
4	531	23.0	803	23	ABL07799
5	512.8	22.2	3700	21	AAZ24476
6	479	20.7	936	23	ABL13733
7	412.2	17.8	1540	23	ABL07231
8	411.4	17.8	3109	21	AAZ24477
					D. melanogaster ac
					Drosophila melanog
					Drosophila melanog
					H. virescens acety
					Drosophila melanog
					Drosophila melanog
					H. virescens acety

9	335.8	14.5	14668	23	ABL07798	Drosophila melanog
10	296.2	12.8	1509	21	AAZ58395	Human PRO2145 nucl
11	296.2	12.8	1509	22	AAC90380	Wild-type human al
12	296.2	12.8	1876	15	AAV12197	Human neuronal nic
13	296.2	12.8	1876	18	AAZ48239	Human neuronal nic
14	296.2	12.8	1876	24	ABV73248	Human neuronal NAC
15	296.2	12.8	1876	24	ABS54875	Human neuronal nic
16	294.6	12.8	1509	22	AAC90385	Mutant human alpha
17	294.6	12.8	1509	22	AAC90386	Mutant human alpha
18	294.6	12.8	1509	19	AAV44687	V274T variant huma
19	293	12.7	1509	22	AAC90387	Mutant human alpha
20	284.4	12.3	2101	18	AAZ59197	Neuronal alpha-bun
21	283.8	12.3	1964	24	ABZ11298	Human polynucleoti
22	267.8	11.6	2769	18	AAZ59196	Neuronal alpha-bun
23	251	10.9	2277	15	AAV12199	Human neuronal nic
24	251	10.9	2277	16	AAQ90387	Alpha 2 subunit of
25	251	10.9	2277	24	ABV73243	Human neuronal NAC
26	251	10.9	2277	24	ABS54870	Human neuronal nic
27	251	10.9	2664	18	AAT48235	Neuronal nicotinic
28	251	10.9	2664	24	ABK92165	Prostate cancer-as
29	245.6	10.6	1416	22	AAC90382	Chimeric alpha7/5-
30	242.6	10.5	1809	23	AAZ591552	DNA encoding novel
31	242.6	10.5	2082	18	AAZ59527	Alpha4 subunit of
32	242.6	10.5	3496	18	AAZ48237	Neuronal nicotinic
33	241.2	10.4	2398	23	ABL26491	Drosophila melanog
34	241	10.4	2082	18	AAZ59528	Alpha4 subunit of
35	240.8	10.4	1869	24	AAZ45873	Modified acetylcho
36	240.8	10.4	1869	24	ABL54794	Modified hen ACR s
37	234.8	10.2	2319	23	ABL04391	Drosophila melanog
38	233	10.1	2210	23	ABL0275	Drosophila melanog
39	232.4	10.1	1896	24	AAZ45867	Modified acetylcho
40	231.4	10.0	2363	15	AAV12196	Human neuronal nic
41	231.4	10.0	2363	24	ABV73245	Human neuronal NAC
42	231.4	10.0	2363	24	ABS54872	Human neuronal nic
43	228	9.9	1869	24	AAZ45864	Modified acetylcho
44	228	9.9	1869	24	ABL54788	Insect nicotinic A
45	225.6	9.8	1908	18	AAZ48236	Neuronal nicotinic

ALIGNMENTS

RESULT 1	
AAZ24475	
ID	AAZ24475 standard; CDNA to mRNA; 2886 BP.
XX	AC
XX	AAZ24475;
XX	DT 17-FEB-2000 (first entry)
XX	
DE	D. melanogaster acetyl-choline receptor DNA from clone Da7.
XX	
KW	Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
KW	neurotransmission; plant protection agent; conductance; AChR; ds.
XX	
OS	Drosophila melanogaster.
XX	
FH	Key
FT	Location/Qualifiers
FT	372..2684
FT	/tag=a
FT	/product="acetyl choline receptor."
PN	DE19819829-A1.
XX	
PD	11-NOV-1999.
XX	
PF	04-MAY-1998; 98DE-1019829.
XX	
PR	04-MAY-1998; 98DE-1019829.
XX	
PA	(FARB) BAYER AG.
XX	
PI	Adamczewski M, Oellers N, Schulte T;

[illegible]

QY 1801 GGAGCACCCTGATCCTAGAGTTCCGACACCGCCCTGTTGAGACACATCCTCCGAGCGG 1860
DB 2172 GGAGCACCCTGATCCTAGAGTTCCGACACCGCCCTGTTGAGACACATCCTCCGAGCGG 2231
QY 1861 AAGCACCAGATCTCTCCAGCTTGAGCTGAAGAGCGCTGTCGAAATCGTGTGGCC 1920
DB 2232 AAGCACCAGATCTCTCCAGCTTGAGCTGAAGAGCGCTGTCGAAATCGTGTGGCC 2291
QY 1921 AAGCTACTAGACATCCATGATGACTTCCGGCACAATTGTCGCCCATGACGCCGCGGA 1980
DB 2292 AAGCTACTAGACATCCATGATGACTTCCGGCACAATTGTCGCCCATGACGCCGCGGA 2351
QY 1981 ACACCTGCCACACACCCGCGCTTCTATCGCAGCGTTTATGGACAAGCGCGATGCGCAGC 2040
DB 2352 ACACCTGCCACACACCCGCGCTTCTATCGCAGCGTTTATGGACAAGCGCGATGCGCAGC 2411
QY 2041 ATTGGGCCAATTGGCAGCAGCCGATGCGCGGATGCGGTCACCCATCATACGTGCAATCAA 2100
DB 2412 ATTGGGCCAATTGGCAGCAGCCGATGCGCGGATGCGGTCACCCATCATACGTGCAATCAA 2471
QY 2101 TCATCAACTGAATATGAATAGTTTAAATCTTAAAGGAAATTCGCTTTTAACTGATCAG 2160
DB 2472 TCATCAACTGAATATGAATAGTTTAAATCTTAAAGGAAATTCGCTTTTAACTGATCAG 2531
QY 2161 CTACGTPAAGATGACGAGTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 2220
DB 2532 CTACGTPAAGATGACGAGTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 2591
QY 2221 GTTGACAGACTGTGCTTATCATATTCACAATGTTGCAATGTTGCAATGTTGCAATGTTG 2280
DB 2592 GTTGACAGACTGTGCTTATCATATTCACAATGTTGCAATGTTGCAATGTTGCAATGTTG 2651
QY 2281 CTACTATCGGCACCATATATTGTCCTCG 2310
DB 2652 CTACTATCGGCACCATATATTGTCCTCG 2681

RESULT 2

ABL27131
ID ABL27131 standard; DNA; 984 BP.
AC ABL27131;
XX
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 32866.
XX DE
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
XX Drosophila melanogaster.
OS
XX WQ200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX PF
XX 23-MAR-2000; 2000US-191637P.
XX PR
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
DR
XX . New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Claim 1; SEQ ID NO 32866; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABBS7737-ABBS72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 984 BP; 332 A; 268 C; 225 G; 159 T; 0 other;

Query Match 38.1%; Score 881; DB 23; Length 984;
Best Local Similarity 98.0%; Pred. No. 1.4e-235;
Matches 903; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

QY 1 ATGAAATATGCACAACTGAACTGACTGAAGTTGACGATGATGAGCTGTGGTGGCAGTA 60
DB 1 ATGAAATATGCACAACTGAACTGACTGAAGTTGACGATGATGAGCTGTGGTGGCAGTA 60
QY 61 AGATTAGCGACTGCGAGCAGCAACTTTAGCAGCAGTAGCAGCACACAGACACCAGCAGC 120
DB 61 AGATTAGCGACTGCGAGCAGCAACTTTAGCAGCAGTAGCAGCACACAGACACCAGCAGC 120
QY 121 AACCAGAGCAGCAACCCAGCAACTTCACACACTGCAACAGGAGCTTAAAGTACAAAACAC 180
DB 121 AACCAGAGCAGCAACCCAGCAACTTCACACACTGCAACAGGAGCTTAAAGTACAAAACAC 180
QY 181 CACAGCAACATTGCAAGCGAGCAGCAATAAGCAGCAACAGGAGCAGCAGTGAAGGAC 240
DB 181 CACAGCAACATTGCAAGCGAGCAGCAATAAGCAGCAACAGGAGCAGCAGTGAAGGAC 240
QY 241 GAGGATGAGCAACCCAGCAGTGAAGCAATGACGAGCAGCAGTGAAGCAATGACGAGCAG 300
DB 241 GAGGATGAGCAACCCAGCAGTGAAGCAATGACGAGCAGCAGTGAAGCAATGACGAGCAG 300
QY 301 AGCAGCAACATTGTTGCGCAAGAGCAGCGCGAGCAACTGCTGCCGCGATGAAGCA 360
DB 301 AGCAGCAACATTGTTGCGCAAGAGCAGCGCGAGCAACTGCTGCCGCGATGAAGCA 360
QY 361 ACAACCCACAAACCAACATAGACTGTGTGCGCAAGCAGCAGTGAAGTGGCTGCG 420
DB 361 ACAACCCACAAACCAACATAGACTGTGTGCGCAAGCAGCAGTGAAGTGGCTGCG 420
QY 421 CGACGAAAGAAACCCAGCAACCCCAACAGCAAGATATCAAGAAACAGCAACTT 480
DB 421 CGACGAAAGAAACCCAGCAACCCCAACAGCAAGATATCAAGAAACAGCAACTT 480
QY 481 AGCATGCTCCCTTCAAAACCGCAACTTCCAGCAGCACTTACAGCAGCAGCAGCAACA 540
DB 481 AGCATGCTCCCTTCAAAACCGCAACTTCCAGCAGCAGCAGCAGCAGCAACA 540
QY 541 ACCAGCTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTATT 600
DB 541 ACCAGCTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTATT 600
QY 601 CCGATATCGACATGATAGATATCCAGCGCCACATTCGCCCTGGCTGTGATGTGCTG 660
DB 601 CCGATATCGACATGATAGATATCCAGCGCCACATTCGCCCTGGCTGTGATGTGCTG 660
QY 661 CAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 661 CAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 721 CTGTTTCAAGAGGATGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 780
DB 721 CTGTTTCAAGAGGATGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 780
QY 781 GCGCAACTGAAATATAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 837
DB 781 GCGCAACTGAAATATAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 837

Db 781 GCGCACTGAGGAGCAGCAGTAGCAGCAGCAACAGCAGCGGCAACAGCAGC 840
Qy 838 AGCAGCAATATTAACGAGCTTAATAACACTCATGGATATTTTATTGATATTTG 897
Db 841 AGCAGCAATATTAACGAGCTTAATAACACTCATGGATATTTTATTGATATTTG 900
Qy 898 AATTATCTCTAAAGTTTC 918
Db 901 AATTATCTCTAAAGCAAGC 921

RESULT 3
ABL27130
ID ABL27130 standard; DNA; 3144 BP.
XX
AC ABL27130;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32863.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
XX Claim 1; SEQ ID NO 32863; 2lpp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX (ABB57737-ABB72072).
XX
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 3144 BP; 1056 A; 676 C; 680 G; 732 T; 0 other;
XX

Query Match 33.68; Score 776.2; DB 23; Length 3144;
Best Local Similarity 89.08; Pred. No. 5.5e-206;
Matches 902; Conservative 0; Mismatches 13; Indels 98; Gaps 2;
Qy 1 ATGAAATATGCACAACTGAACTGACCTGAGTTGACGATGATGAGTGGTGGCAGTA 60
Db 1001 ATGAAATATGCACAACTGAACTGACCTGAGTTGACGATGATGAGTGGTGGCAGTA 1060
Qy 61 AGATTAGCGCACTGCAGCAGCAACTTTAGCAGCAGTAGCAGCAAGCAACCAACAGCAGC 120
Db 1061 AGATTAGCGCACTGCAGCAGCAACATCAGCAGCAGTAGCAGCAGCAAGCAACCAACAGCAGC 1120

Qy 121 AACACGAGGCAACACAGCAACTCACAACACTGCAACCAAGGAGCTTAAGTACAAAACAC 180
Db 1121 AACAAAGGCGACAAACAGCAACTCACAACACTGCAACCAAGGAGCTTAAGTACAAAACAC 1180
Qy 181 CACAGCAACATTTGCAAGGAGCAGCAGCAATAGCAGCAACAGGAGCAGCATCGAAGGAC 240
Db 1181 CACAGCAACATTTGCAAGGAGCAGCAGCAATAGCAGCAACAGGAGCAGCATCGAAGGAC 1240
Qy 241 GAGGATGTAGCCAAACACCGGTAGAGCAATGACCAGCAGCGCATCTGCAACAGCTAGAC 300
Db 1241 GAGGATGTAGCCAAACACCGGTAGAGCAATGACCAGCAGCGCATCTGCAACAGCTAGAC 1300
Qy 301 AGCAGCAACATTTGTCGCCAAAGACAGCGCAGCAGCAACTGTCGCCGCGATGAGCA 360
Db 1301 AGCAGCAACATTTGTCGCCAAAGACAGCGCAGCAGCAACTGTCGCCGCGATGAGCA 1360
Qy 361 ACAACCCCAACCAACCAACATAAGACTGTGTGACGCAAGGAGCAACGATTCGCTGCGC 420
Db 1361 ACAACCCCAACCAACCAACATAAGACTGTGTGACGCAAGGAGCAACGATTCGCTGCGC 1420
Qy 421 CGACGAAAAAGAAAAACCCAGCAACCCCAACCAACAGATATCA----- 463
Db 1421 CGACGAAAAAGAAAAACCCAGCAACCCCAACCAACAGATATCAAGGTAAACATTAATAAC 1480
Qy 464 ----- 463
Db 1481 ATCATATTTAACTAAATATATAGAAATTTAGAAAAATTAATGCAACCCCTCAGCATTTGAATT 1540
Qy 464 -----AGAAACAACAGCAACTTAGCATGCTCCCTTCAAAACGCGCA 505
Db 1541 TGGTCTTTTACAAATTCAGAAACACAGCAACTTAGCATGCTCCCTTCAAAACGCGCA 1600
Qy 506 AATCCACGAGACCTACAGCAGCACCAACAGCAGCAACAGCTGTTCGACAGCCACCTACA 565
Db 1601 AATCCACGAGACCTACAGCAGCACCAACAGCAGCAACAGCTGTTCGACAGCCACCTACA 1660
Qy 566 TGCATATGTCAGCGCAGGAGCAATGAGTTTCAGTATTCGATATTCGAGACATGATAGATAT 625
Db 1661 TGCATATGTCAGCGCAGGAGCAATGAGTTTCAGTATTCGATATTCGAGACATGATAGATAT 1720
Qy 626 CCACGGCCACATTCGCTGGTGTTCATGCTGTCAGAGTGTCTGCTGCTGCTGCTGCAAC 685
Db 1721 CCACGGCCACATTCGCTGGTGTTCATGCTGTCAGAGTGTCTGCTGCTGCTGCTGCAAC 1780
Qy 686 AGTGGCAACTTCACGTGCAACAGCGATCGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCAAC 745
Db 1781 AGTGGCAACTTCACGTGCAACAGCGATCGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCAAC 1840
Qy 746 CCATCGCTTCATTTCTTATTTAGGCACTTTGCGAGCACTGCAAAATAGCAGC--A 802
Db 1841 CCATCGCTTCATTTCTTATTTAGGCACTTTGCGAGCACTTTCGAGGCACTGAGGAGCAGCAGTA 1900
Qy 803 GCAGCAGTAGCAGCAGCAACAGCAGCAACCAACAGCAGCAGCAATATTAACGAGCTTA 862
Db 1901 GCAGCAGCAACAGCAGCAACAGCGGCAACAGCAGCAGCAGCAATATTAACGAGCTTA 1960
Qy 863 ATAACTACTCATGGATATTTTATTGATATTTTGAATTTATCTGCTAAAGTT 915
Db 1961 ATAACTACTCATGGATATTTTATTGATATTTTGAATTTATCTGCTAAAGTT 2013

RESULT 4
ABL07799
ID ABL07799 standard; cDNA; 803 BP.
XX
AC ABL07799;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17879.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.

XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US09231.
 XX PR 23-MAR-2000; 2000US-191637P.
 XX PR 11-JUL-2000; 2000US-0614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-656860/75.
 XX DR P-PSDB; ABB63696.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX PS Claim 1; SEQ ID NO 17879; 21pp + Sequence Listing; English.
 XX CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 803 BP; 211 A; 199 C; 190 G; 203 T; 0 other;

Query Match 23.0%; Score 531; DB 23; Length 803;
 Best Local Similarity 88.4%; Pred. No. 9.2e-138;
 Matches 616; Conservative 0; Mismatches 15; Indels 56; Gaps 1;

OY 1054 GACGAGAAATCAATGCTAGTCACTAATGTGTGGTTAAACTGGAGTGAACGACATG 1113
 DB 1 GACGAGAAATCAATGCTAGTCACTAATGTGTGGTTAAACTGGAGTGAACGACATG 60
 OY 1114 ATCTCCCTGGAACACCTCCGACTATGCGGAGTTAAGGATCTCGAATACCGCGCAT 1173
 DB 61 ATCTCCCTGGAACACCTCCGACTATGCGGAGTTAAGGATCTCGAATACCGCGCAT 120
 OY 1174 CGCATCTGGAAGCCGAGCTGCTGATGTACAACAGTGGGATGAGGGATTTGACGGCACC 1233
 DB 121 CGCATCTGGAAGCCGAGCTGCTGATGTACAACAGTGGGATGAGGGATTTGATGGCACC 180
 OY 1234 TACCAGAGCAAGTGGTGGTGGCGGAACAACGGCTGTCTATACGTTCCCGCGGGGATC 1293
 DB 181 TACCAGAGCAAGTGGTGGTGGCGGAACAACGGCTGTCTATACGTTCCCGCGGGGATC 240
 OY 1294 TTCAGTCCAGTGCAGATCGACATCAGTGGTGTCCCTTCGATGACCGCGGTGCGAG 1353
 DB 241 TTCAGTCCAGTGCAGATCGACATCAGTGGTGTCCCTTCGATGACCGCGGTGCGAG 300
 OY 1354 ATGAGTTCCGCGAGTTGACCTACGACGATTTCCAGCTGGATTACAATTACAAGATGAA 1413
 DB 301 ATGAGTTCCGCGAGTTGACCTACGACGATTTCCAGCTGGATTACAAGTTGGT----- 343
 OY 1414 ACTGGCGGTGATATCAGCAGTTACGTGCTCAACGCGAGTGGGAACCTACTGTTGGT----- 1473
 DB 344 -----TCAGTGTGCC 354
 OY 1474 GCAACAGTACGAGATCTATTACAACCTGTCGCCGGAACCCCTATATAGACATCACCTTC 1533
 DB 1474 GCAACAGTACGAGATCTATTACAACCTGTCGCCGGAACCCCTATATAGACATCACCTTC

DB 355 GGCAAAACCTAACGAAATCTATTACAACCTGTCGCCGGAAACCCCTATATAGACATCACCTTC 414
 OY 1534 GCCATCATCATCCGCCGAGCAACACTGTACTATTCTTCAACCTGATCATACCTTGTGTA 1593
 DB 415 GCCATCATCATCCGCCGAGCAACACTGTACTATTCTTCAACCTGATCATACCTTGTGTA 474
 OY 1594 CTGATTGCTCCATGCGCCTTGTCTCGGATTCAACCTGCGCGGAGATTCGGGTGAAAAATTA 1653
 DB 475 CTGATTGCTCCATGCGCCTTGTCTCGGATTCACTCTGCGCGGAGATTCGGGTGAAAAATTA 534
 OY 1654 TCGCTGGGTGTACCATCTTCTCTCGCTGACCGGTGTTTCTGAATATGTTGCCGAGACA 1713
 DB 535 TCACGTGGGTGTACCATCTTCTCTCGCTGACCGGTGTTTCTGAATATGTTGCCGAGACA 594
 OY 1714 ATGCGCGCTACTTCCGATGCGGTGCGATTGTGGATAC 1750
 DB 595 ATGCGCGCTACTTCCGATGCGGTGCGATTGTGGATAC 631
 RESULT 5
 AA224476
 ID AA224476 standard; cDNA to mRNA; 3700 BP.
 XX AC AA224476;
 XX DT 17-FEB-2000 (first entry)
 XX DE H. virescens acetyl-choline receptor DNA from clone Hva7-1.
 XX KW Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
 KW neurotransmission; plant protection agent; conductance; AChR; dS.
 XX OS Heliothis virescens.
 XX FH Key Location/Qualifiers
 FT CDS 335..1825
 FT /*tag= a
 FT /product= "acetyl-choline receptor"
 XX DE19819829-A1.
 XX PD 11-NOV-1999.
 XX PF 04-MAY-1998; 98DE-1019829.
 XX PR 04-MAY-1998; 98DE-1019829.
 XX PA (FARB) BAYER AG.
 XX PI Adamczewski M, Oellers N, Schulte T;
 XX DR WPI; 2000-014207/02.
 XX DR P-PSDB; AAY50815.
 XX PT New nucleic acid encoding a nicotinic acetylcholine receptor from
 PT insects, used to identify potential insecticides -
 XX PS Claim 1a; Page 14-17; 26pp; German.
 XX CC This invention describes a novel nucleic acid (NA) encoding a nicotinic
 CC acetyl-choline receptor (I) from insects which can be used as an
 CC insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
 CC (also vectors containing it, its regulatory regions, and antibodies
 CC directed against (I)-encoded proteins) are used to screen for: (a) plant
 CC protection agents that alter conductance of AChR, potentially useful as
 CC insecticides, or (b) genes which encode polypeptides that are involved in
 CC formation of functionally related AChR in insects. (I) are also used to
 CC isolate and characterize the specified regulatory regions and for
 CC recombinant production of (II). This sequence encodes an acetyl-choline
 CC receptor isolated from Heliothis virescens.
 XX SQ Sequence 3700 BP; 893 A; 953 C; 944 G; 910 T; 0 other;

Query Match		22.28; Score 512.8; DB 21; Length 3700;
Best Local Similarity		62.5%; Pred. No. 2.6e-132;
Matches		878; Conservative 0; Mismatches 502; Indels 24; Gaps 4;
Qy	925	GGATATCATGAAAGAGACTGTTACAGATCTTTTGGATCCTTATATACACTAGAACGT 984
Db	425	GGGTACACAGAGAGCGCTACTGCACACCTATTTGGACCACACTACACGTACTGGAGAGG 484
Qy	985	CCGCTTCTCAATGAATCGGACCGTAACTAATTAAGCTTTTGGTTTAACTTTAAATGCAAAAT 1044
Db	485	CCGCTGCTCAACAGAGCGACCGCTCCAGCTCTCTTCGGCCTCAGCTCATGCGAGATC 544
Qy	1045	ATCGATGTGACGAGAAAATCAATTTAGTACATTAATGTGTGTTTAAACATGGAGTGG 1104
Db	545	ATCGACGTGACGAGAGAACAGCTTTTAAACAAACATCTGGCTAAAACATAGATGG 604
Qy	1105	AAGCACATGAATCTCCGCTGGACACCTCCGACTATGGCGGAGTTAAGGATCTCCGNATA 1164
Db	605	AATGATATGAATTTGAGGTGGACACTTCAGATTTTCGGCGGGGTCAAGAGATTTAAGAGTG 664
Qy	1165	CCGCGCATCGCATCTGGAAGCGGAGCTGCTGATGTACACAGTGGGATGAGGATTT 1224
Db	665	CCACCCACAGACTATGGAACACAGAGTCTTATGTACACAGCGCGGACGAAGGTT 724
Qy	1225	GACGGCACCTACAGACGAGCGTGGTGGTGGGAAACAAACGGCTGTCTATACGTTCCG 1284
Db	725	GACAGCACGTATCCAACGAACGTGGTGGTGGGAAACAAACGGCTGTCTGTAGTGGCG 784
Qy	1285	CCGGGGATCTCAAGTCAGCTGCAAGATCGACATCAGCTGGTTCCCTTCGATGACCAG 1344
Db	785	CCGGCATCTTCAAGAGCACCTGCAAGATCGACATCAGCTGGTTCCCTTCGACGACCAA 844
Qy	1345	CGTGGCAGATGAAGTTGGCAGTTGGACCTAGCAGGATTCAGCTGGATTTACAAATTA 1404
Db	845	CGATGCCAGATGAAGTTGGCAGCTGGACTTATGATGTTATCAGTTGGATCTACAACTA 904
Qy	1405	CAAGATGAAGTGGCGGTGATATCAGCAGTTAGCTGTCTCAACGCGAGTGGGAACACTG 1464
Db	905	CAGGATGAAGGGCGGAGATATAAGCAGTTTGTCAAGAAATGGCAATGGAGTTAATA 964
Qy	1465	GGTGTGCGCGCAACCTFAAGAGATCTATTACAACTGCTGCCGGAACCTTATATAGAC 1524
Db	965	GGAGTCCCGCAACGCGACAGATCTATTACAACTGTTGTCCGAGCCATATACATCGAC 1024
Qy	1525	ATCACCTTGGCATCATCCGCGGACGAACACTGTACTATTCTTCAACCTGATCATA 1584
Db	1025	ATCACGTTTGGCGTGGTATCCGAGAAACAGCTCTACTACTTCTTCAATCTCATCGTG 1084
Qy	1585	CTTGTGTACTGATTCCTCCATGGCCTTGTCTGGATTCACCTTGGCGCCAGATTCGGGT 1644
Db	1085	CCCTGTGTCTCATCTCGCTCCATGGCTCTATTGGGGTTCACTTGGCTCCAGACTCCGGA 1144
Qy	1645	GAATAATATCGTGGGTGTACCATCTGTCTCTGCTGACCGGTCTTCTGAATATGTTT 1704
Db	1145	GAATAATGTTCTTTAGTGTGACGATATATCTGTCTGAGGTGTCTCTCAACATGGTG 1204
Qy	1705	GCCGAGCAATTCGCGGTACTTCCGATGCGGTGGCAATTTG-----TGGATACG 1752
Db	1205	GCGGAGACGATGCCAGCAGCTCGGACGCGCTGCTGCGCACCTACTTCAACTGC 1264
Qy	1753	ATCGTGTGTTTG--TGTGGTGGCATGGATATTTGCAATGAGTCGCGCCAGGACCGC 1810
Db	1265	ATCATGTTATGTTGGTGTCTCTCGCTGTCTCCACCATCTGATTCCTTCAACTACCCAC 1324
Qy	1811	TGATCTTAGAGTTCCCGACACGCGCTTTCGGACACATCCTCCGACGGAA-----GCAC 1866
Db	1325	CGGCACGACAGACTCAGAAATGAGTGAATTTGGATTCGTTGGTGTCTTTATTTGGCTG 1384
Qy	1867	CAGATACTCTCCAGCTTTGAGCTGAAAGAGCGCTCTGCGAAATCGCTGTCTGGCCCAAGTA 1926
Db	1385	CCGTGGGTGCTGCGCATGTACGCGCCGCGTCTCGCGACGACGCGCGCGCGCGCGTA 1444
Qy	1927	CTAGACATCGATGATGATCTTCCGGCACAAATTTGTCGCCCCCATGAGCGCGCGGGAACACTG 1986

Db	1445	CTCCGCGCGGACCTGGAGCTGCGCGAGCGCTCTCCAAAGTCGCTCTAGCGAAGCTG 1504
Qy	1987	CCACACAACCCGCTTTCTATCGCACGGTTTATGGACAAGCGACGATGGCAGCATTTGGG 2046
Db	1505	CTCGACATCGATGACGACTTCCGCCACCCCAAGCGAGCGAGCGCAATGCTGCCGATAC 1564
Qy	2047	CCAATTGGCAGCACCCGAATGCGCGATGCGGTCCACCATCATATAGTGCATCAATAATCA 2106
Db	1565	TACAGGGGGGTGAGGAGATGCGCGGGGTTGGCGCGCACAGTTGCTTC-----GGT 1618
Qy	2107	ACTGAATGAATAGTTTAACTTTAAAGGAATTCGCTTTTATACTGATCAGTACGT 2166
Db	1619	GTGAGCTACGAGCTCTCCCTCATTTCTGAAGAGATTAGAGTCTACAGATCAGATCGCG 1678
Qy	2167	AAAGATTACCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 2226
Db	1679	AAGAGACAGCAATGCGGACATTTCCGCGACTGGAGTTCCGCCCATGTTGCTGGAC 1738
Qy	2227	AGACTGTGCTTATATTTACAAATGTTCCGAATTTAGCCACAATAGCTGACTACTA 2286
Db	1739	AGACTGTGCTTATATTTACCTTGTTCACAAATCATCGCACGCTAGCGTGTCTG 1798
Qy	2287	TCGGCACCACATATTTGCTCTG 2310
Db	1799	TCGGCACCACATATGTTGCTG 1822
RESULT 6		
ABLL3733		
ID	ABLL3733	standard; cDNA; 936 BP.
XX	ABLL3733;	
XX		
DT	26-MAR-2002	(first entry)
XX		
DE	Drosophila melanogaster	expressed polynucleotide SEQ ID NO 35681.
KW	Drosophila;	developmental biology; cell signalling; insecticide;
KW	pharmaceutical;	gene; ss.
OS	Drosophila melanogaster.	
XX		
PN	WO200171042-A2.	
XX		
PD	27-SEP-2001.	
XX		
PF	23-MAR-2001;	2001WO-US09231.
XX		
PR	23-MAR-2000;	2000US-191637P.
PR	11-JUL-2000;	2000US-0614150.
XX		
PA	(PEKE)	PE CORP NY.
XX		
PI	Venter JC,	Adams M, Li PWD, Myers EW;
XX		
DR	WPI;	2001-656860/75.
DR	P-PSDB;	ABB69630.
XX		
PT	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -	
XX	Claim 1; SEQ ID NO 35681; 21pp + Sequence Listing; English.	
XX	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLL16176-ABLL30511), expressed DNA sequences (ABLL1840-ABLL16175) and the encoded proteins (ABLL5773-ABLL72072).	

CC	The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO									
CC	at ftp.wipo.int/pub/published_pct_sequences.									
XX										
QQ	Sequence 936 BP; 238 A; 213 C; 239 G; 246 T; 0 other;									
	Query Match	20.7%	Score 479;	DB 23;	Length 936;					
	Best Local Similarity	73.5%;	Pred. No. 3.5e-123;							
	Matches 611;	Conservative 0;	Mismatches 220;	Indels 0;	Gaps 0;					
QY	913	GTTTGCCTACGAGATATCATGAAAGAGACTGTTACACGATCTTTTGGATCTTATAAT	972							
DB	94	GCTTTGTGCGCTGGACCCCATGAGAGCGCTACTCCACGCCCTTCTGGACAACACTACAAC	153							
QY	973	ACACTAGAAGCTCCCGTTCTCAATGAATCGAGCCCGTTACAATTAAGCTTTGGTTAACT	1032							
DB	154	AGCCTGGAGGCTCGGTGGTCAATGAATTCGATCCATTCGAATGAGCTTCGGAGCTAACCA	213							
QY	1033	TTAATGCAAAATATTCAGATGTGGACGAGAAAATCAATTTGTAGTCACTAATGTGTGGTTA	1092							
DB	214	CTCATGCAGATTATTCAGATGTGGACGAGAAATCAACTGCTTTATAACGAATAATTTGGCTC	273							
QY	1093	AAACTGGAGTGGAAACGACATGAATCTCCGCTGGAAACACCTCCGACATATGCGGAGTTAAG	1152							
DB	274	AAATTTGGAATTTGGAACGATATGAATCTTCGATGGAATTCGAGTGAATTCGGTGTGTGCGG	333							
QY	1153	GATCTCGGAATACCGCGCATCTGCAAGCGGACGCTGTGTGGGGAACACACGCTCGTGT	1212							
DB	334	GATCTCGGAATTCGGCACATCCGCTATGGAACCGGATGACTGATGTACAACAGTGGCC	393							
QY	1213	GATGAGGGATTTGACGGCACCTACACAGAGAAAGCTGTGTGGGGAACACACGCTCGTGT	1272							
DB	394	GACGAGGGCTTCGATGGAAGCTAGCGCACAAATGTGTGTTCGCAATAATGGGAGCTGT	453							
QY	1273	CTATAGTTCGCGCGGGGATCTTCAAGTCAGCTGCAAGATCGACATFCAGTGGTTCGCC	1332							
DB	454	CTGTAGCTACCGCGCAGTATATTAAAGTCAACGTGAAGATCGACATTCAGTGGTTCCTCA	513							
QY	1333	TTTCAGTACACAGCGGTGCGAGATGAAGTTTCGGGAGTTGGACCTACGACGATTCACAGCTG	1392							
DB	514	TTTCAGCTACGAGATGTGAATTTGGTTCTGGGACCTACGATGGTTCAGTTG	573							
QY	1393	GATTTCACATTCACAGATGAACCTGGCGGTGATATCAGCAGTTACGCTCAACGGCGAG	1452							
DB	574	GACCTGCAGTTGCAGGACGAGCTGTGGGCGACATTCCTAGCTTTATAACCAATGGGAA	633							
QY	1453	TGGGAATCTAGGTGTGCCCGGCAACGCTAACGAGATCTATTACACTGCTGCCCGGAA	1512							
DB	634	TGGGACTTGTGTAGTGTGCCCGGTAAACGAAATGAAATCTACTATAATTGCTGCCAGAA	693							
QY	1513	CCCTATATGACATCACTTCGCCCATCATCATCCGCGGAGACACTGTACTATTCTTC	1572							
DB	694	CCATTATGACATAACATTTCGCCCATTTGATAAGGCGCAAAACGTTGTACTATTTTTC	753							
QY	1573	AACTGTATCATACCTTGTGTACTGATTGCTTCCTCATGCCCTTGCTCGGATTCACCCCTCGCG	1632							
DB	754	AATCTGATTGTGCGGTGCTGCTGATCGCTCCATGSCACTGCTAGGGTTACACTGCCA	813							
QY	1633	CCAGATTCGGGTGAAAATATATCGCTGGGTGTTTACCATCTGTCTCGCTGACCGTGT	1692							
DB	814	CCAGATTTCTGTTGAAAAGCTTTCGCTTGGAGTTACAATTTCTATTATCGCTTACAGTCTTC	873							
QY	1693	CTCAATATGTTCCGCGAGACAATTCGGGCTACTTCCGATCGCGGTGCAATG	1743							
DB	874	CTCAACATGTTGCCGGAACAATTCGCCGGGACCTCCGATGCGGTACCGCTG	924							
RESULT 7										
ABL07231										
ID	ABL07231 standard; cDNA; 1540 BP.									
XX										
AC	ABL07231;									
XX										

DT	26-MAR-2002 (first entry)	
XX	Drosophila melanogaster expressed polynucleotide SEQ ID NO 16175.	
DE	Drosophila melanogaster expressed polynucleotide SEQ ID NO 16175.	
XX	Drosophila; developmental biology; cell signalling; insecticide;	
KW	pharmaceutical; gene; ss.	
KW	Drosophila melanogaster.	
XX		
XX	W0200171042-A2.	
PN		
XX	27-SEP-2001.	
PD		
XX	23-MAR-2001; 2001WO-US09231.	
XX		
PF	23-MAR-2000; 2000US-191637P.	
XX		
PR	11-JUL-2000; 2000US-0614150.	
XX		
XX	(PEKE) PE CORP NY.	
XX		
PA		
XX		
PI	Venter JC, Adams M, Li PWD, Myers EW;	
XX		
XX	WPI; 2001-656860/75.	
DR	P-PSDB; ABB63128.	
DR		
XX		
PT	New isolated nucleic acid detection reagent for detecting 1000 or more	
PT	genes from Drosophila and for elucidating cell signalling and cell-cell	
PT	interactions -	
XX		
XX	Claim 1; SEQ ID NO 16175; 2lpp + Sequence Listing; English.	
XX		
CC	The invention relates to an isolated nucleic acid detection reagent	
CC	capable of detecting 1000 or more genes from Drosophila. The invention is	
CC	useful in developmental biology and in elucidating cell signalling and	
CC	cell-cell interactions in higher eukaryotes for the development of	
CC	insecticides, therapeutics and pharmaceutical drugs. The invention	
CC	discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA	
CC	sequences (ABL01840-ABL16175) and the encoded proteins	
CC	(ABB57737-ABB72072).	
CC	The sequence data for this patent did not form part of the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequences.	
XX		
XX	Sequence 1540 BP; 412 A; 390 C; 376 G; 362 T; 0 other;	
Query Match	17.88; Score 412.2; DB 23; Length 1540;	
Best Local Similarity	69.28; Pred. No. 2.2e-104;	
Matches	578; Conservative 0; Mismatches 253; Indels 4; Gaps 1;	
QY	909 TAAAGTTTGCTAGCAGGATATCATGAAAAAGAGACTGTTACACGATCTTTTGGATCCTTA 968	
Db	106 TAAAGAAGCTGTCAAGGACCTCATGAAAAGCGCTGCTGAACCACTGCTGTCCACCTA 165	
QY	969 TAATACACTAGAAGCTCCCGTTCTCAATGAATCGGACCCGTTTCAATTAAGCTTTGGTTT 1028	
Db	166 CAATACGCTGGAGCGACCCGCTGGCCAATGAATCGGAGCCCTCGAGGTTAAGTTCGGACT 225	
QY	1029 AACTTTAATGCAAAATTATCGATGTGGACGAGAAAAATCAATTGCTAGTCACTAATGTGTG 1088	
Db	226 GAGCGTGCACGATCATCGACGTGGATGGAAGAATTCAGATTTCTGACCAACAATCGGTG 285	
QY	1089 GTTAAAACTCGAGTGGAAACACATGAATCTCCGCTGGAAACACCTCCGACTATCGCGGAGT 1148	
Db	286 GTTAAATTTGGATGGAGACGACTACATCTGCGCTGGAATGAACGGAATACGCGGGGT 345	
QY	1149 TAAGGATCTCGGAATACCGCGCATCGCATCTTGGAAAGCCGAGCTGCTGATGTACACAG 1208	
Db	346 CAAGGATCTACGAATCACGCGCCCAACACAGCTGTGGAAGCCGACGTGCTCATGTACAACAG 405	
QY	1209 TGCGGATGAGGGATTTGACGCGCACTTACCAGACGAACGTGGTGGTGGGGAACAACCGGCTC 1268	
Db	406 CGCGGATGAGGGATTCGATGGCAGTATCACACCAACATTTGTTGTCAAAACATACACGCAG 465	

RESULT 7
ABL07231
ID ABL0
XX
AC ABL0
XX

QY 1269 GTGCTATACGTTCCCGCGGGGATCTCAAGTCGACGTGCAAGATCGACATCAGTGGTT 1328
 Db 466 TTGCTGTAGTCGCCCGCCCGTGTATCTTCAAGACCATGCAAGATGACATCAGTGGTT 525
 QY 1329 CCCTTCGATGACACGGGTGCGAGATGAAGTTGCGGAGTTGGACCTACACGAGTCCCA 1388
 Db 526 CCATTTGATGACCAACATTCGGAATGAAATTCGGTAGTTGGACTTACGATGGAATCA 585
 QY 1389 GCTGGATTTACAATACAAGATGAACCTGGCGGTGTATATACGAGTTTACGTGCTCAACGG 1448
 Db 586 GTTGGATTTGGTTTGAATTCGGAAGATGAGGGGATCTTTCCGATTTCAACAATGG 645
 QY 1449 CGAGTGGGACTACTGGGT---GTGCCCCGGAACGTAACGAGATCTATTACACTGCT 1504
 Db 646 CGAGTGTACTTGGTTTACCATTCCGCGGAAGAAGATACGATAGTCTAGCCCTGCT 705
 QY 1505 GCCCGGAACCTATATAGATACATCACCCTTCGCCATCATCCGCGGACGAACTGTACT 1564
 Db 706 GCCAGAACCATATGTCGATATCACCTTTACTATACAAATTCGTGCGCGTACATATATT 765
 QY 1565 ATTCTTCAACCTGATCATACCTTGTGTACTGATTCGCTCCATGCGCTTCTCGGATTC 1624
 Db 766 ATTTTTCATTTAATTTGTCCTATGTGCTAATCTCATCGATGGCCCTACTGGCTTCA 825
 QY 1625 CCCTGCCCGCAGATTCGGGTGAATAATATCGTGGGTGTACCATCTTCTCTCGGTGA 1684
 Db 826 CATTCGCCCGGATTCGGCGGAGAACTGACGTGGCGTAACTATATCTACTATCAATA 885
 QY 1685 CCGTGTCTTGAATATGGTTGCCGAGACAATGCCGCTACTTCGGATGCGGTGCC 1739
 Db 886 CAGTATTTCTAAACCTTGTCCGAGTCCATGCCGACAACGTGGATGCTGTTC 940

RESULT 8

AAZ24477
 ID AAZ24477 standard; cdna to mRNA; 3109 BP.

AC AAZ24477;

DT 17-FEB-2000 (first entry)

XX H. virescens acetyl-choline receptor DNA from clone Hva7-2.

XX Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
 KW neurotransmission; plant protection agent; conductance; ACHR; ds.

XX Heliothis virescens.

XX DEL9819829-AL.

XX 11-NOV-1999.

XX 04-MAY-1998; 98DE-1019829.

XX 04-MAY-1998; 98DE-1019829.

XX (FARB) BAYER AG.

XX Adamczewski M, Oellers N, Schulte T;

XX WPI; 2000-014207/02.

DR P-PSDB; AAY50816.

XX New nucleic acid encoding a nicotinic acetylcholine receptor from

PT insects, used to identify potential insecticides

XX Claim 1a; Page 19-22; 26pp; German.

XX This invention describes a novel nucleic acid (NA) encoding a nicotinic
 CC acetyl-choline receptor (r) from insects which can be used as an
 CC insecticide. Inhibitors of (r) interfere with neurotransmission. (I)
 CC (also vectors containing it, its regulatory regions, and antibodies
 CC directed against (I)-encoded proteins) are used to screen for: (a) plant

CC protection agents that alter conductance of Achr, potentially useful as
 CC insecticides, or (b) genes which encode polypeptides that are involved in
 CC formation of functionally related Achr in insects. (I) are also used to
 CC isolate and characterize the specified regulatory regions and for
 CC recombinant production of (II). This sequence encodes an acetyl-choline
 CC receptor isolated from *Heliothis virescens*.

XX Sequence 3109 BP; 923 A; 610 C; 742 G; 834 T; 0 other;

Query Match 17.8%; Score 411.4; DB 21; Length 3109;
 Best Local Similarity 68.8%; Pred. No. 5.3e-104;
 Matches 565; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

QY 924 AGGATATCATGAAAAGAGACTGTACACGATCTTTTGGATCCCTTATATACACTAGAACG 983
 Db 151 AGGTCTCTACGAGAAGAGACTCTGAAACGGTGTCTGGCGAACTACAAACCCCTGGAGCG 210
 QY 984 TCCCGTCTCAATGAATCGGACCCGTTACAATTAAGCTTTTGGTTTAACCTTAATGCAAT 1043
 Db 211 ACCGGTGGCCACAGAGACGCAACCGCTAGAGGTGACGTTGCGCTTGACCTTGACGAAAT 270
 QY 1044 TATCGATGTGACGAGAGAAAATCAATTCGTAGTCACTAATGTGTGGTTAAACTGGAGTG 1103
 Db 271 CATTCAGCTGGAGAGAAGATCACTACTTATAACCAATATATGGCTGCTGTGGAGTG 330
 QY 1104 GAACGACATGAATCTCGCTGGACACCTCCGACTATGCGGAGGTTAAGGATCTGCGAAT 1163
 Db 331 GAATGACTACAACTGAGGTGGAACGACGAGTATGCGGGGTCAAGGACCTCAGGAT 390
 QY 1164 ACCGCCCATCGCATCTGGAAGCGGACGTCGTATGATACAACAGTCGCGATGAGGAT 1223
 Db 391 CACGCCCAACAAGTTGTGGAAGCGGACGCTTATATATATAGTCTGACGAGGTT 450
 QY 1224 TGACGGCACCTACAGACGAACTGTGTGTCGGAACAACGGCTGCTGTATACGTTCC 1283
 Db 451 TGACGGACCTACAGACCAACGCTGTGTGTCAGAAGCGCGGCACTGCTGTACGTGCC 510
 QY 1284 GCGGGGATCTTCAAGTCGAGCTGCAAGATCGACATCAGCTGGTTCCTCCCTCGATGACCA 1343
 Db 511 ACCTGGCATATTCAAGAGACATGCAAGATGGACATCGCTGGTTCCTCTCGACGACCA 570
 QY 1344 GCGGTGGAGATGAAGTTCGCGAGTTGACCTAGCAGGATTCACGCTGGATTTACAAT 1403
 Db 571 ACATGTGATATGAAGTTCGCTAGCTGGACATATGACGGCAATCAGTTGGATCTGGTCT 630
 QY 1404 ACAAGTGAACCTGCGGTGATATCAGCAGTTACGTCTCAACGGCGAGTGGAACTACT 1463
 Db 631 AAAAGATGAGCAGGCGGCGCTATCTCGGACTTCATAACAATGGGAGTGTATCTAAT 690
 QY 1464 GGGTGTGCCCGGAACGTAACGAGATCTATTACACTGCTGCCCGGAACCTATATAGA 1523
 Db 691 AGGAATGCCAGGCAAAAAGAACACAATAACATACGCTGTGCCCGGAGCCCTACGTGGA 750
 QY 1524 CATCACCCTTCGCATCATCTCCGACCAACACTGTACTATTCTTCAACCTGATCAT 1583
 Db 751 CGTCACTTCACCATCATGATAAGAGACGAAACCTTGTACTTCTTCAACCTGATCTGT 810
 QY 1584 ACCTTGTGTACTGATTCCTCCATGGCTTGTGCTGGATTCACCTCGCGGACAGATTCGGG 1643
 Db 811 CCGGTGGTCTGATCTCATCTGATGGCACTCTCTGGCTTCACACTGCCACGACCTCGG 870
 QY 1644 TGAAAAATATCGTGGGTGTTACCATCTTGTCTCTCGCTGACCGGTGTTCTGAATATGGT 1703
 Db 871 AGAAAACTCACACTTGGAGTCACTATTCTTCTATCTGCTGCGGTGTTCTCTCAACCTGGT 930
 QY 1704 TGCCGAGACAATGCCGCTACTTCCGATGCGGTGCCATTGT 1744
 Db 931 AGCCGAGACCTGCGCACAGGTCTCCGACGCTATCCCCCTGT 971

RESULT 9

ABL07798
 ID ABL07798 standard; cdna; 14668 BP.

XX ABL07798;
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 17876.
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
XX Drosophila melanogaster.
XX WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US09231.
XX 23-MAR-2000; 2000US-191637P.
XX 11-JUL-2000; 2000US-0614150.
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX P-PSDB; ABB63695.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX Claim 1; SEQ ID NO 17876; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX (ABB57737-ABB72072).
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 14668 BP; 4616 A; 3078 C; 2662 G; 4312 T; 0 other;
Query Match 14.5%; Score 335.8; DB 23; Length 14668;
Best Local Similarity 99.4%; Pred. No. 1.7e-82;
Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1053 GGACGAGAAAATCAATTGCTACTAATGTGTGTTAAACTGGAGTGAACGACAT 1112
DB 1000 GGACGAGAAAATCAATTGCTACTAATGTGTGTTAAACTGGAGTGAACGACAT 1059
QY 1113 GAATCTCCCTGGAACACCTCCGACTATGCGGAGTTAAGGATCTCGGAATACCGCGCA 1172
DB 1060 GAATCTCCCTGGAACACCTCCGACTATGCGGAGTTAAGGATCTCGGAATACCGCGCA 1119
QY 1173 TCGCATCTGGAGCCGAGCTGCTGATGTACACAGTGGGATGGGATTTACGGCAC 1232
DB 1120 TCGCATCTGGAGCCGAGCTGCTGATGTACACAGTGGGATGGGATTTACGGCAC 1179
QY 1233 CTACACAGCAAGCTGGTGGTGGGAAACACGCTGCTGTATAGTTCCCGGGGAT 1292
DB 1180 CTACACAGCAAGCTGGTGGTGGGAAACACGCTGCTGTATAGTTCCCGGGGAT 1239
QY 1293 CTTCAAGTCGAGTCGAAGATCGACATCACGTGGTTCCTTCGATGACCGGTCGCA 1352
DB 1240 CTTCAAGTCGAGTCGAAGATCGACATCACGTGGTTCCTTCGATGACCGGTCGCA 1299
QY 1353 GATGAAGTTCGGCAGTTGGACCTACGACGGATTCAGCT 1391

DB. 1300 GATGAAGTTCGGCAGTTGGACCTACGACGGATTCAGCT 1338
RESULT 10
AAC58395
ID AAC58395 standard; cDNA; 1509 BP.
XX AAC58395;
XX AAC58395;
XX 29-JAN-2001 (first entry)
XX Human PRO2145 nucleotide sequence SEQ ID NO:76.
XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
XX proliferation; tumorigenesis; identification; cancer; cytostatic;
XX nontropic; neuroprotective; antiinflammatory; immunosuppressive;
XX immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
XX neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
XX hypothalamic disorder; glandular disorder; macrophagal disorder;
XX epithelial disorder; stromal disorder; blastocoealic disorder;
XX inflammatory disorder; immunologic disorder; ss.
XX Homo sapiens.
XX WO200053755-A2.
XX 14-SEP-2000.
XX 06-JAN-2000; 2000WO-US00376.
XX 08-MAR-1999; 99WO-US05028.
XX 02-JUN-1999; 99WO-US12252.
XX 23-JUN-1999; 99US-0141037.
XX 07-JUL-1999; 99US-0143048.
XX 26-JUL-1999; 99US-0145698.
XX 30-NOV-1999; 99WO-US28313.
XX 20-DEC-1999; 99WO-US30911.
XX 05-JAN-2000; 2000WO-US00219.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
XX Watanabe CK, Wood WI;
XX WPI; 2000-572270/53.
XX P-PSDB; AAB24088.
XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
XX treatment, diagnosis and prevention of cancer -
XX Claim 50; Fig 57; 286pp; English.
XX The present invention describes an isolated antibody that binds to
XX one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
XX PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
XX PRO1025, PRO1030, PRO1037, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
XX PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,
XX PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
XX growth. The PRO polypeptides and nucleotides are useful in the
XX treatment, diagnosis and prevention of cancer. The antibodies and other
XX anti-tumour compounds may be used to treat various conditions, including
XX those characterised by overexpression and/or activation of the amplified
XX PRO genes. Exemplary conditions or disorders to be treated with such
XX antibodies and other compounds include benign or malignant tumours
XX (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
XX colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic
XX carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
XX leukaemias and lymphoid malignancies, other disorders such as neuronal,
XX glial, astrocytal, hypothalamic and other glandular, macrophagal,
XX epithelial, stromal and blastocoealic disorders, and inflammatory,
XX angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
XX primers and hybridisation probes used in the isolation of the human PRO

CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
CC PRO polynucleotide and protein sequences given in the exemplification of
CC the present invention.
XX
SQ Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 other;

Query Match 12.8%; Score 296.2; DB 21; Length 1509;
Best Local Similarity 60.7%; Pred. No. 5.8e-72;
Matches 506; Conservative 0; Mismatches 318; Indels 9; Gaps 1;

QY 911 AAGTTTGCCTAGCAGGATATCATGAAAGAGACTGTTACACGATCTTTTGATCCTTATA 970
DB 53 ACGTGTCCTCCGCAAGGAGTTCAGAGGAGCTTTTACAGAGAGCTGGTCAAGAACTACA 112

QY 971 ATACACTAGAACGTCCTCGTTCTCAATGAATCGGACCGCTTTACAAATTAAGCTTTGGTTAA 1030
DB 113 ATCCCTGGAGAGCGCGTGGCCAAATGACTCGCAACCACTCACCGTCTACTTCTCCCTGA 172

QY 1031 CTTTAATGCAAAATATGAGTGTGGACGAGAAATCAATTTGCTAGTCACTAATGTGTGGT 1090
DB 173 GCCTCTGCAGATCATGAGCTGGATGAGAAGAACCAAGTTTAAACCACCAACATTTGGC 232

QY 1091 TAAACTGGAGTGAAGACATGAATCTCCGCTGGACACCTCCGACTATGGCGGAGTTA 1150
DB 233 TGCAAATGTCTTGACAGACTACTATTTACAGTGAATGTGTGAGATATCCAGGGGTGA 292

QY 1151 AGGATCTGCGAAATACCCGCGCATCGCATCTGGAAGCGGACGTGCTGATGATCAACAGTG 1210
DB 293 AGACTGTCTGTTCCAGATGGCCAGATTTGGAACCAAGACATTTCTCTATAACAGTG 352

QY 1211 CGGATGAGGATTTGACGGCACTTACAGACGACGTGGTGGTGGCGGAACAACGGTCTGT 1270
DB 353 CTGATGAGCGCTTGTAGCGCACATTCACACTAACGTTGGTGGTGAATTTCTCGGGCAT 412

QY 1271 GTCTATACGTTCCGCGGGGATCTCAAGTCGAGCTGCAAGTGCAGATCGACATCACGTTGPTCC 1330
DB 413 GCCAGTACCTGCTCCAGGATATTTCAAGAGTTCTCTGCTACATCGATGATGAGTGTGTTTC 472

QY 1331 CCTTCGATGACGACGCGTGGAGATGAAGTTCCGCGAGTTGGACCTACGACGATTCACAGC 1390
DB 473 CTTTGTGATGTCAGCACTGCAAACTGAAGTTTGGGTCTCTGTCTTACGGAGGCTGGTCT 532

QY 1391 TGGATTTACAATTTACAAGATGAACCTGGCGGTGATATCAGCAGTATCGTCTCAACGGCG 1450
DB 533 TGGATCTGCAGATGCAGAGGCA-----GATATCAGTGGCTATATCCCAATGGAG 583

QY 1451 AGTGGGAACCTACTGGGTGTCGCGGCAACGTAACGAGATCTATTACAACCTGTGCCCGG 1510
DB 584 AATGGGACCTAGTGGGAATCCCGGCAAGAGGAGTGAAGTCTATGATGCTGCAAG 643

QY 1511 AACCTATAGACATCACCTTCGCCATCATCATCCCGGACGACACTGTACTATTCT 1570
DB 644 AGCCCTACCCGATGTCACTTCACTACAGTACCATTGCGCCGCGAGACGCTCTACTATGGCC 703

QY 1571 TCACCTGATCATACCTTTGTGTACTGATGCTCCATCGGCTTGTGCTCGGATTCACCTGC 1630
DB 704 TCACCTGCTGATCCCTGCTGTGCTATCTCCGCGCTCGCCCTGCTGGTGTCTCTGCTTC 763

QY 1631 CGCAGATTCGGGTGAATAATATTCGCTGGGTGTTACCATCTGCTCTCGTACCGCTGT 1690
DB 764 CTGAGATTCGGGGGGAAGATTTCCCTGGGGATTAACAGTCTTACTCTCTCTTACCGTCT 823

QY 1691 TTCTGAATATGTTTGGCGAGACAATGCGGCTACTTCCGATGCGGTGCCATTG 1743
DB 824 TCATGCTGCTGCTGCTGAGATCATGCCGCAACATCCGATTCGTTCCGTACCATTTG 876

RESULT 11

AAC90380

ID AAC90380 standard; cDNA: 1509 BP.

XX

AC AAC90380;

XX

DT 14-MAR-2001 (first entry)
XX Wild-type human alpha7 ligand gated ion channel coding sequence.
XX
KW Human; alpha7 nicotinic acetylcholine gated ion channel;
KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.
OS Homo sapiens.
XX WO200073431-A2.
XX 07-DEC-2000.
XX
PF 25-MAY-2000; 2000WO-US11862.
XX
XX 27-MAY-1999; 99US-0136174.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX Groppi VE, Wolfe ML, Berkenpas MB;
PI P-PSDB; AAB50012.
XX
DR WPI; 2001-061524/07.
XX P-PSDB; AAB50012.
XX
PT Special cell culture medium for treating cells and for inducing
PT mammalian cell lines to conduct calcium ions, comprising specified
PT concentrations of ions of sodium, calcium and potassium at specified pH
XX
XX
PS Example 5; Pages 60-61; 77pp; English.
XX
CC The present sequence is the coding sequence for wild-type human alpha7
CC nicotinic acetylcholine gated ion channel. The human alpha7 ion channel
CC was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3)
CC chimeric ligand gated ion channel (see AAC90382 and AAB50014). The
CC alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells
CC in the present invention, resulting in preferential calcium ion
CC conductance by the cells.
XX
SQ Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 other;

Query Match 12.8%; Score 296.2; DB 22; Length 1509;
Best Local Similarity 60.7%; Pred. No. 5.8e-72;
Matches 506; Conservative 0; Mismatches 318; Indels 9; Gaps 1;

QY 911 AAGTTTGCCTAGCAGGATATCATGAAAGAGACTGTTACACGATCTTTTGATCCTTATA 970
DB 53 ACGTGTCCTCCGCAAGGAGTTCAGAGGAGCTTTTACAGAGAGCTGGTCAAGAACTACA 112

QY 971 ATACACTAGAACGTCCTCGTTCTCAATGAATCGGACCGCTTTACAAATTAAGCTTTGGTTAA 1030
DB 113 ATCCCTGGAGAGCGCGTGGCCAAATGACTCGCAACCACTCACCGTCTACTTCTCCCTGA 172

QY 1031 CTTTAATGCAAAATATGAGTGTGGACGAGAAATCAATTTGCTAGTCACTAATGTGTGGT 1090
DB 173 GCCTCTGCAGATCATGAGCTGGATGAGAAGAACCAAGTTTAAACCACCAACATTTGGC 232

QY 1091 TAAACTGGAGTGAAGACATGAATCTCCGCTGGACACCTCCGACTATGGCGGAGTTA 1150
DB 233 TGCAAATGTCTTGACAGACTACTATTTACAGTGAATGTGTGAGATATCCAGGGGTGA 292

QY 1151 AGGATCTGCGAAATACCCGCGCATCGCATCTGGAAGCGGACGTGCTGATGATCAACAGTG 1210
DB 293 AGACTGTCTGTTCCAGATGGCCAGATTTGGAACCAAGACATTTCTCTATAACAGTG 352

QY 1211 CGGATGAGGATTTGACGGCACTTACAGACGACGTGGTGGTGGCGGAACAACGGTCTGT 1270
DB 353 CTGATGAGCGCTTGTAGCGCACATTCACACTAACGTTGGTGGTGAATTTCTCGGGCAT 412

QY 1271 GTCTATACGTTCCGCGGGGATCTTCAAGTCGAGCTGCAAGTGCAGATCGACATCACGTTGPTCC 1330
DB 413 GCCAGTACCTGCTCCAGGATATTTCAAGAGTTCTCTGCTACATCGATGATGAGTGTGTTTC 472

QY	1331	CTTTCGATGACACGCGGTGGAGATGAAGTTCCGGAGTTGGACCTACGACGGAATCCAGC	1399
Db	473	CCTTTGATGTGCAGCACTGCAAAACCTGAAGTTTGGGTCTTGGTCTTACGGAGGCTGGTCT	532
QY	1391	TGATTTACAAATTACAGATGAACCTGCGGTCATATACGACAGTTACGTCCTCAACGGCG	1450
Db	533	TGGATCTGCAGATGCAGGAGGCA-----GATATCAGTGGCTATATCCCAATGGAG	583
QY	1451	AGTGGGAACCTACTGGGTGTGCCCGCAAAAGTTAACGAGATCTATTACAACTGCTGCCCGG	1510
Db	584	AATGGGACCTAGTGGGAATCCCGCGCAAGAGGAGTGAAGGTTCTATGATGCTGCAAG	643
QY	1511	AACCTATATAGACATCACTTCGCCCATCATATCCGCCGACGACACACTGATATTTCT	1570
Db	644	AGGCCTACCCCGATGTCACTTCCACAGTACCACTGCGCGCAGAGGCTCTACTATGGCC	703
QY	1571	TCAACCTGATACACTTGTGTACTGATTGCCCTCCATGGCTGTGCTCGGATTCACCTGC	1630
Db	704	TCAACCTGTGATCCCTGTGCTCATCTCCGCCCTCGCCCTGCTGGTGTCTCTGCTTC	763
QY	1631	CGCCAGATTCGGGTGAAAATTTATCGCTGGGTGTTTACCATCTTCGCTCGCTGACCGTGT	1690
Db	764	CTCAGATTCGGGGAGAAGATTTCCTGGGGATAACAGTCTTACTCTCTCTTACCGTCT	823
QY	1691	TTCTGATATGGTTCGGGAGACAATGCGGCTACTTCCGATGCGGTGGCCATTG	1743
Db	824	TCATGTGCTGCTGGTGGATGATCATGCCGCAACATCCGATTCGGTACCATTG	876
RESULT 12			
AAV12197			
ID	AAV12197 standard; cDNA; 1876 BP.		
AC	AAV12197;		
XX			
DT	14-MAY-1998 (first entry)		
XX			
DE	Human neuronal nicotinic acetylcholine receptor alpha-7 subunit cDNA.		
XX			
KW	Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit;		
KW	brain tissue; screening; NACHR; antibody; ds.		
XX			
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
FT	73..1581		
FT	/*tag= a		
FT	/product= "neuronal nicotinic acetylcholine receptor		
FT	alpha-7 subunit"		
XX			
PN	WO9420617-A2.		
XX			
PD	15-SEP-1994.		
XX			
PF	08-MAR-1994; 94WO-US02447.		
XX			
PR	08-MAR-1993; 93US-0028031.		
XX			
PA	(SALK) SALK INST BIOTECHNOLOGY IND ASSOC.		
PA	(SIBI-) SIBIA NEUROSCIENCES INC.		
XX			
PI	Elliott KJ, Ellis SB, Harpold MM;		
XX			
DR	WPI; 1994-303024/37.		
DR	P-PSDB; AAW44153.		
XX			
PT	Human neuronal nicotinic acetylcholine receptor subunits and DNA -		
PT	also transformed cells useful for screening cpds. which modulate		
PT	activity of the receptor		
XX			
PS	Claim 8; Page 78-79; 99pp; English.		
XX			
CC	The present sequence encodes a human neuronal nicotinic acetylcholine		

CC The present sequence encodes a human neuronal nicotinic acetylcholine

receptor (NACHR) subunit. The cells expressing the alpha and/or beta NACHR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NACHR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits or specific receptor subunit combinations with a variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells that express a variety of subtypes

Sequence 1876 BP: 369 A; 553 C; 530 G; 423 T; 1 other: 50

Query Match	12.8%;	Score 296.2;	DB 15;	Length 1876;
Best Local Similarity	60.7%;	Pred. No. 6.5e-72;		
Matches 506;	Conservative	0;	Mismatches 318;	Indels 9;
				Gaps 1;

Qy	911	AAGTTTCCCPAGCAGGATATCATGAAAGAGACTGTGTACACGATCTTTTGGATCCCTTATA	970
Db	125	ACGTGTCCCTGCAAGGCGAGTTCCAGAGGAAGCTTTTCAAGGAGCTGGTTCAGAACTACA	184
Qy	971	ATACACTAGAACGTCGCCGTTTCTCAATGAATCGGACCCGGTTTACAAATTAAGCTTTGGTTTAA	1030
Db	185	ATCCCTTGGAGAGCCCGTGGCCAAATGACATCGCAAGCACATCACCGCTCTACTTCTCCCTGA	244

Qy	1031	CTTTAAATGCAATATT	CGATGCGACGAGAAAAAT	CAATTGCTAGTCACTAAT	GTGTGGT	1090
Dh	245	GCCTCTTCAGATCAT	CGACGTGGATCAGAGCAAC	CAAGTTTTTAA	CACCAATTTGGC	304

[illegible]

QY 1151 AGGATCTCGGAATACCGCCGCATCGCATCTGGAACGGACCTGCTCATGTACAACAGTG 1210

QY 1211 CGGATGAGGGGATTTGACGGCACTACACAGACGAACGTGGTGGGAAACACGGGTCGT 1270

425 CAGAGACCCCTTTGACGCCACATGACACATACAGTGTTGGGAGGATCTCTCGGGGAT 434

QY 1271 GTCATACGTTCCGCCGGGATCTTCAAGTGCACGTCGACATCGATCAGTGGTTCC 1330

DD 485 GCACGACCTGCTCCAGGCATATTCACAGAGTCTTGCTACATCGATGACGCTGGTTTC 544

QY 1331 CCTTCGATGACCAGCGGTGCGAGATGAAGTTTCGGCAGTTGGACCTACGACGATTCCAGC 1390

Db	545	CGTTTGATGTGCGACACTGCAAACTGAAGTTTGGGTCTCTGTGCTTACGGAGGCTGTGCTCT	604
Qy	1391	TGGATTTCAAATACAGATGAAACTGGCGGTGATATCAGCAGTTACGTGTCTCAACGGCG	1450

DB	Sequence	Length
605	TGGATCTCAGATGCAGAGGCA-----GATATCAGTGGCTATATCCCAATGGAG	655
QY	1451 AGTGGGAACACTACTGGTGTGCCCGGCAACGTAACGAGATCATTTACAACCTGCTGCCCGG	1510

Db	656	AATGGGACCTAGTGGGAAATCCCGGGCAAGAGAGTGAAGGTTCTATGAGTGCTGCNAAG	715
Ov	1511	AACCCCTATATAGACATCACCTTCGCGCATCATCGCGCGCAAGCACTGTACTATTCT	1570

Db	716	AGCCCTACCCCATGTCAACTTTCACACTGACCATGCCCGCAGGACGCTCTACTATGGCC	775
Dv	1571	TGAAAAACACATCATATACCTTTGCTGCATGTAATGCTCCATCACGCCCCGCTGCTACCCCTGC	1630

Db
776 TCAACCTGCTGATCCCGTGTGGCTCATCTCGGCCCTCGCCCTGCTGGTGTCTCTTC 835

Db 836 CTGCAGATTCGGGGAGAAATTCCTGGGATAACAGTCTACTCTCTCTACCGTCT 895

1691 TTCTGAATATGGTTGCCGAGACAATGCCGGCTACTTCCGATGCCGGTGCCATTG 1743

Db	896	TCATGTCGTCGGTGGATCATGCCGCAACATCCGATTCGGTACCATTG	948
RESULT 13			
AAAT48239			
ID	AAAT48239	standard; DNA; 1876 BP.	
XX	AAAT48239;		
XX	09-APR-1997	(first entry)	
XX	Neuronal	nicotinic acetylcholine receptor alpha-7 subunit DNA.	
XX	Neuronal	nicotinic acetylcholine receptor; nAChR; neurotransmitter;	
XX	ligand-gated	receptor; ds.	
XX	Homo sapiens.		
XX	Key	Location/Qualifiers	
XX	CDS	73..1581	
XX	FT	/*tag= a	
XX	PN	W09641876-A1.	
XX	PD	27-DEC-1996.	
XX	PP	07-JUN-1996; 96WO-US09775.	
XX	PR	07-JUN-1995; 95US-0484722.	
XX	(SIBI-)	SIBIA NEUROSCIENCES INC.	
XX	PI	Elliot KJ, Harpold NM;	
XX	WPI;	1997-065463/06.	
XX	P-PSDB;	AAW09025.	
XX	Nucleic acids	encoding nicotinic acetylcholine receptor sub-units -	
XX	used in	screening to determine the effect of drugs on the receptor	
XX	Disclosure;	Page 71-73; 108pp; English.	
XX	A DNA	sequence (AAAT48239) codes for the alpha-7 subunit (AAW09025) of	
XX	the human	neuronal nicotinic acetylcholine receptor (nAChR). Host	
XX	cells, esp.	mammalian cells or amphibian oocytes, carrying alpha-7	
XX	nucleic acids,	opt. in combination with other alpha and/or beta	
XX	subunit	nucleic acids (see also AAAT48232-38, AAAT48240-41), express	
XX	recombinant	nAChR subunits useful for identifying cpds. that	
XX	modulate	the activity of human nAChRs.	
XX	Sequence	1876 BP; 369 A; 553 C; 423 G; 423 T; 0 other;	
XX	Query Match	12.8%; Score 296.2; DB 18; Length 1876;	
XX	Best Local Similarity	60.7%; Pred. No. 6.5e-72;	
XX	Matches 506;	Conservative 0; Mismatches 318; Indels 9; Gaps 1;	
Qy	911	AAAGTTCCCTAGCAGGATATCATGAAAGAGACTGTTACAGATCTTTTGGATCCTTATA	970
Db	125	ACGTGTCCTCGCAAGCGAGTTCAGAGGAAGCTTTACAAGGAGCTGGTCAAGAACTACA	184
Qy	971	ATACACTAGAACGTCCCGTTCTCAATGAATCGGACCGCTTACAATTAAGCTTTGGTTAA	1030
Db	185	ATCCCTTTGGAGAGCGCCGTGGCCCAATGACTCGCAACCACTACCGGTCTACTTCTCCCTGA	244
Qy	1031	CTTTTAATGCAAAATPATCGATGTGGACGAGAAAAATCAATTGCTAGTCACCTAAATGTTGGT	1090
Db	245	GCCTCCTGCACATCATGACGTGGATGAGAAGAACCAAGTTTAAACCAACCAACATTTGGC	304
Qy	1091	TAAACATGGAGTGGAAACGACATGAATCTCCGCTGGAAACACCTCCGACTATGGCGGAGTTA	1150
Db	305	TGCAAAATGCTCTTGACAGACAGACTATTTACAGATGGAATGTCTCAGAAATATCCAGGGGTGA	364

Qy	1151	AGGATCGCAATACCCGCCCATCGCATCTGGAGCGGAGCGTCTGATGTACAACAGTG	1211
Db	365	AGACTGTCTGTTTCCCAAGATGGCCAGATTTTGGAAACACAGACATCTTCTCTATAACAGTG	424
Qy	1211	CGGATAGGAGATTGTACGGCACCTTACCAGACGACCTGGTGGTGGCGGAACAACGGCTCGT	1270
Db	425	CTGATGAGCGCTTGGAGCCACATTCACACTAACGTGTTGGTGAATCTCTTCGGGCATT	484
Qy	1271	GTCTATACGTTCCGCGGGGATCTTCAAGTCGACGTCAAGATCGACATCAGCTGGTTC	1330
Db	485	GCCAGTACCTGCCCTCCAGGCATATTAAGAGTTCTCTGCTACATCGATGTACGCTGGTTTC	544
Qy	1331	CCTTCGATGACCGGTGCGAGATGAAGTTCGSCAGTTGSGACCTACGACGGATTCCAGC	1390
Db	545	CCTTTGATGTGACGACTGCAAACTGAAGTTGGTGCTGCTTACGGAGGCTGGTCT	604
Qy	1391	TGGATTTCACAAATTACAAGATGAAACTGGCGGTGATATCAGCAGTTACGTGCTCAACGGCG	1450
Db	605	TGGATCTGCAGATGCAGGAGCA-----GATATCAGTGGCTATATCCCAATGGAG	655
Qy	1451	AGTGGGAACACTGGGTGTGCGCGGCAACGTAACGAGATCTATTACAACGTGCGCCGG	1510
Db	656	AATGGGACCTAGTGGGAATCCCGGCAAGAGGAGTGAAGGTTCATAGAGTGTGCAAG	715
Qy	1511	AACCTATATAGACATCACCTTCGCCATCATCAPCCGCCGACGAACACTGTACTATTCT	1570
Db	716	AGCCTACCCGATGTCACCTTCACAGTGACCATGCGCCGACGACGCTCTACTATGCCC	775
Qy	1571	TCAACCTGATCATACCTTTGTACTGATGTCCTCCATGGCGTTCGTCGGATTACCCCTGC	1630
Db	776	TCAACCTGCTGATCCCTGTGCTCATCCGCGCTCGCCCTGCTGGTGTTCCTGCTTC	835
Qy	1631	CGCCAGATTCCGGTGAATAATATPCGTGGGTGTATCATCTTGTCTCTCGCTGACCGTGT	1690
Db	836	CTGCAGATTCCGGGAGAGATTTCCTCGGGATAACAGTCTACTCTCTTACCGTCT	895
Qy	1691	TTCTGAATATGTTGCCGAGACAATGCCGGCTACTTCCGATGCGGTGCCATTG	1743
Db	896	TCATGCTGCTGCTGGCTGAGATCATGCCCGCAACATCCGATTCGGTACCATTG	948
RESULT 14			
ABV73248			
ID	ABV73248 standard; cDNA; 1876 BP.		
XX			
AC	ABV73248;		
XX			
DT	22-JAN-2003 (first entry)		
XX			
DE	Human neuronal NACHr alpha7 subunit encoding cDNA.		
XX			
KW	Human; neuronal; nicotinic acetylcholine receptor; NACHr; drug screening;		
KW	immunochemistry; NACHr alpha7 subunit; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
FH	73..1581		
CDS	/*tag= a		
FT	/product= "NACHr alpha7 subunit"		
FT	/note= "neuronal nicotinic acetylcholine receptor"		
XX			
PN	W0200259266-A2.		
XX			
PD	01-AUG-2002.		
XX			
PF	29-OCT-2001; 2001WO-US50985.		
XX			
PR	01-NOV-2000; 2000US-0703951.		
XX			
PA	(MERI) MERCK & CO INC.		
XX			
PI	Gillespie A, Claeps BO, Chavez-Noriega LE, Siegel R, Elliott KJ;		

Gillespie A, Claeps BO, Chavez-Norlega LE, Siegel R, Elliott KJ;

Best Local Similarity 60.7%; Pred. No. 6.5e-72;
Matches 506; Conservative 0; Mismatches 318; Indels 9; Gaps 1;

```
Qy 911 AAGTTTCCTAGCAGGATATCATGAAAGAGACTGTTACAGCATCTTTTGGATCCTTATA 970
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 125 ACGTGTCCCTGCGAGGCGAGTTCAGAGGAGCTTTACAGGAGCTGGTCAAGAACTACA 184
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 971 ATACACTAGAACGTCCTGCTCAATGAATCGGACCGTTTACAATTAAGCTTTGGTTAA 1030
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 185 ATCCCTTGGAGAGGCCGCTGGCCAATGACTCGCAACCACCTCACCGTCTACTTCCCTGA 244
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1031 CTTTAATGCAATATCGATGTGGACGAGAAAATCAATTCGTAGTCACCTAATGTGTGGT 1090
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 245 GCCTCTCGCAGATCATGACGTGGATGAGAAGAACCAAGTTTAAACCACCAACATTTGC 304
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1091 TAAACTGGAGTGAACGACATGAATCTCGCTGGRACACCTCGGACTATGGCGGAGTTA 1150
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 305 TGCNAATGCTTGGACAGATCACTATTTACAGTGAATGTGCAGAATATCCAGGGGTGA 364
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1151 AGGATCTGCAATACCCCGCATCGCATCTGGAAGCGGACGTCGTGATGTACAACAGTG 1210
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 365 AGACTGTTGCTTTCCAGATGGCCAGATTTGGAAACCAGACATTTCTTCTATAACAGTG 424
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1211 CGGATGAGGATTTGACGGCACCTACACAGACGACGTGGTGGCGGAACAACGGCTCGT 1270
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Db 425 CTGATGAGCGCTTTGACGGCACATTCACACATAACGTGTTGGTGAATTCCTCTGGGCATT 484
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1271 GTCTATACGTTCCCGCGGGATCTTCAAGTCGAGTCGCAAGATCGACATCACGTGGTTC 1330
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Db 485 GCCAGTACCTGCCCTCAGGCATATTCAAGAGTTCCTGCTACATCGATGTACGTGGTTTC 544
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1331 CCTTCGATACCAAGCGGTGGGAGATGAAGTTCGGCAGTTGGACCTACGACGGATTCACG 1390
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 545 CCTTTGATGTGCAGCACTGCAAACTGAAGTTTGGGTCTCTGCTTTACGGAGGCTGCTCCT 604
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1391 TGGATTTACAAATTACAAAGATGAACCTGGCGGTGATATCAGCAGTTAGCTCTCAACGGCG 1450
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 605 TGGATCTGCAGATGACGAGGCA-----GATATCAGTGGCTATATCCCAATGGAG 655
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1451 AGTGGAACTACTGGGTGTCGCCGGAACGTAACGAGATCTATTACAACCTGCTGCCCGG 1510
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 656 AATGGGACCTAGTGGGAATCCCGGCAAGAGAGTGAAGTTCATGAGTGTGCTGCAAG 715
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1511 AACCTATATAGATCACTCTGCCATCATCATATCCGCGCAGCAACTGTACTATTCT 1570
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 716 AGCCTACCCCGATGTCACCTTCACAGTGACCATGCGCGCAGCAGCTCTACTATGGCC 775
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1571 TCACCTGATCATACCTTGTACTGATTCCTCCATGGCTTGCCTCGGATTCACCTGC 1630
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Db 776 TCACCTGCTGATCCCTGTGTCTCATCTCCGCCCTCGCCCTGCTGTGTCTCTCTCT 835
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1631 CGCCAGATTCGGGTGAAAAATTATCGCTGGGTGTTACATCTTCTCTCGTGCACCGTGT 1690
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 836 CTGCAGATTCGGGGAGAAGATTTCCCTGGGGATAACAGTCTTACTCTCTTACCGTCT 895
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1691 TTTGAAATATGTTGCCGAGACAAATGCCGGCTACTTCCGATGGCGTCCCATTTG 1743
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 896 TCATGCTGCTGCTGGTGAATCATGCCCCGCAACATCCGATTCGGTACCATTG 948
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Job time : 625.968 secs

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OM nucleic - nucleic search, using sw model

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Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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5: gb_ov:*
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8: gb_pl:*
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14: gb_vi:*
15: em_ba:*
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25: em_pl:*
26: em_ro:*
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29: em_vi:*
30: em_hgt_hum:*
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32: em_hgt_other:*
33: em_hgt_mus:*
34: em_hgt_pln:*
35: em_hgt_rod:*
36: em_hgt_mam:*
37: em_hgt_vrt:*
38: em_sy:*
39: em_hgt_hum:*
40: em_hgt_mus:*
41: em_hgtg_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
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2	2310	100.0	2886	6	E58346	E58346 Nucleic acid	
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5	776.2	33.6	42079	2	AC017620	AC017620 Drosophila	
c	7	776.2	33.6	158758	3	AC092243	AC092243 Drosophila
c	6	776.2	33.6	186803	3	AC092225	AC092225 Drosophila
8	776.2	33.6	272521	3	AE003642	AE003642 Drosophila	
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23	320.2	13.9	2116	3	AY036614	AY036614 Drosophila	
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25	313.8	13.6	2106	10	RATNARAD	L31619 Rattus rattus	
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ALIGNMENTS

RESULT 1
AX009610
LOCUS AX009610
DEFINITION Sequence 1 from Patent EP0962528.
ACCESSION AX009610
VERSION AX009610.1 GI:9996842
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1
AUTHORS Adamczewski, M.D., Schulte, T.D. and Oellers, N.D.
TITLE Nucleic acids encoding acetylcholin-receptor subunits from insects

JOURNAL Patent: EP 0962528-A 1 08-DEC-1999;
BAYER AG (DE)
FEATURES Location/Qualifiers
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RESULT 2
E58346
LOCUS E58346
DEFINITION Nucleic acid encoding insect acetyl choline receptor subunit.
ACCESSION E58346
VERSION E58346.1 GI:13019345
KEYWORDS JP 2000023680-A/1.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2886)
REFERENCE Martin, A., Nadja, E. and Thomas, S.
AUTHORS Nucleic acid encoding insect acetyl choline receptor subunit
TITLE Patent: JP 2000023680-A 1 25-JAN-2000;
JOURNAL BAYER AG
COMMENT OS Drosophila melanogaster
PN JP 2000023680-A/1
PD 25-JAN-2000
PF 26-APR-1999 JP 1999118159
PR 04-MAY-1998 DE 19819829.9
PI MARTIN ADAMUTSUSUKI, NADJA ERASU, THOMAS SCHULTE PC
C12N15/09, A01K67/033, C07K14/705, C07K16/28, C12N1/21, C12N5/10, PC
C12Q1/68.
PC G01N33/15, G01N33/50, (C12N1/21, C12R1:19), C12N15/00, C12N5/00 CC
FH Key Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 3

AF272778

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

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AF272778 2907 bp mRNA linear INV 29-APR-2002

Drosophila melanogaster nicotinic acetylcholine receptor Dalp5

subunit (nAcRalpha-34E) mRNA, nAcRalpha-34E-A allele, complete cds.

AF272778

AF272778.1 GI:20152839

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 2907)

Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.

Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,

Dalp5, Dalp6 and Dalp7, in Drosophila melanogaster Identify a

New and Highly Conserved Target of Adenosine Deaminase Acting on

RNA-Mediated A-to-I Pre-mRNA Editing

Genetics 160 (4), 1519-1533 (2002)

21969411

11973307

2 (bases 1 to 2907)

Direct Submission

Grauso, M. and Sattelle, D.B.

Submitted (27-MAY-2000) Human Anatomy and Genetics, MRC-FGU,

University of Oxford, South Park Road, Oxford OX1 3QX, UK

Location/Qualifiers

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DEFINITION subunit (nAcRalpha34E) mRNA, nAcRalpha34E-B allele, complete cds,
alternatively spliced.
ACCESSION AY036613
VERSION AY036613.1 GI:20340268
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Prosopterygota; Drosophila.
REFERENCE 1 (bases 1 to 2834)
AUTHORS Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
TITLE Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
JOURNAL Genetics 160 (4), 1519-1533 (2002)
MEDLINE 21969411
PUBMED 11973307
REFERENCE 2 (bases 1 to 2834)
AUTHORS Grauso,M. and Sattelle,D.B.
TITLE Direct Submission
JOURNAL MRC-FGU Human Anatomy and Genetics,
Submitted (26-MAY-2001) MRC-FGU Human Anatomy and Genetics,
University of Oxford, South Parks Road, Oxford OX1 3QX, UK
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GUAN, P., HALLIS, M., HALLIS,
Hernandez J P. Houck-J.

GUAN, P., HALLIS, M., HALLIS,
Hernandez J P. Houck-J.

Wei, M. H., Ibegwam, C., Jalali, M., Kalush, F., Karpen, G. H., Ke, Z., Kennison, J. A., Ketchum, K. A., Kimmel, B. E., Kodira, C. D., Kraft, C., Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A. A., Li, J., Li, Z., Liang, Y., Lin, X., Liu, X., Mattel, B., McIntosh, T. C., McLeod, M. P., McPherson, D., Merkulov, G., Milshina, N. V., Mobarry, C., Morris, J., Moshrefi, A., Mount, S. M., Moy, M., Murphy, B., Murphy, L., Muzny, D. M., Nelson, D. L., Nelson, D. R., Nelson, K. A., Nixon, K., Nusskern, D. R., Pacleb, J. M., Palazzolo, M., Pittman, G. S., Pan, S., Pollard, J., Puri, V., Reese, M. G., Reinert, K., Remington, K., Saunders, R. D., Scheeler, F., Shen, H., Shue, B. C., Siden-Kiamos, I., Simpson, M., Skupski, M. P., Smith, T., Spier, E., Spradling, A. C., Stapleton, M., Strong, R., Sun, E., Svirskas, R., Tector, C., Turner, R., Venter, E., Wang, A. H., Wang, X., Wang, Z. Y., Wasserman, D. A., Weinstock, G. M., Weissbach, J., Williams, S. M., Woodgett, W., Wu, D. C., Wu, D. C., Yang, S., Yao, Q. A., Ye, J., Yeh, R. F., Zaveri, J. N., Zhong, W., Zhou, X., Zhu, S., Zhu, X., Smith, H. O., Gibbs, R. A., Myers, E. W., Rubin, G. M. and Venter, J. C.

The genome sequence of *Drosophila melanogaster*
 Science 287 (5461), 2185-2195 (2000)
 20196006
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2 (bases 1 to 272521)
 Celisner, S. E., Adams, M. D., Kronmiller, B., Wan, K. H., Holt, R. A., Evans, C. A., Gocayne, J. D., Amanatides, P. G., Brandon, R. C., Rogers, Y., Banzon, J., An, H., Baldwin, D., Banzon, J., Beeson, K. Y., Busam, D. A., Carlson, J. W., Center, A., Champs, M., Davenport, L. B., Dietz, S. M., Dodson, K., Dorsett, V., Dou, L. E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R. F., Garg, N. S., George, R. A., Gonzalez, M., Houck, J., Hoskins, R. A., Hostin, D., Howland, T. J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A., McIntosh, T. C., Moy, M., Murphy, B., Nelson, C., Nelson, K. A., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanavong, S., Pittman, G. S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Tyler, D., Williams, S. M., Zaveri, J. S., Smith, H. O., Venter, J. C. and Rubin, G. M.

Sequencing of *Drosophila melanogaster* genome
 Unpublished

3 (bases 1 to 272521)
 Misra, S., Crosby, M. A., Matthews, B. B., Bayraktaroglu, L., Campbell, K., Hradecky, P., Huang, Y., Kaminker, J. S., Prochnik, S. E., Smith, C. D., Tupy, J. L., Bergman, C. M., Berman, B. P., Carlson, J. W., Celisner, S. E., Clamp, M. E., Drysdale, R. A., Emmert, D., Frise, E., de Grey, A. D. N. J., Harris, N. L., Kronmiller, B., Marshall, B., Millburn, G. H., Richter, J., Russo, S., Searle, S. M. J., Smith, E., Shu, S., Smutniak, F., Whitfield, E. J., Ashburner, M., Gelbart, W. M., Rubin, G. M., Mungall, C. J. and Lewis, S. E.

Annotation of *Drosophila melanogaster* genome
 Unpublished

4 (bases 1 to 272521)
 Adams, M. D., Celisner, S. E., Gibbs, R. A., Rubin, G. M. and Venter, C. J.

Direct Submission
 Submitted (06-SEP-2002) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA

6 (bases 1 to 272521)
 FlyBase
 Direct Submission
 Submitted (23-JAN-2003) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA
 On Sep 16, 2002 this sequence version replaced gi:7298121.
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CDS

Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and Rubin,G.M.
Direct Submission
Submitted (08-MAR-2000) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, MS 64-121, Berkeley, CA
94720, USA
On or before Mar 22, 2000 this sequence version replaced
gi:2337897, gi:1945578, gi:2337896, gi:2347073, gi:2337894,
gi:3097819, gi:895619, gi:3097823.
Submitted by the Berkeley Drosophila Genome Project. For more
information, visit the BGP Web site: <http://www.fruitfly.org/> This
is the finished sequence of 34C4-36A7.
The orientation of this sequence along the chromosome is left to
right. This sequence was annotated by Sima Misra
(simaf@fruitfly.berkeley.edu) on behalf of the Berkeley Drosophila
Genome Center. Coding sequences are predicted based on
computational analysis, using both gene and CDS prediction programs
and matches to other sequences. These predictions and matches have
been evaluated by the annotators and may have been refined by hand.
The annotators have also used their judgement about which matches
to include in this record. The annotations on this sequence can be
examined in more detail from
<http://www.fruitfly.org/publications/Adh.html>
The annotation syntax used in this record is documented at
ftp://ftp.ebi.ac.uk/pub/databases/edgp/sequence_annotation.README.v
1.2.

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SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Epiphytodea; Drosophilidae; Drosophila.
1 (bases 1 to 1683)
MILLAR,N.S.
Direct Submission
Submitted (31-MAR-2003) Millar N.S., Department of Pharmacology,
University College London, Gower Street, London, WC1E 6BT, UNITED
KINGDOM

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Qy 973 AACTAGACGTCCTGCTTCATGATCGAGCCGTTACAAATTAAGCTTTGGTTTAACT 1032
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VERSION	AF143846	7-1 subunit mRNA, complete cds.	
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REFERENCE		Heliothis virescens	
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		Schulze, T., Oellers, N. and Adamczewski, M.	
		Putative alpha subunits of insect nicotinic acetylcholine receptors	
		more similar to vertebrate alpha 7 subunits and C. elegans Ce21	
		than to other insect nicotinic acetylcholine receptor alpha	
		subunits	
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 3629)		
AUTHORS	Schulze, T., Oellers, N. and Adamczewski, M.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-APR-1999) 2F-BTB, Bayer AG, Bldg. Q 18., Leverkusen		
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ORIGIN			1 others

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Db	1385	CCGTGGGTGCTGCGATGTCAACGCCCGGCTTCGCGACGACGCGCGCGCGCGCGCGTA	1444
Qy	1927	CTAGACATCATGATGACTTTCGGCAAAATGTGCCCCCATGATCGCCCGCGGAACACTG	1986

Db	1445	CCTCCGCGCGGACCTGGAGCTGGCGGACGCTCTCTCCAAGTGGCTCTCTAGCGACGCTG	1504
Qy	1987	CCACACACCCGGCTTTCTATCGCAGCGTTTATGGACAAGCGACGATGCGACGATTTGGG	2046
Db	1505	CTGCACATCATGACGACTTCCGCCACCCCAAGCGAGCAGCGCAATGCTGCCGATAC	1564
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Db	1565	TACAGGCGGGTGAGGAGAAATGGCGCGGGTTGGCGCGGCACAGTTGCTTC-----GGT	1618
Qy	2107	ACTGAATATGAATTAGTGTAACTTAAAGAAATTCGCTTTTATACTGATCATGACTACGT	2166
Db	1619	GTCGACTACGAGCTCTCCCTCATTTCTGAAGAGATTAGACTCATCAGATCAGATGCGC	1678
Qy	2167	AAAGATCAGCAGTGCATATGACATTCGCAATGATTGGAATTTTCAGCATATGTCGTTGAC	2226
Db	1679	AAGCAGCAGAGATGCGGACATTCGCGCGACTGGAAGTTGCGCGCCATGCTCGTGAC	1738
Qy	2227	AGACTGTCCTTATCATATTTACAAATGTTTCGCAATATTTAGCCACAATAGCTGACTACTA	2286
Db	1739	AGACTGTGCTTATTATCTTTACCTCTTTCACAATCATCGCCACGCTAGCGTGTGCTG	1798
Qy	2287	TCGCGCCACATATTTGTTCTCG	2310
Db	1799	TCGCGCCACATCATGTTGTTCTCG	1822
RESULT 12			
AX009612			
LOCUS	AX009612	3700 bp	DNA linear PAT 06-SEP-2000
DEFINITION	Sequence 3 from Patent EP0962528.		
ACCESSION	AX009612		
VERSION	AX009612.1	GI:9996844	
KEYWORDS			
SOURCE	Heliothis virescens (tobacco budworm)		
ORGANISM	Heliothis virescens		
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;		
	Noctuoidea; Noctuidae; Heliothinae; Heliothis.		
REFERENCE	1		
AUTHORS	Adamczewski,M.D., Schulte,T.D. and Oellers,N.D.		
TITLE	Nucleic acids encoding acetylcholin-receptor subunits from insects		
JOURNAL	Patent: Ep 0962528-A 3 08-DEC-1999;		
	BAYER AG (DE)		
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BASE COUNT	893 a 953 c 944 g 910 t		
ORIGIN			
Query Match	22.2%;	Score 512.8;	DB 6; Length 3700;
Best Local Similarity	62.5%;	Pred. No. 4 le-129;	
Matches	878; Conservative 0; Mismatches 502; Indels 24; Gaps 4;		
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QY 1753 ATCGTGTGTTTG--TCTGGCTGCCATGATATTGGATAGTGCCTCCAGACGACCG 1810
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QY 1927 CTAGACATCGATGATGATCTCCGGACAAATTTGCGCCCATGACGCGCGCGGGAAC 1986
Db 1445 CTTCCCGCGCGACCTGGAGTGGCGAGCGCTCTCCAAAGTCGCTCTAGCAACGTTG 1504
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Db 1739 AGACTGTGCTTATATATTTACCTGTTTCAACAATCATGCCAGGCTAGCGTGTGCTG 1798
QY 2287 TCGGACACCATATATTTCTCTCG 2310
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RESULT 13
E58347
LOCUS
DEFINITION Nucleic acid encoding insect actyl choline receptor subunit.
ACCESSION E58347
VERSION E58347.1 GI:13019346
KEYWORDS JP 2000023680-A/2.
SOURCE Heliothis virescens (tobacco budworm)
ORGANISM Heliothis virescens
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.
REFERENCE 1 (bases 1 to 3701)
AUTHORS Martin,A., Nadja,E. and Thomas,S.
TITLE Nucleic acid encoding insect actyl choline receptor subunit
JOURNAL Patent: JP 2000023680-A 2 25-JAN-2000;
BAYER AG
COMMENT OS Heliothis virescens
PN JP 2000023680-A/2
PD 25-JAN-2000
PF 26-APR-1999 JP 1999118159
PR 04-MAY-1998 DE 19819829.9
PI MARTIN ADAMUTSUBUSUKI,NADJA ERASU,THOMAS SCHULTE PC
C12N15/09,A01K67/033,C07K16/28,C12N1/21,C12N5/10, PC
C1201/68,
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BASE COUNT 893 a 953 c 944 g 910 t 1 others
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Query Match 22.2%; Score 512.8; DB 6; Length 3701;
Best Local Similarity 62.5%; Pred. No. 4.1e-129;
Matches 878; Conservative 0; Mismatches 502; Indels 24; Gaps 4;

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RESULT 14
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LOCUS Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6
DEFINITION subunit variant type I (nAcRalpha-30D) mRNA, complete cds,
alternatively spliced.
ACCESSION AF321445
VERSION AF321445.1 GI:20152844
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 2023)
AUTHORS Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
TITLE Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
JOURNAL 21969411
MEDLINE 11973307
PUBMED 2 (bases 1 to 2023)
REFERENCE 1 (bases 1 to 2023)
AUTHORS Grauso,M. and Sattelle,D.B.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
3QX, UK

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BASE COUNT
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Best Local Similarity 58.5%; Pred. No. 2.4e-111;
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RESULT 15

AF321447

LOCUS

DEFINITION

AF321447

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AF321447 2023 bp mRNA linear INV 29-APR-2002
Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6
subunit variant type III (nAcRalpha-30D) mRNA, complete cds,
alternatively spliced.
AF321447
AF321447.1 GI:20152848

Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
AUTHORS Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
TITLE Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalphaa6 and Dalphaa7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing

JOURNAL Genetics 160 (4), 1519-1533 (2002)
MEDLINE 21969411
PUBMED 11973307

REFERENCE
AUTHORS Grauso,M. and Sattelle,D.B.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
3QX, UK

FEATURES
source Location/Qualifiers
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ORIGIN

Query Match
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Mismatches 574; Indels 18; Gaps 2;

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Db 1821 GGTACGGTGTGCTCTCGCTCCGACATAATCGT 1856

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